

studied to determine if resistance genes are present, defects in plant genomes can also be studied in this way. Similarly, the method permits determination of the pathogens which integrate into the genome, such as retroviruses and other integrating viruses such as influenza virus, have undergone shifts or mutations, which may require different approaches to therapy. This method is also applied to eukaryotic pathogens, such as trypanosomes, different types of Plasmodium, etc. The method essentially eliminates sequencing of non-coding portions. This sequence represents a polynucleotide isolated from human colon cancer cell cDNA library

Sequence 155 BP; 41 A; 30 C; 33 G; 49 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
7.00	100.00%	155	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	35.00%	Indels:	0
DB:	7	Gaps:	0

10-799-747-116 (1-20) x ACD97494 (1-155)

Qy 5 SerValLeuSerPheLeuLeu 11
Db 12 AGTGTTCCTTCCTTCCTC 32

RESULT 11

AAT20076/C
ID AAT20076 standard; cDNA to mRNA; 263 BP.

AC AAT20076;

DT 17-JUN-1996 (first entry)

DE Human gene signature HUMGS01218.

Gene signature; messenger RNA; relative abundance; frequency;

human; cloning; mapping; non-biased library; diagnosis; detection;

cell typing; abnormal cell function; ss.

OS Homo sapiens.

PN WO9514772-A1.

PD 01-JUN-1995.

PP 11-NOV-1994; 94MO-JP001916.

12-NOV-1993; 93JP-00355504.

PA (MATS/) MATSUBARA K.

(OKUBO/) OKUBO K.

PI Matsubara K, Okubo K;

DR WPI; 1995-206931/27.

XX Single-stranded DNA for identifying gene signatures - isolated from 3'-

PT directed human cDNA library that reflects relative abundance of corresp.

PT mRNA in specific human tissues.

XX Claim 1; Page 554; 2245pp; Japanese.

CC A single-stranded DNA (or its complementary strand or the corresp. double

CC -stranded DNA) which comprises one of the 7837 "GS" sequences given in

CC AAT19001-T6837 and which is able to hybridize to part of human genomic

CC cDNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were

CC obtained from 3'-directed cDNA libraries prepared from various human

CC tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using

CC poly(T) as the sole primer. Since the 3'-untranslated sequence is unique

CC to a particular mRNA species, almost all the 3'-oriented cDNAs hybridize

CC with specific mRNAs. Each library is constructed so as to reflect

CC accurately the relative abundance of different mRNAs in the particular

CC tissue from which it was derived. The appearance frequency of a given GS

CC in a cDNA library can be determined (esp. using primers and probes

CC derived from the GS sequences) as a means of diagnosing abnormal cell

CC function or for recognising different cell types

XX Sequence 263 BP; 92 A; 34 C; 43 G; 92 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
7.00	100.00%	263	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	35.00%	Indels:	0
DB:	2	Gaps:	0

US-10-799-747-116 (1-20) x AAT20076 (1-263)

Qy 5 SerValLeuSerPheLeuLeu 11

Db 82 AGTGTTCCTTCCTTCCTC 62

RESULT 12

ADG93542
ID ADG93542 standard; DNA; 264 BP.

AC ADG93542;

DT 01-JAN-2004 (first entry)

DE E. faecium DNA sequence SEQ ID 3169.

Gene; urinary tract infection; bacteraemia; endocarditis; wound;

abdominal-pelvic infection.

OS Enterococcus faecium.

PN US6583275-B1.

PD 24-JUN-2003.

PP 30-JUN-1998; 98US-00107532.

PR 02-JUN-1997; 97US-0051571P.

PR 14-MAY-1998; 98US-0085598P.

PA (GENO-) GENOME THERAPEUTICS CORP.

PI Doucette-Stamm LA, Bush D;

DR WPI; 2003-799836/75.

XX P-PSDB; ADC97196.

XX New isolated nucleic acid derived from Enterococcus faecium encoding an

XX Enterococcus faecium polypeptide useful for detection, prevention and

XX treatment of a pathological condition resulting from a bacterial

XX infection.

XX Example 1; SEQ ID NO 3169; 243pp; English.

CC The invention relates to an isolated nucleic acid derived from

CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having

CC one of 10 fully defined sequences given in the (or comprising 40

CC sequential nucleotides chosen from any of the nucleic acids, its

CC complement or sequences hybridizing to it). Also included are a

CC recombinant vector comprising the nucleic acid operably linked to

CC transcription regulatory element, a cell comprising the vector and a

CC single-stranded probe comprising the nucleic acid. The nucleic acids are

CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.

CC The nucleic acids is useful for diagnosing pathological conditions

CC resulting from E. faecium bacterial infection (e.g. urinary tract

CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic

CC infection) and for screening drugs such as agonists and antagonists. The

CC nucleic acid is useful for recombinant production of Candida albicans -

Qy = SEQ ID 116 10/749 717
Db = SEQ ID 1076 EP 067476 A1

PT Single-stranded DNA for identifying gene signatures - isolated from 3'-
 PT directed human cDNA library that reflects relative abundance of corresp.
 PT mRNA in specific human tissues.

PS Claim 1, Page 1777-78; 2245pp; Japanese.

XX A single-stranded DNA (or its complementary strand or the corresp. double
 CC -stranded DNA) which comprises one of the 7837 "GS" sequences given in
 CC AAT19001-1726837 and which is able to hybridise to part of human genomic
 CC DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were
 CC obtained from 3'-directed cDNA libraries prepared from various human
 CC tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using
 CC poly(U) as the sole primer. Since the 3'- untranslated sequence is unique
 CC to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise
 CC with specific mRNAs. Each library is constructed so as to reflect
 CC accurately the relative abundance of different mRNAs in the particular
 CC tissue from which it was derived. The appearance frequency of a given GS
 CC in a cDNA library can be determined (esp. using primers and probes
 CC derived from the GS sequences) as a means of diagnosing abnormal cell
 CC function or for recognising different cell types

Sequence 336 BP; 95 A; 62 C; 62 G; 112 T; 0 U; 5 Other;

Query Match 8.9%; Score 127; DB 2; Length 336;
 Best Local Similarity 100.0%; Pred. No. 8.7e-35;
 Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 763 GAAAAAATACCTTCACTGCTCCACGAGTGAATCCGCCACCTCCACTGACTAGTA 822
 Db 14 GAAAAAATACCTTCACTGCTCCACGAGTGAATCCGCCACCTCCACTGACTAGTA 73
 QY 823 GAATTTGTAATTTAATCTTACTCTTATTTGGAATCAAGTTGGAATGTTGCTTAT 882
 Db 74 GAATTTGTAATTTAATCTTACTCTTATTTGGAATCAAGTTGGAATGTTGCTTAT 133
 QY 883 GTTCAGA 889
 Db 134 GTTCAGA 140

RESULT 8
 ADE81840/c
 ID ADE81840 standard; cDNA; 493 BP.
 XX
 AC ADE81840;
 XX
 DT 29-JAN-2004 (first entry)

Arabidopsis thaliana expressed polynucleotide seq id 611.

KM Genetically modified organism; transgenic organism; plant;
 KM inhibitor testing; activator testing; modifier testing; fungicide;
 KM insecticide; genetic function; genetic regulation; cellular metabolism;
 KM gene; ss.

XX Arabidopsis thaliana.

XX US2003115639-A1.

XX 19-JUN-2003.

XX 26-JAN-2001; 2001US-0070961.

XX 27-JAN-2000; 2000US-0178466P.

XX (GORLACH J.
 PA (ANYI) AN Y.
 PA (HAMT) HAMILTON C M.
 PA (PRIC) PRICE J L.
 PA (RAIN) RAINES T M.
 PA (YUYU) YU Y.
 PA (RAME) RAMEKA J G.
 PA (PAGE) PAGE A.

QY = SEQ 12 10/799747
 Db = SEQ 6136 EP 067916 A1

PA (MATH) MATHEW A V.
 PA (LEDF) LEDFORD B L.
 PA (WOES) WOESSNER J P.
 PA (HAAS) HAAS W D.
 PA (GARC) GARCIA C A.
 PA (KRICK) KRICKER M.
 PA (SLAT) SLATER T.
 PA (DAVI) DAVIS K R.
 PA (ALLE) ALLEN K.
 PA (HOFF) HOFFMAN N.
 PA (HURB) HURBAN P.
 PI Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y,
 PI Rameka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD,
 PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N,
 PI Hurban P;
 XX WPI; 2003-810930/76.

PT Novel Arabidopsis thaliana nucleic acids useful for generating
 PT genetically modified transgenic organisms, for screening biologically
 PT active agents such as fungicides, insecticides.

PS Claim 1, SEQ ID NO 611; 44pp; English.

XX The invention describes a nucleic acid (I) comprising a sequence capable
 CC of hybridising under stringent conditions to any one of 998 fully defined
 CC Arabidopsis thaliana sequences (1) as given in specification e.g., 360,
 CC 1137, 455, 219, 472 nucleotides, etc, or its fragment. (I) is useful as a
 CC hybridisation probe to complementary molecules in a cDNA library. (I) is
 CC also useful for generating genetically modified and transgenic organisms,
 CC usually plant cells and plants. A protein encoded by (I) is useful in
 CC screening assays to determine the effect of candidate inhibitors,
 CC activators or modifiers of the gene product. The protein is also useful
 CC for screening biologically active agents e.g., fungicides and
 CC insecticides. A genetically modified cell, comprising an exogenous
 CC nucleic acid, where the nucleic acid comprises transcription regulatory
 CC sequences operably linked to a sequence capable of hybridising under
 CC stringent conditions to (1) is useful in the study of genetic function
 CC and regulation, for alteration of the cellular metabolism and for
 CC screening compounds that may affect the biological function of the gene
 CC or gene product. This sequence represents an Arabidopsis thaliana
 CC polynucleotide of the invention.

SO Sequence 493 BP; 146 A; 115 C; 70 G; 162 T; 0 U; 0 Other;

Query Match 3.1%; Score 45; DB 9; Length 493;
 Best Local Similarity 100.0%; Pred. No. 2.4e-06;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1390 TGAATTTAAAAA
 Db 52 TGAATTTAAAAA
 1434
 8

RESULT 9
 AAH25190

ID AAH25190 standard; cDNA; 1231 BP.

XX AAH25190;

XX 22-AUG-2001 (first entry)

XX Nucleotide sequence of a human transferrin.

XX Human: transferrin; autoimmune disease; rheumatoid arthritis;
 KM hyperproliferative disorder; neoplasm; cardiovascular disorder;
 KM cardiac arrest; cerebrovascular disorder; cerebral ischemia;
 KM angiogenesis; nervous system disorder; Alzheimer's disease; infection;
 KM ocular disorder; corneal infection; wound healing;
 KM epithelial cell proliferation; aging; organ transplant; ss.
 XX Homo sapiens.

Reference
SN 10/199747

SCAN THIS
Reference

N



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(54) **GENE SIGNATURE.**

(57) A 3'-directed cDNA library which accurately reflects the abundance ration of mRNA in a cell has been prepared from various human tissues, and sequencing of the cDNAs contained in the library has be conducted to examine the incidence of each cDNA in each tissue. As each cDNA has expression information with each tissue corresponding to the mRNA concentration, these cDNAs are usable as a probe or primer for detecting cell anomoly or discriminating cells. The cloned gene can produce porteins utilizable as a medicine or the like.

EP 0 679 716 A1

Fields of the Invention

The present invention relates to purified single-stranded DNA molecules, purified single-stranded DNA molecules complementary thereto or purified double-stranded DNA molecules consisting of said single-stranded DNA molecules, which can specifically hybridize to human genomic DNA, human cDNA or human mRNA at particular sites. The DNA molecules of the present invention can be used for detecting the overall or individual expression status of mRNAs coding for the corresponding cellular proteins, detecting and diagnosing cellular abnormalities due to disease and viral infection, or distinguishing and identifying the cell type, and efficiently cloning genes expressed in a tissue-specific manner. The present invention further includes cloned DNA molecules which can be used to produce proteins useful as pharmaceutical products or the like.

Related Arts

Recognizing the importance of the most fundamental attribute of mRNA, that is, "the nature of the cell is determined by the expression pattern of genes as reflected in the population of mRNA", the inventors of the present invention have proposed "body mapping" as a unique approach to their objective. This is an entirely novel attempt to prepare "the information on gene expression" for presumably about 200 different kinds of cells and tissues present in the human body and elucidate when, where and to what extent a certain gene is expressed, and map genes to the respective organ or cell type in which they are expressed.

While a variety of cells in the living body express various proteins depending on their respective biological functions, the intracellular concentrations of these proteins vary according to the cell type, stage of development and differentiation, environment, etc.

In general, genes are classified into "genes encoding proteins essential for the life of the cell" and "genes encoding proteins responsible for functions specific to the cell". Of these two, "genes encoding proteins essential for the life of the cell" are expressed constantly in all types of cells and also called "housekeeping genes", while "genes encoding proteins responsible for functions specific to the cell" are often expressed specifically in a particular type of cells or a particular group of cells, and also may be specifically expressed at a particular stage of cellular development and differentiation. Furthermore, they are often "inducible genes" and the amount of their expression varies depending upon the environment to which cells are exposed. In other words, cells may grow as a result of the expression of "genes encoding proteins essential for the life of the cell" and display their specific functions as a result of the expression of "genes encoding proteins responsible for functions specific to the cell".

However, under abnormal cellular conditions due to disease or infection, the expression of genes within individual cells is altered as compared with that under the normal conditions. Especially, during viral infection, RNAs encoding virus-specific proteins are synthesized in large amounts within the cell, leading to the production of said protein in large amounts. In other words, the alteration in the expression level of genes within the cell, especially as reflected in the concentration of intracellular mRNA, can lead to such abnormal cellular conditions as seen in diseases.

Thus, the function of each cell in the living body is closely related to the expression status of genes within the cell. Accordingly, in order to elucidate the function of each cell at molecular level or to investigate the pathogenesis of a disease at molecular level, it becomes necessary to comprehend the expression status of cellular genes, especially the intracellular concentration of each mRNA.

A theoretically possible approach to this objective is the extraction and analysis of all cellular proteins for determination of expression status. However, although it may be possible to isolate a specific protein, in most cases it is almost impossible to completely isolate all of these proteins, because a great variety of proteins are expressed within the cell.

Another approach is to directly estimate the concentrations of cellular mRNAs corresponding to all intracellular proteins. However, although it may be possible to isolate a specific mRNA, it is practically impossible to completely isolate all of these mRNAs and directly estimate their amounts, because a great variety of mRNAs are synthesized simultaneously within the cell and furthermore they may be unstable and susceptible to enzymatic degradation during their extraction.

This invention aims to provide DNA molecules which can be used as probes or primers required for detecting the overall or individual expression status of mRNAs coding for the corresponding cellular proteins, detecting or diagnosing cellular abnormalities due to disease or virus infection, recognizing and identifying various cell types, and efficiently cloning genes expressed in a tissue-specific manner. Moreover, the present invention aims to provide cloned DNA molecules which can be used to produce proteins useful as pharmaceutical products.

Summary of the invention

In general, the genetic information flows in order from DNA to mRNA and to protein (F. H. C. Crick, 1958). That is, "the information for the amino acid sequence of a protein" is first transcribed into mRNA and then translated into protein.

To explain this in further detail mammalian genes commonly comprise a region encoding a protein and a region regulating the expression of said gene. The regions of a gene encoding protein (called "exons") are often separated by intervening sequences (called "introns"). When a gene is transcribed into RNA, the introns of the precursor RNA (pre-mRNA) are excised and exons are connected in tandem to form a contiguous structure coding for a particular protein (this process is called "splicing"). On the other hand, the region regulating the expression of gene comprises, in addition to the regions directly regulating transcription such as a promoter and operator which are present upstream of the transcription region, untranslated regions are located both upstream (5') and downstream (3') of the coding region. In particular, 3' untranslated region (3' UTR) is important for regulating expression, since it contributes to the transport and stability of mRNA. During the processing of pre-mRNA, a methylated cap is added at its 5' end, the 3' untranslated region is cleaved at a specific site, a poly(A) tail is attached by adding 100 - 200 adenylate residues to the cleaved end, and the coding regions are spliced together to form mRNA. The protein is then synthesized after attachment of ribosomes to the mRNA.

The inventors of the present invention have elucidated that, in general, when the intracellular level of a particular mRNA is high, the expressed amount of the corresponding protein is also elevated, and also that it is possible to estimate the relative concentration of each intracellular protein by estimating relative intracellular concentration of the corresponding mRNA [DNA sequence 2, 137-144 (1991); Nature genetics, 2, 173-179 (1992)].

Basically in the present invention, mRNA is extracted from a particular cell and cDNA is synthesized by conventional methods using reverse transcriptase. However, in the present invention, cDNA is synthesized using a method developed by the inventors of the present invention so as to reflect the relative intracellular concentration of mRNA. A cDNA library is constructed and a group of cDNAs representing the population of total mRNA are cloned and sequenced.

An approach which appears to be similar to the one used by the inventors of the present invention but is entirely different, is the method of cloning of a cDNA library constructed by the random priming by Venter et al.

Venter's group randomly cloned cDNAs from commercially available cDNA libraries derived from brain cells (catalog No. 936206, 936205 or 935, Stratagene, California) and determined their base sequences [Science 252, 1651-1656 (1991); Nature 355, 632-634 (1992)].

While the method used by Venter et al. involves sequencing of cDNAs obtained by random priming, this method has the following drawbacks:

- 1) Since random cloning of various regions of a single-stranded mRNA may often lead to the formation of many cDNA fragments without any mutual overlapping portions, it is difficult to determine whether these cDNA fragments are derived from the same mRNA or a different one,
- 2) The longer a mRNA strand, the higher the chance for said mRNA to be reverse-transcribed into cDNA, and
- 3) Since the availability of each primer to be used among random primers differs depending on their base sequences, the relative frequency of cDNA synthesis is variable.

From aforementioned reasons, the relative frequency of appearance of cDNA does not reflect the relative concentration of cellular mRNA. Consequently, it is impossible to determine the relative concentration of each mRNA and the actual population of intracellular proteins by using the method of Venter et al.

However, with the method developed by the inventor of the present invention, it is possible to construct a cDNA library which precisely reflects the relative concentration of mRNA without any of the aforementioned complications. Since, in the present invention, cDNA is synthesized using only "poly-T" as the primer, the 3' ends of the cDNA have "a poly A tail". Therefore, the synthesis of cDNA with "poly-T" as the sole primer is initiated from the 3' end resulting in the formation of 3'-oriented cDNA. Since the 3' untranslated sequence is unique to a particular mRNA species and not present in other mRNA species [Birnstiel, M. L., et al., Cell 41, 349-359 (1985)], almost all the 3' end-oriented cDNAs hybridize with specific mRNAs. Digestion of the resulting cDNA with a restriction enzyme MboI which recognizes the specific four-base sequence GATC results in the formation of cDNA extending from the 3'-terminus to the first MboI restriction site. In the present invention, each cDNA thus cloned and included in "a cDNA library faithfully reflecting the relative intracellular concentration of mRNA" is called a "gene signature" (abbreviated as GS hereinafter). A GS includes not only the double-stranded DNA but also each single-stranded DNA thereof.

The present invention relates to a purified single-stranded DNA, purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA (or a single-stranded DNA complementary thereto) comprising any of the base sequences listed under the sequence identification number (SEQ ID NO) 1 - 7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA. The present invention also relates to probes and primers consisting of said single-stranded DNA. The present invention also relates to a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA (or a single-stranded DNA complementary thereto) which is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1 - 7837 (wherein T is read as U) or any portion thereof at its 3' region and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA. The present invention also relates to probes and primers consisting of said single-stranded DNA.

The present invention is explained further in detail as follows.

The DNA of the present invention not only includes a single-stranded DNA (or a single-stranded DNA complementary thereto) comprising any of the base sequences listed under SEQ ID NO 1 - 7837 but also includes a single-stranded DNA containing a portion of said single-stranded DNA (or said single-stranded DNA complementary thereto) if it hybridizes to human genomic DNA, human cDNA or human mRNA.

Furthermore, the DNA of the present invention not only includes a single-stranded DNA (or a single-stranded DNA complementary thereto) which is complementary to a mRNA containing any of the base sequences listed under SEQ ID NO 1- 7837 (wherein T is read as U) or any portion thereof at its 3' region but also includes a single-stranded DNA (or a single-stranded DNA complementary thereto) containing a portion of said single-stranded DNA (or said single-stranded DNA complementary thereto) if it hybridizes to human genomic DNA, human cDNA or human mRNA.

In addition, the DNA of the present invention not only includes a single-stranded DNA or a single-stranded DNA complementary thereto but also includes a double-stranded DNA consisting of said single strands.

Obviously, the term "contain" as used herein does not necessarily mean that the DNA of the present invention contains at a single site without interruption (1) "a single-stranded DNA (or a single-stranded DNA complementary thereto) comprising any of the base sequences listed under SEQ ID NO 1-7837 or a portion thereof" or (2) "a single-stranded DNA (or a single-stranded DNA complementary thereto) which is complementary to a mRNA containing any or any portion of the base sequences listed under SEQ ID NO 1 - 7837 (wherein T is read as U) at its 3' region or a portion of said single-stranded DNA." In other words, the term "contain" is applicable also to the case where one or more exogenous bases are inserted in the base sequence of the DNA (1) or (2).

The hybridization to a particular site of human genomic DNA, human cDNA or human mRNA can be achieved under standard conditions (see e.g., Molecular Cloning: A Laboratory Manual, Sambrook, J., et al., Cold Spring Harbor Laboratory Press, 1989). In the following preferred embodiment, there will be described methods for constructing a cDNA library which reflects precisely the relative intracellular concentration of mRNA, cloning cDNA groups which correspond to total mRNA, and determining the base sequence of each cDNA.

First, cells from specific tissues, for example, cells from organs, for example, cells derived from human liver (HepG2) are grown, and the total mRNA is extracted by standard procedures. mRNA thus obtained is attached to a vector to construct a cDNA library.

For example, mRNA is attached to the vector plasmid pUC19, which has the M13 sequences flanking the cloning site, as follows.

pUC19 is cleaved by HincII and PstI and poly-T of 20 bp - 30 bp is added to the PstI-digested end to which the 3'-end poly-A tail of the mRNA is hybridized (Fig. 1a). After the DNA strand is extended with conventional methods using reverse transcriptase, a double stranded DNA is formed with DNA polymerase (Fig. 1b). The double stranded DNA thus obtained is cleaved with the restriction enzyme MboI which recognizes a specific four base sequence (Fig. 1c).

MboI, which recognizes a four base sequence (GATC), cleaves the DNA within a few hundred bases from the poly-A tail. Since MboI is found to digest, without exception, about 300 human cDNAs which were randomly selected from the GenBank data base by the inventor of the present invention, this enzyme cleaves the cDNA to be cloned at a specific site. In addition, as pUC19 is prepared in dam⁺ E. coli, e.g., E. coli JM109 and since its adenine at the MboI recognition site is methylated (G^mATC), it is not cleaved by MboI.

Subsequently, in order to prepare a vector containing the double-stranded DNA which has previously been attached to pUC19 and has the MboI-cleaved end, the pUC19 DNA is digested with BamHI to make termini cohesive with the MboI-cleaved end. Since the recognition sequence of BamHI (GGATCC) contains that of MboI (GATC), the extended portion of the double-stranded DNA is not cleaved with BamHI.

The resulting double-stranded DNA is then circularized by standard ligation methods, and the recombinant vector plasmid thus prepared is introduced into *E. coli*, e.g., *E. coli* DH5 in order to make a cDNA library.

With this method, only a clone containing the base sequence upstream of the poly-A tail of the mRNA is obtained.

Since the average size of the inserted cDNA fragment is relatively small, 270 bp, it is free from biased cloning resulting from variations in the efficiency of cDNA synthesis and transformation that occur in the case of larger sized DNAs. Furthermore, because instability due to repeated base sequences and the like is eliminated, the cDNA library of the present invention faithfully represents the relative concentration of mRNA in the cell.

Furthermore, when the cDNA inserted into the vector is relatively short, it is possible to accurately amplify the cDNA fragment using the sequence of the vector flanking it as a primer. It is also possible to determine the base sequence from the 5' end directly by the PCR without interference from the 3' poly-A tail which will reduce the accuracy of sequence determination.

Amplification of the GS, i.e., the cDNA fragment inserted into the vector, is performed as follows.

The *E. coli* cells in which the cDNA library is introduced are grown using standard methods and lysed. Debris contained in the bacterial lysate are removed by centrifugation and the supernatant containing the vector DNA is recovered. The vector DNA thus obtained is used as the DNA template for amplification by the PCR (Fig. 1d, amplification with PCR primers 1 and 2).

Base sequences flanking both ends of the GS is properly selected for use as primers and the PCR is performed under standard conditions. PCR products thus obtained are subjected to the elongation reaction using fluorescence primers complementary to the vector sequence flanking the 5' end of the GS, and the sequence is determined with an autosequencer (Fig. 1d, sequence determination with dye primer).

Based on the results of the sequence determination of each GS, the species and the frequency of appearance of the GS in each tissue or cell type are analyzed.

As to each cell type not only normal cells but also cells under pathogenic conditions (such as tumor cells, virus infected cells, etc.) can be used without any restriction. For example, liver cells (from fetus, neonate or adult), various hematopoietic cells (granulocytic, monocytic, etc.), lung cells, adipocytes, endothelial cells, osteoblasts, colon mucosa cells, retinal cells and hepatoma cells (HepG2, etc.), and promyelocytic leukemia cells (HL60, etc.) will be used. The appearance frequency for each GS is described for each cell type in Tables 1 through 219. There, patent number represents "SEQ ID NO for each GS", size represents the "length of each GS", and F represents the "sum of appearance frequencies in the cells studied". In addition, hepG2 stands for "hepG2 (a liver cancer cell line)", HL60 stands for "HL60 promyelocytic leukemia cell line", granulo stands for "granulocytoid, HL60 stimulated by DMSO", mono stands for "monocytoids, HL60 stimulated by TPA", 40 w liver stands for "40 w neonatal liver", 19 w liver stands for "liver of a 19 weeks old fetus, adult liver is "adult liver", lung stands for "adult lung", adipose stands for "subcutaneous adipose tissue", endothel stands for "primary cultured aortic endothelium", osteoblast stands for "primary cultured osteoblast", colon mucosa is "colon mucosa", small cell carci stands for "small cell carcinoma of lung", retina is "retina", cerebral cortex is "cerebral cortex", adenocarci (lung) stands for "adenocarcinoma of lung", squamous cell ca (lung) stands for "squamous cell carcinoma of lung", keratinocyte stands for "primary cultured keratinocyte", fibroblast stands for "primary cultured fibroblast", Alzheimer stands for "Alzheimer temporal lobe", cerebellum stands for "cerebellum", visceral fat is "visceral fat", corneal epithelium is "corneal epithelium", peripheral granulocyte is "peripheral granulocyte", neuroblastoma is "neuroblastoma" and taste bud of tongue is "taste bud of tongue".

"Accession number of target mRNA" represents the accession number of the entry in GenBank Release 79 whose base sequence has homology with that of each GS, "match %" represents the percent homology of the GS sequence relative to that of said homologous sequence, "match starts at (GS)" represents the base position counted from the 5'-end of the GS at which the region for homology calculation starts, "match starts at (GenBank)" represents the base position counted from the 5'-end of the GenBank sequence at which the region for homology calculation starts, and "GenBank target size" represents the whole length of the GenBank sequence corresponding to the GS. The columns in Tables 1 - 219 represent the same items as in Table 1.

Based on the data in Tables 1 - 219, each GS can be classified into several groups. A GS, which is expressed at high frequency in a specific cell or groups of cells with similar property, for example,

promyelocytic leukemia cell, granulocyte and monocyte and not expressed entirely or expressed very little in other cells (groups), is a likely GS corresponding to the gene encoding "the protein responsible for functions specific to the cell" (e.g., GS0001553, GS0002047, GS004895, etc.). On the other hand, a GS, which is expressed commonly in every kind of cell, most likely corresponds to the gene encoding "the protein essential for the life of the cell" (e.g., GS0000019, GS0000155, GS000861, etc.). In addition, some GSs are expressed at low frequency (e.g., GS0000013, GS0002399, GS0003155, etc.).

Since the GS with the sequence determined as described above will reflect the population of mRNA expressed in a particular cell, it must be possible to find the relative concentration of mRNA in each cell by determining the appearance frequency for each GS in a cDNA library derived from that cell. Therefore, to confirm the correlation between the appearance frequency for each GS in a cDNA library and the relative concentration of cellular mRNA, the GS thus obtained was labeled with ³²P by standard methods and used as the probe in the following hybridization test. mRNA isolated from a specific cell is hybridized to said ³²P-labeled probe under standard conditions. The results of this Northern hybridization test were such that, when a GS found with high appearance frequency in a cDNA library was used as a probe, a dense band was formed, confirming the correlation of the frequency of appearance of the GS with the relative concentration of mRNA in the cell (see Example 5).

Similarly, the colony hybridization test of the cDNA library constructed as described above with a ³²P-labeled probe prepared as described above showed a close correlation between the frequency of appearance of the GS and the number of colonies hybridized with said GS (see Example 6), confirming the correspondence of the frequency of appearance of the GS and relative concentration of the GS in a cDNA library.

From the above results, by determining the appearance frequency of each GS in a cDNA library derived from a variety of cells, it has become possible to determine the expression status of the gene (or mRNA) corresponding to each GS. This fact implies conversely that each GS may be useful for industrial purposes as a specific probe or primer encoding information about the expression status of its corresponding gene (or mRNA) for each cell. For example, when it is proven that "a certain GS appears at high frequency only in a cDNA library derived from tissue A, that is, the gene corresponding to said GS is specifically expressed only in tissue A", by conventional cloning of the corresponding full-length cDNA using said GS as a probe or primer, it is possible to clone a full-length gene which is expressed in a tissue-specific manner.

Furthermore, for example, when it is proven that "the frequency of appearance of a certain GS is low in a cDNA library derived from tissue B, that is, the appearance frequency of the gene corresponding to said GS is low in tissue B", by examining the expression frequency of the gene corresponding to said GS in a test sample of tissue B from a patient using said GS as a probe or primer, it may be possible to identify the pathogenic gene, wherein an unusually high expression frequency of said gene being a strong indication that said GS may be the gene involved in the pathogenesis. Furthermore, by conventional methods for cloning said full-length cDNA using said GS as a probe or primer, it is possible to isolate said pathogenic gene and elucidate its characteristics.

In practice, the DNA of the present invention may be used as a probe or primer for detecting and diagnosing disease, cloning a pathogenic gene or related gene, cloning a viral gene, identifying and recognizing cell types, cloning a species-specific promoter and gene mapping.

One GS corresponds to one mRNA. It is therefore obvious that any portion of cDNA complementary to each mRNA carry the same "information for expression" as the GS. Accordingly, the DNA of the present invention is not restricted to "the DNA comprising the GS itself or portion thereof", but also includes the DNA comprising, for example, "a full-length cDNA complementary to each mRNA" and "the non-GS region of the cDNA complementary to each mRNA or a portion thereof". They can be used as a probe or primer comprising the same "expression information" as that of the GS and can be used as a probe or primer in a similar manner as a GS. For example, by using a GS or a portion thereof as a probe or primer, it is obviously possible for those skilled in the art to readily isolate "a full-length cDNA corresponding to each mRNA" or "the non-GS region of the cDNA complementary to each mRNA or a portion thereof". For example, as described hereinafter, conventional techniques such as "5' RACE", "nesting" and "inverse PCR" can be used.

An example of the method for detecting disease using the GS of the present invention will be described. As shown in Tables 1 - 219, with the method described above it is possible to detect a GS present specifically in a cDNA library constructed from each tissue by detecting and comparing the frequency of appearance of GS in each tissue. It is also possible to identify a GS corresponding to a protein which is expressed commonly in various tissues or which is expressed at low frequency. These GSs are denatured and then fixed on an appropriate filter, for example, nylon filter or nitrocellulose filter. It is

convenient to use a single filter with many GSs fixed on it. Usage of a single filter on which many denatured DNAs are fixed is well known. An example may be "the Escherichia coli Gene Mapping Membrane" (Takarashuzo, code No. 9035). It is a single nylon filter on which the cosmid contigs of genomic DNA of E. coli are fixed. It is possible to prepare a filter comprising a group of specific GSs corresponding to proteins expressed in a particular tissue, a filter comprising a group of GSs corresponding to proteins commonly expressed in various tissues, or a filter comprising a group of GSs corresponding to proteins expressed at low frequency. The single-stranded GSs fixed on these filters are then hybridized to labeled complementary DNA fragments synthesized using "random primers" prepared from template mRNA extracted from a test tissue, using four labeled nucleotides and reverse transcriptase (labeled mRNA can also be hybridized to the filters). Similarly, labeled complementary fragments synthesized using mRNA extracted from normal tissue as the template are hybridized (labeled mRNA can also be hybridized to the filters). If the profile of hybridization to a group of GSs has been categorized beforehand by comparing the hybridization profile of various pathogenic tissues to that of corresponding normal tissues, it is possible to diagnose the pathogenic condition of a particular test tissue by comparing the hybridization profile of the test tissue with that of the corresponding normal tissue and assigning that profile to a certain category. Virus infection can be detected in the same manner as in the case of other diseases.

Next, an example of the method for cloning pathogenic genes or their related genes using the GS of the present invention is described. As described above, using the filter on which denatured GSs are fixed, the GS-hybridization profile of various pathogenic tissues and that of corresponding normal tissues are compared. A considerable difference in the hybridization intensity between normal and pathogenic tissues will be an indication that the particular GS corresponds to a pathogenic gene. If a filter comprising only GSs specific for a particular tissue is applied to a sample from that particular tissue, the probability for detecting the GS with a great difference in hybridization intensity is elevated. Also a filter comprising GSs corresponding to proteins whose expression is low will facilitate the identification of the GS corresponding to the pathogenic gene by detecting an intense signal, because the hybridization signal for these GSs is usually weak. Once a GS corresponding to a pathogenic gene is found, said pathogenic gene can be cloned by established methods such as genomic Southern hybridization using said GS as a probe and/or a primer.

Furthermore, a method for cloning a full-length gene using a GS as a probe or primer is described in detail. Cloned genes isolated in the present invention are also appropriate for use in the production of proteins useful as pharmaceutical products. mRNA is extracted from tissues by conventional methods and cDNA libraries are then prepared (See Molecular Cloning, 2nd ed. Vol. 2, Section 8 New York; Cold Spring Harbor Laboratory). In this case, it is desirable to extract mRNA from tissues in which the target gene is highly expressed. One method to detect a specific gene in libraries thus prepared is, for example, to select positive clones via hybridization using a whole or partial GS as a probe. In general, since a GS is specific for a particular mRNA, hybridization can be carried out under certain stringent conditions. Probes used are at least more than 25 bases long, preferably more than 50 bases long, and more preferably more than 100 bases long.

Furthermore, if cDNA libraries, in which the cDNA for a specific gene is concentrated, are prepared, they will be preferable for selecting said specific gene. One method useful for this purpose is carried out as follows: 1) preparation of an affinity chromatographic column of resin on which the denatured GS corresponding to the specific gene is fixed; 2) application of mRNA extracted from a tissue to said column and retention of the mRNA species corresponding to the specific gene on said column; 3) elution and concentration of said retained mRNA; and finally 4) preparation of cDNA libraries using said concentrated mRNA species as the template. Another method is the selective amplification of cDNA corresponding to the specific gene by the PCR. Selective amplification of a specific gene is carried out as follows: using a partial sequence of a GS localized toward the 3' end of the specific gene as primer, cDNA is synthesized from mRNA with reverse transcriptase and 4 NTPs. To the 3' end of a single-stranded cDNA thus obtained a homopolymer such as poly-T is attached by the action of "terminal deoxynucleotidyl transferase (TdT)". In addition, using "a primer complementary to the homopolymer" and "a primer used in said reverse transcriptase reaction, or a primer whose sequence is included in the same GS but is located proximal to the 5' end", cDNA corresponding to the specific gene may be selectively amplified by the PCR [see 5'RACE (5' Rapid Amplification of cDNA ends): PNAS, Vol. 85, pp. 8998 - 9002 (1988); Nucleic Acids Res., Vol. 17, pp. 2919-2932 (1989)]. In addition, instead of the attachment of a homopolymer, there is another method comprising the following steps: 1) a single stranded anchor DNA is linked to the 3' end of a single stranded cDNA using "T4 DNA ligase"; and 2) said cDNA is amplified by the PCR using a primer complementary to said anchor DNA [Nucleic Acids Res., Vol. 19, pp. 5227-5232 (1991)]. Said primer is desirably more than 13 bases long, preferably more than 15 bases long, and more preferably more than 18

bases long. Furthermore, in order to enhance the efficiency of heat denaturation in the cycling reaction, said primer is preferably less than 50 bases long and more preferably less than 30 bases long. By linking said amplified DNA to a vector, a cDNA library concentrated with respect to the target gene is prepared.

In addition, it may be also possible to isolate a cDNA clone corresponding to the specific gene directly from the PCR products. Specifically, the PCR products are first separated by gel electrophoresis, subjected to Southern blotting analysis using the denatured GS as a probe, and examined for the presence of a band which specifically hybridizes to said GS. If a GS-hybridized band is detected, it is highly possible to isolate the cDNA clone corresponding to the specific gene by excising said band from the gel and subjecting it to direct cloning.

As described above, in order to further amplify the specific gene previously amplified by the PCR, it may be possible to perform the second PCR of the primary PCR products by replacing either or both primers previously used with a primer having the base sequence internal to said two primers (nesting) (Journal of Virology, Vol. 64, p. 864 (1990)). Nesting may be performed directly upon the products of the primary PCR. Alternatively, if a band which specifically hybridizes to the GS is detected by the Southern blotting analysis of the primary PCR products, nesting may be performed for the DNA obtained by excision of the band followed by extraction. In the case where a band which specifically hybridizes to the GS is detected by the Southern blotting analysis of nested products using the denatured GS as a probe, it is highly possible to successfully isolate the cDNA clone corresponding to the target gene by excising said band from the gel and subjecting it to direct cloning.

The isolated cDNA clone corresponding to the target gene may often correspond to the full-length mRNA, but it may be a cDNA with the 5' end deleted. In the case where the 5' end is deleted it is possible to isolate the full-length cDNA clone by conventional methods. For example, by screening a cDNA library using a probe comprising the base sequence in the 5' end region of the cloned cDNA, since the target position of said probe is shifted further toward the 5' end of the full-length cDNA than in the case of using a GS as a probe, it is possible to isolate only longer cDNA clones as the positive clone. Also by synthesizing cDNA using "a primer comprising the base sequence in the 5' end region of the cloned cDNA" with mRNA as the template followed by PCR amplification of "a single stranded cDNA having a homopolymer or anchor DNA sequence at the 5' end" and using "the primer used for previous cDNA synthesis or a primer having the sequence internal to that of said primer" and "a homopolymer or a primer complementary to anchor primer" as described above for the 5' RACE method, only the sequence toward the 5' side of the cDNA may be selectively amplified since the position of said primer is shifted further toward the 5' side of the full-length cDNA. Even if the cDNA thus obtained has a deletion at the 5' end, the population of cDNA fragments covering the full-length of the long cDNA may be obtained by repeating this procedure. It may be easy for those skilled in the art to obtain a full-length cDNA by suitably linking said cDNA fragments having overlap segments together.

Alternatively, by performing the inverse PCR (Inverse PCR: Genetics, Vol. 120, p. 621 (1988); Molecular Cloning, 2nd ed., Vol. 2, 14.12-14.13 (New York: Cold Spring Harbor Laboratory)), it may be possible to isolate a cDNA clone extending externally from the GS, that is, in the genomic DNA region. Specifically, the target DNA (genomic DNA or cDNA) is digested with restriction enzymes into fragments of about 2-3 kb and then circularized by ligating the cleaved ends. By performing the PCR for said DNA using "a set of primers which are complementary to the cDNA clone isolated using the GS or the GS as a probe or primer, and thereby making the direction of DNA synthesis mutually opposite (outward), it may be possible to amplify the DNA region extending externally from the GS. There is known a method to isolate a full-length genomic DNA of a specific gene by repeating this procedure (Nucleic Acids Res., Vol. 16, p. 8186 (1988)).

In addition, although "Taq polymerase" is conventionally used in the PCR described above, the cloning procedure may be more efficiently performed using the "LAPCR (long and accurate PCR)" technique (Nature Genet., Vol. 7, p. 350-351 (1994), Nature., Vol. 369, p. 684-685 (1994)).

Furthermore, needless to say that by linking said full-length gene thus obtained to a suitable expression vector followed by its expression in an appropriate host, it is possible to obtain the corresponding gene product (Molecular Cloning, 2nd ed.).

Next, there will be described an example of the method for identifying and recognizing cell types using the GS of the present invention. As shown in Tables 1 - 219, based on the appearance frequency of GS in each tissue and its comparison among tissues, it is possible to identify those GSs specifically present in a cDNA library constructed for each tissue. These "tissue-specific GSs" are fixed on a filter. It will be more convenient if GSs specific to each tissue are collected and fixed on a filter as a whole (e.g., a GS block specific for hepatocytes or cerebral cortex cells). As described above, to this filter are hybridized labeled complementary fragments synthesized using "random primers" prepared from mRNA extracted from test tissues or cells, "nucleotide containing 4 labeled nucleotides", and "reverse transcriptase". (Directly labeled

mRNA can also be hybridized to the filters.) Depending on the type of tissues or cells, intense hybridization signals will be observed with the GS groups specific to said tissue or cell. Furthermore, a tissue-specific promoter can be cloned by structure analysis of the 5' upstream sequence through the cloning of the corresponding gene using established methods such as genomic Southern hybridization with the "tissue-specific GS" as the probe and/or primer.

These tissue-specific promoters thus obtained are useful for gene therapy in the future.

Gene therapy in a narrow sense aims to supplement the defective protein of patients using gene technology, and in this case it is necessary to express the exogenous gene in a desired tissue in a desired quantity. For this purpose, a promoter which is known to be expressed in a specific tissue in a desired quantity (in most cases a large quantity is desired) is highly useful. Although, at present, a virus promoter is often used, it can be inactivated by endogenous modification such as methylation. Promoters provided by tissue-specific GSs will be ideal substitutes for viral promoters.

There will be described the method for chromosomal assignment of DNA corresponding to the GS of the present invention using the probe derived from the GS obtained as described above.

First, the Southern blotting method will be described.

According to this method, for example, chromosomes are isolated from a lymphoblast cell line of human normal karyotype (e.g., GM0130b), and then a monochromosomal hybrid cell is prepared by introducing each human chromosome into non-human cells, such as rodent cells, and cultured on a large scale by standard methods. Then the DNAs extracted from said hybrid cells are digested with various restriction enzymes and subjected to agarose gel electrophoresis. Then, the electrophoresed DNAs are hybridized to ³²P-labeled GS prepared as described above and used as the probe. By identifying the hybrid cell the DNA of which is hybridized to said probe, it is possible to identify the chromosome in which the DNA corresponding to the GS of the present invention is present. Southern hybridization test of the total human genomic DNA using each labeled GS as a probe formed a single band corresponding to the GS, indicating that the DNA of the present invention can be used as a desirable probe for human genomic DNA. It is obvious that a desirable probe for human genomic DNA can be used also as a desirable probe for human cDNA and human mRNA.

A method similarly using the PCR to determine chromosomal localization of the GS of the present invention will be described.

To prepare most appropriate primers, base sequences are selected from the sequence of the GS in question by conventional methods, for example, by using the computer software OLIGO4.0 (National Biosciences) and the oligonucleotides (20-24mer) having the selected sequences are synthesized. The preferred size of the sequence to be amplified by the PCR is from 50mer to 100mer.

Using the primers thus synthesized and the chromosomal DNA extracted from the monochromosomal hybrid cell as such as the template, amplification by the PCR is performed in a conventional manner. Resulting PCR products are subjected to non-denatured acrylamide gel electrophoresis and stained with ethidium bromide for fluorescent detection. The sizes of these PCR products are then determined.

Chromosomal assignment is confirmed when the presence of a PCR product of correct size is confirmed.

It is evident that a chromosome or chromosomes in which the DNA corresponding to a GS is localized can be identified by using these procedures. It has also become evident that the DNA of the present invention can be used as desirable primers for human genomic DNA since a single band has resulted from amplification of the total human genomic DNA by the PCR using primers designed based on each tested GS. Obviously, a desirable primer for human genomic DNA is also a desirable primer for human cDNA and human mRNA.

Brief Description of Figures

Fig. 1 shows the preparation of 3' Mbol cDNA library.

Fig. 2 shows the results of tests of primers. A shows the location of primers on the vector; and B shows the electrophoretic patterns of DNA fragments amplified using the primers (A). Primers used are as follows: lane 1, FW (-40)/RV (-14); lane 2, FW (-40)/RV (-36); lane 3, FW (-40)/RV (-71); lane 4, FW (-40)/RV (-29); and lane 5, FW (-47)/RV (-48). Artifacts are indicated by arrows.

Fig. 3 shows the electrophoretic pattern of PCR products using FW(-40) and RV(-14) as primers. The lane at the right end shows the electrophoretic pattern of size markers and the other lanes show the PCR products using FW(-40)/RV(-14) as primers.

Fig. 4 shows the mRNA concentration reflecting the frequency of appearance of each GS in the cDNA library: especially, Figs 4A - 4D; experimental results; Fig. 4E, photographs of colonies; and Fig. 4F,

summary.

Fig. 5 shows the appearance frequencies for various cDNAs in the 3'-directed HepG2 cDNA library.

Fig. 6 shows the genetic mapping of each GS (gs) using PCR.

Fig. 7 shows the genetic mapping of each GS (gs) using PCR.

5 Fig. 8 shows the genetic mapping of each GS (gs) using PCR.

Fig. 9 shows the genetic mapping of each GS (gs) using PCR.

Fig. 10 shows the genetic mapping of each GS (gs) using PCR.

Fig. 11 shows the chromosomal mapping of GS001418 (gs001418) using PCR.

Fig. 12 shows the chromosomal mapping of GS001457 (gs001457) using PCR.

10 Fig. 13 shows Southern blotting of human total chromosomes using the GS as a probe.

Fig. 14 shows Southern blotting of human total chromosomes using the GS as a probe.

Fig. 15 summarizes the characteristics of hybrid cells used for Southern hybridization.

Fig. 16 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000152 (clone s14g02) as a probe.

15 Fig. 17 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000041 (clone s650) as a probe.

Fig. 18 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000181 (clone hm01e01) as a probe.

20 Fig. 19 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000055 (clone c13a18) as a probe.

Fig. 20 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000180 (clone s479) as a probe.

Fig. 21 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000094 (clone s173) as a probe.

25 Fig. 22 shows Southern blotting of chromosomal DNA from the hybrid cells using junk (clone hm01g02) as a probe.

Fig. 23 shows the chromosomal mapping of each GS by Southern blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BglII and E/B stands for double cleavage with EcoRI and BamHI.

30 Fig. 24 shows the chromosomal mapping of each GS by Southern-blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BglII and E/B stands for double digestion with EcoRI and BamHI.

Fig. 25 shows the chromosomal mapping of each GS by Southern blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BglII and E/B stands for double digestion with EcoRI and BamHI.

Fig. 26 shows the chromosomal mapping of each GS by Southern blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BglII and E/B stands for double digestion with EcoRI and BamHI.

35 Preferred embodiments of the invention

In the following section, there will be explained preferred embodiments of the present invention. However, the present invention will not be restricted to these preferred embodiments.

40 [Example 1]

Preparation of mRNA

45 Cytoplasmic RNA was extracted from a liver cancer cell line HepG2 (Aden., et al., Nature 282, 615-617, 1979) using standard procedures [Sambrook, J., et al., Molecular Cloning, 2nd ed. (New York: Cold Spring Harbor Laboratory), vol. 1, pp. 7.3-7.36, 1989]. Briefly, HepG2 cells grown in Dulbecco's modified Eagle medium supplemented with 10% FCS were lysed in RNA extraction buffer [0.14 M NaCl, 1.5 mM MgCl₂, 10 mM Tris-HCl (pH 8.6), 0.5% NP-40, 1 mM DTT, 1000 units/ml RNase inhibitor (Pharmacia)] by using a
50 Vortex mixer for 30 sec and then left standing on ice for 5 min. Nuclei and other cell debris were precipitated by centrifuging at 12,000 g for 90 sec, and the supernatant was deproteinized with Proteinase K followed by phenol extraction. RNA was precipitated by isopropanol and rinsed with 70% ethanol. Finally, the poly A⁺ fraction was collected by oligo dT column fractionation (Aviv., et al., Proc. Natl. Acad. Sci. USA 69, 1408-1412, 1972).

55

[Example 2]

Preparation of vector primer DNA and construction of cDNA libraries

5 To prepare a vector primer, pUC19 DNA amplified in JM109 cells (Yanisch-Perron, C., et al., *Gene* 33, 103-119, 1985) was digested with PstI to completion and a poly T-tail was added with terminal transferase (Pharmacia) to a mean length of 26. This process was monitored by the incorporation of ³H-deoxythymidine triphosphate [Okayama, H., et al., *Methods in Enzymology* (San Diego: Academic Press), vol. 154, pp. 3-28, 1987]. The product was digested by HincII, and the resulting short fragments were eliminated by
10 chromatography with Sepharose S-300. Then the T-tailed plasmid was purified by an oligo dA column and stored in 50% ethanol at a concentration of 1 µg/µl.

Fig. 1 shows the outline of the construction of the cDNA library. Two micrograms each of the cytoplasmic Poly A⁺ RNA and the vector primer DNA were co-precipitated in 70% ethanol containing 0.3 M Na-acetate and the pellet was dissolved in 12 µl of distilled water. For the first strand synthesis, after heat
15 denaturation at 76°C for 10 min, 4 µl of 5 x reaction buffer [250 mM Tris-HCl (pH 8.3), 375 mM KCl, 15 mM MgCl₂], 2 µl of 0.1 M DTT and 1 µl of 10 mM each of dATP, dCTP, dGTP and dTTP were added to the sample at 37°C. The reaction was initiated by the addition of 200 units of reverse transcriptase MMLV-H-RT (BRL), and after incubation at 37°C for 30 min, stopped by transferring the reaction tube onto ice. For the second strand synthesis, to the aforementioned reaction mixture the following was added: 92 µl of
20 distilled water, 32 µl of 5 x E. coli reaction buffer [100 mM Tris-HCl (pH 7.5), 20 mM MgCl₂, 50 mM (NH₄)₂SO₄, 500 mM KCl, 250 µg/ml of BSA, 750 µM βNAD], 3 µl of 10 mM each of dATP, dCTP, dGTP and dTTP, 15 units of E. coli ligase (Pharmacia), 40 units of E. coli polymerase (Pharmacia), and 1.5 units of E. coli RNase H (Pharmacia). The reaction mixture was then incubated at 16°C for 2 h and heated to 65°C for 15 min. Then 20 units each of BamHI and MboI were added, and the reaction mixture was incubated at
25 37°C for 1 h and heated again at 65°C for 30 min. Finally, the sample was diluted up to 1 ml with 1 x E. coli reaction buffer, and 100 units of E. coli ligase were added. The resulting mixture was incubated at 16°C overnight. An aliquot of this mixture was used to transform competent E. coli DH5 cells (Toyobo). Transformants were selected by ampicillin resistance. The product was named "3' MboI cDNA library".

30 [Example 3]

Amplification of cDNA insert by PCR

The plasmid-carrier E. coli colonies were picked into 96-well plates containing 125 µl of LB medium
35 (Davis, R. W., et al., *Advanced Bacterial Genetics*. New York: Cold Spring Harbor Laboratory, 1980) in each well and incubated in a moist chamber at 37°C for 24 h. A replica culture was made for every plate using a 96-pinned replica device (Sigma) and the master plates were stored at -80°C for future use. After overnight incubation at 37°C, 50 µl of the culture from each well of these replicas were transferred to polycarbonate 96-well plates (Techne). Bacteria were collected by centrifugation in an Omnispin H4211 rotor (Sorvall) at
40 1500 rpm for 5 min, resuspended in 50 µl of water, covered with a layer of mineral oil and lysed at 95°C for 30 min in a metal bath. Debris were removed by centrifugation at 3600 rpm for 30 min in the same rotor.

Five microliters of the supernatant were added to 20 µl of distilled water and kept at 95°C for 10 min under a layer of mineral oil. Then the denatured lysate was subjected to PCR by adding 25 µl of 2 x reaction mixture [40 mM Tris-HCl (pH 8.9 at 23°C), 3 mM MgCl₂, 50 mM KCl, 200 µg gelatin/ml]
45 containing 5 pmol each of primers, 5 nmol each of dATP, dCTP, dGTP, dTTP and 1.25 units of Taq DNA polymerase (Cetus) at 70°C. Temperature cycling reactions were carried out immediately after addition of the reaction mixtures using a thermal cycler either for microfuge tubes (PJ1000, Perkin Elmer Cetus) or for a 96-well plate (PHC-3, Techne); 35 repeated cycles of 30 sec at 96°C, 1 min at 55°C, and 2 min at 72°C without a final extension step were performed.

50 For this method, the correct choice of primers for the PCR reaction is crucial. Therefore, preliminary tests were performed using the following primers with a predicted T_m of above 60 °C.

The primers tested were a pair of primers, FW(-47) and RV(-48), which are identical to the commercially available 24 mer primers, a second pair of primers, [FW(-40) and RV(-29)], which are a longer version (21 mer) of the well-tested sequencing primers, and the primers RV(-71) and RV(-14), which have a triplet
55 sequence at the 3' terminus identical with that in FW(-40) but is in the opposite orientation (Fig. 2A).

In most of the cases where various combinations of primers were tested, short PCR artifacts appeared, besides the expected major products (Fig. 2B, arrows indicate the PCR artifacts.). These artifacts could be reduced by raising the annealing temperature, lowering the primer concentration or lowering the substrate

concentration but in all cases the yield of the products was not high enough to serve as a template for the sequencing reaction without concentration thereof.

However, since one pair of primers [SW(-40) and RV(-14)] did not yield artifacts (Fig. 3), this pair was selected for further tests, and was found to give reproducible results. Similar results were obtained with randomly selected cDNA clones. Therefore, only this pair of primers SW(-40) and RV(-14) was used as the primers of the present embodiment.

[Example 4]

10 DNA sequencing

The PCR products were drop-dialyzed against TE [10 mM Tris-HCl (pH 8.0), 1 mM EDTA] on millipore filter (VS 0.025 μ m) for 90 min while stirring. Forty-eight samples are easily applied on a single filter of 150 mm diameter. Without further purification the samples were subjected to the Cycle Sequencing protocol (Applied Biosystems, 1991) using dye labeled primers with minor modifications. For dideoxycytidine sequencing reaction, 2 μ l of the dialyzed PCR reaction product (about 0.2 pmol of template DNA) were added to 3 μ l of a reaction mixture containing 0.4 pmol of FAM M13 (-21) Primer (Applied Biosystems) in 160 mM Tris-HCl (pH 8.9), 40 mM $(\text{NH}_4)_2\text{SO}_4$, 10 mM MgCl_2 , 50 μ M dATP, 12.5 μ M dCTP, 75 μ M 7-deaza-dGTP (Boehringer Mannheim Biochemicals), and 50 μ M dTTP, 25 μ M dddCTP, 0.8 unit of Taq Polymerase (Perkin Elmer Cetus), and subjected to 15 plus 15 cycles of the reaction (95 °C 30 sec, 60 °C 1 sec, 70 °C 1 min and 95 °C 30 sec, 70 °C 1 min) according to the manufacturer's recommendation in a 96-well plate using a thermal cycler (PHC-3, Techne). The three other sequencing reactions for dideoxyguanosine, dideoxyadenosine, and dideoxythymidine were performed in parallel (with TMRA, JOE, and ROX primers respectively, supplied by Applied Biosystems) in an identical fashion, except that twice the volume of all the ingredients was added to the dideoxyguanosine and dideoxythymidine reactions. Each sample, from a set of four was cooled to 4 °C, pooled, precipitated with ethanol, resuspended in 6 μ l of a solution of formamide/50 mM EDTA (5/1 by v/v), loaded onto sequencing gel and analyzed by a DNA autosequencer (Model 373A Ver 1.0.1, Applied Biosystems).

30 [Example 5]

The frequency of appearance of each GS of the cDNA library reflects mRNA population.

To confirm that our 3'-directed regional cDNA library was a non-biased representation of the mRNA population in HepG2 cells, the inserts of four cDNA clones (EF-1 α , α 1-antitrypsin, hnRNP core protein A1 and inter- α -trypsin inhibitor) from the clones redundantly obtained by random selection of cDNA were radiolabeled and used as probes in a Northern analysis of poly A⁺ mRNA from the HepG2 cells. (The results are shown in Fig. 4A-D, and summarized in Fig. 4F.) The relative band intensity of the four mRNA species demonstrated that their relative ratios were 52, 24, 1 and 1.2, respectively (lane iii in Fig. 4F). Then the same set of probes was used for measuring the number of colonies hybridizing with each probe in the same cDNA library of 8,800 clones (Fig. 4E).

The clonal frequencies were 307, 128, 7 and 9, or in ratio, 44, 17, 1 and 1.3, respectively (lane iv in Fig. 4F). These two estimates agreed, showing that the cDNA library used is a non-biased representation of the mRNA population. The ratio was practically unchanged when different preparations of mRNA from the same cell were tested.

Fig. 4 shows the proportionality of the composition of the 3'-directed cDNA library and of the mRNA. Fig. 4A, 2 μ g of poly A⁺ RNA from HepG2 cells was electrophoresed in lanes 1-4 of a formamide agarose gel containing ethidium bromide (5 μ g/ml) and then exposed to UV. Lane 5 is the RNA ladder (BRL) used as size markers (kb). In Fig. 4B, the filter was northern blotted using the following ³²P-labeled 3'-specific cDNA probes: Elongation factor-1 α (lane 1), α 1-antitrypsin (lane 2), hnRNP core protein A1 (lane 3), inter- α -trypsin inhibitor (lane 4). In Fig. 4C, one pmol each of the non-labeled cDNA fragments [EF-1 α (lane 1), α 1-antitrypsin (lane 2), hnRNP core A1 (lane 3), inter- α -trypsin inhibitor (lane 4), were electrophoresed in a 2% agarose gel, then photographed. Fig. 4D is a Southern analysis of the blotted filter from Fig. 4C, using the same set of radioactive probes. Lane 5 shows the migration pattern of the reference 1 kb ladder (BRL). Hard copies of these screen images were taken at 8 h for b, and 1 h for d. The radioactivity in each band was counted directly in a scinti-scanner (β -603; Betagen) and registered in (i) and (ii) in Fig. 4F. The observed band intensities were corrected based on the band intensities in Fig. 4D (ii in Fig. 4F), and normalized relative to the value of probe 3 (hnRNP core A1, lane iii in Fig. 4F) as 1 (iii in Fig. 4F). These values represent the relative content of each mRNA species in the original mRNA preparation. Fig. 4E

shows the results of colony hybridization of the membranes carrying 8,800 colonies of the 3'-directed cDNA library using the same set of the four radioactive probes. Positive colonies were counted and registered (iv in Fig. 4F), then normalized with the value of HnRNP core protein A1 as 1. The numbers in B, D and E in Fig. 4 represent the probe No. in Fig. 4F. Fig. 4F shows a remarkable agreement between the values of lanes (iii) and (v).

[Example 6]

Population study of the cDNA library

To analyze further the composition of the cDNA library, 7 and 10 clones were selected from the redundant (group I) and solitary (group II) sequence groups, respectively, and these inserts were used as radiolabeled probes for colony hybridization (Fig. 6). The frequencies of the colonies that hybridized with group I probes were roughly identical to those that were randomly picked and sequenced. These frequencies were about 3.5%-0.1%. Nearly 52% of the cDNA library population consisted of the redundant sequence group containing 173 species. When 8 probes from group II were tested, 18 positive colonies were identified among 26,400 colonies screened, giving an average frequency of 0.007%. Two probes did not hybridize with any of the 26,400 colonies, resulting in the average frequency of <0.004%. Thus, the average frequency of the 10 probes in group II was several orders of magnitude less than the lowest of group I.

The results are summarized in Fig. 5, showing the appearance frequencies of various DNA species in the 3'-directed HepG2 cDNA library. In Fig. 5, seven cDNA probes (a15 through tb042) were selected from the 162 identified genes in the redundant group (group I), and ten (s155 through s632) were randomly chosen from the solitary group (group II). In columns A, B and C, each one of the insert DNAs was radiolabeled and used as a probe for colony hybridization tests of 982 (A), 8,800 (B) or 26,400 colonies (C). NT indicates "not tested". The DDBJ entry names of the 17 clones listed in this table are HUM000A15, HUM000C321, HUM00TB038, HUMHM01B02, HUM0C13A04, HUMHM02D02, HUM00TB042, HUM000S155, HUM000S159, HUM000S639, HUM000S635, HUM000S170, HUM000S154, HUM000S167, HUM000S645, HUM000S647, and HUM000S632.

[Example 7]

Analyses of sequencing errors

All the sequence data presented in this specification were obtained by repeated cycles of enzymatic amplification of the plasmid inserts, followed by cycle sequencing with Taq polymerase. Sequences of 60 clones that showed data bank matches were examined for discrepancies from the data bank entries. It was found that the accuracy in the region 1-100 bp distant from the cloning site was 98.7%, indicating that the primers or probes designed with the sequence in this region could be obtained practically without any erroneous sequences or even if they contain any errors, they are functionally without problems.

[Example 8]

Mapping of GS by PCR

<cDNA sequence>

cDNA library was constructed from mRNA of DMSO treated HL60 cells. The methods for construction of the 3'-directed cDNA library and for sequence analysis of the library components are the same as described in Examples 1-4.

<PCR primer>

Primer design was performed by using the computer software OLIGO 4.0 (National Biosciences) which eliminates possible formation of inter- or intra-molecular secondary structures. In addition to the primer design, transfer of oligonucleotide sequences to the local database and synthesizer were semiautomated using a Macintosh computer linked with a network. DNA oligomers were synthesized on an automated DNA synthesizer (Model 394, Applied Biosystems) on a 40 nmol scale. The synthesized oligomers were used as

PCR primers without further purification.

(Preparation of Genomic DNA)

5 The human genomic DNA was extracted from the normal karyotype lymphoblastoid cell line GM0130b.
 Mouse and Chinese hamster genomic DNAs were purchased from Clontech. Monochromosomal hybrid cells utilized for mapping panel were commonly used ones which have been described previously. Briefly, chromosomes 3, 4, 9, 11, 12, 13, 15, 22 and Y were carried in human-Chinese hamster monochromosomal hybrid cells, and chromosomes 1, 2, 5, 6, 7, 8, 10, 11, 12, 14, 15, 16, 17, 18, 19, 20, 21 and X were carried
 10 in the human-mouse monochromosomal hybrid cells A9 series. The integrity of the hybrid cells were monitored by *in situ* hybridization.

(Amplification by Polymerase Chain Reaction)

15 PCR was performed according to standard protocols (Saiki, R. K., et al., Science 230, 1350-1354, 1985), using 10 pmol of each primer on a whole 20 μ l scale reaction, with 35 thermal cycles of 30 sec at 94°C, 60 sec at an annealing temperature, and 90 sec at 72°C, using a Perkin-Elmer 9600 thermal cycler. Annealing temperature was determined according to the "optional annealing temperature" estimated by the Program OLIGO.

20 (Analysis of the PCR Products)

The PCR products were run on an 8% polyacrylamide non-denatured gel (Acrylamide:Bis-acrylamide = 19:1, 1 mm thick) at 300 V for 1 h, followed by staining in 90 mM Tris-borate, 2 mM EDTA buffer solution
 25 containing 0.25 μ g/ml ethidium bromide for 15 min. The size of the amplification products were determined relative to the 10 bp DNA ladder (BRL). Detection of fluorescence was performed by using a laser fluorescent image analyzer (FM-BIO, Hitachi Software Engineering). The image data were transferred to a computer for analysis.

30 (Results of Analysis of the PCR Products)

Among various species of 3'-directed cDNA-GSs obtained from granulocytoid cells, 195 novel GSs which did not match the sequences deposited in Genbank Release 76 were selected and used for designing primers for the PCR. The PCR was performed with these primers using the total human genomic
 35 DNA as the template.

Among the 195 primer pairs, 191 (98%) yielded products whose size matched those expected within 5 nt. The results are summarized in Figs. 6 - 10 whose figure legends are as follows: GS, gene signature; CN, clone name; Chromosomal position, chromosome numbers to which GSs were mapped; Sequence of primers, DNA sequences of primers (Sense, sense strand; anti-sense, anti-sense strand); AT, annealing
 40 temperature; HO, Observed size of PCR products with total human genomic DNA (nt); HE, Expected size of PCR products with total human genomic DNA (nt); MO, Observed size of PCR products with mouse genomic DNA (nt); CO, Observed size of PCR products with Chinese hamster genomic DNA (nt); G, Number of "hits" of GS in the granulocytoid (DMSO treated HL60) cDNA library after analyzing altogether 1000 clones; T, Total number of "hits" of the GS after analyzing altogether 3000 clones from the three
 45 cDNA libraries of HL60 with and without induction by DMSO or TPA. Question marks ("??") indicate that the PCR products did not yield a clear band.

"M" indicates that the PCR products yielded a band which was indistinguishable from the band observed after the reaction using mouse DNA as the template. Similarly, "C" indicates that the PCR products yielded a band which was indistinguishable from the band after the reaction using Chinese
 50 hamster DNA as the template.

The overall rate of success of the PCR was 191/195 (98%), although GSs were randomly selected from the cDNA sequences, indicating that the quality of the cDNA library used in this work was reliable, and that the sequence analyses and primer designs were performed appropriately. Thus, the possible chances of failure of the PCR caused by presence of an intron(s) in the relevant cDNA sequences is negligible in
 55 working with the GS, as introns virtually do not lie in the poly A proximal 3'-region of vertebrate genes (Wilcox et al., Nucleic Acids Res. 19, 1837-1843, 1991). This is a big advantage compared to the use of partial fragmented cDNA sequences obtained from randomly primed cDNA libraries (Adams et al., Science 252, 1651-1656, 1991) or from 5'-directed cDNA libraries.

(Chromosomal assignments of GS)

The 191 primer pairs that yielded PCR products from total human DNA were used for chromosomal assignments of the GSs with the monochromosomal hybrid cell panel. At least 119 GSs were assigned to a single chromosome. As an example, GS001418, shown in Fig. 11, was assigned to chromosome number 3. With some clones, extra products were obtained, some of which were assigned to the same chromosome, whereas others to different chromosomes. An example, GS001457, is shown in Fig. 12. Sixty-two (33%) clones yielded the expected PCR products with two or more different chromosomes. Thirty-five cases (18%) yielded PCR products whose size were indistinguishable from background rodent genomic DNA. Among these, 21 GSs produced products indistinguishable from mouse and Chinese hamster DNA. Ten GSs yielded no expected PCR products with the monochromosomal cell panel DNA although the expected PCR products from total human genomic DNA were observed. The 10 cases probably arose from a small deletion in the hybrid cells. Five clones obtained from HepG2 cDNA library have been analyzed also by Southern blot analysis. Four out of the 5 GSs (GS000053, GS000120, GS000271 and GS000279) gave consistent results with those obtained by the PCR. One GS (GS000228), which was uncertainly assigned to chromosome Y because of the weak signal detected by the Southern blot method, was assigned to chromosome 11 by PCR.

[Example 9]

Mapping of GS by Southern blot method

(Cell lines)

Total human genomic DNA was isolated from the human normal karyotype lymphoblastoid cell line GM0130b. Monochromosomal hybrid cells used as the mapping panel are shown in Fig. 15. Hybrid A9(neo-x)-y cells as described by Koi, et al. (Jpn. J. Cancer Res. 80, 413-418, 1989) were donated by Dr. M. Oshimura, Faculty of Medicine, Tottori University, passaged 3 times and frozen for storage. The loss or rearrangements of chromosomes could have occurred during this period. The GM series was obtained from the Mutant Cell Repository, National Institute of General Medical Science (NIGMS) (Camden, NJ). To confirm that human chromosomes remained intact in the hybrid cells after storage in liquid nitrogen, metaphase spreads of the hybrid cells were monitored by chromosome staining based on *in situ* hybridization using biotinylated total human DNA as the probe (Durnam, D. M., et al., Somatic cell Mol. Genet. 11, 571-577, 1985). Intact, as well as translocated or fragmented human chromosomes were easily detected by this means. In a hybrid cell mapping panel, chromosomes 11, 12 and 15 were represented by the hybrid cell lines A9(neo-11)-1, A9(neo-12)-4 and A9(neo-15)-2, respectively, and in another panel, they were represented by the hybrid cell lines GM10927A, GM10868 and GM11418, respectively.

(Isolation of genomic DNA and Southern blotting)

High molecular weight DNA was extracted from cells using sodium dodecyl sulfate (SDS) and Proteinase K, followed by phenol-chloroform extraction and ethanol precipitation. DNAs were digested overnight with a combination of two restriction enzymes including EcoRI, BamHI and BglII. About 5 µg of each digest was electrophoresed in an 0.8% agarose gel, then transferred to Hybond N⁺ membrane (Amersham) with 0.4 N NaOH. The membrane was rinsed in 2 x SSC and stored at 4 °C for subsequent use.

Clones containing a novel sequence and having more than 150 bp were selected as probes. The cDNA inserts of the clones were amplified by the PCR. The PCR products were isolated by electrophoresis through a 2% low-melting temperature agarose gel (Nusieve : SeaPlaque, 3 : 1), followed by excision. The gel was removed by melting at 65 °C and digesting with β-Agarose I (Bio Labs) at 40 °C for 1 h. The probes were labeled with [α -³²P]dCTP by random priming using a commercial kit (Amersham). Hybridization proceeded at 65 °C in a high salt buffer containing 6xSSC, 1x Denhardt's solution and 0.5% SDS, in the presence of 0.1 mg/ml of sonicated, denatured salmon sperm DNA. The membranes were washed in 2xSSC, 0.1% SDS at 65 °C for 30 min, then twice for 30 min in 0.1xSSC, 0.1% SDS at 65 °C, and analyzed using a Fuji BAS-2000 imaging analyzer.

(Analyses with Genomic DNA)

Among the HepG2 3'-directed cDNA libraries described in Examples 1 and 2, 160 novel clones were selected and used as probes for Southern blots.

5 Total human genomic DNA was isolated from a cell line GM0130b that has a normal karyotype, and digested with the restriction enzymes, EcoRI, BamHI and BglII alone or in combination. The GS clones used as probes were the 3'-directed cDNAs. Each of these cDNAs covers a region between the poly(A) site and the nearest MboI site (GATC) (Okubo, K., et al., Nature Genetics 2, 173-179, 1992) and thus do not have restriction sites for BamHI or BglII. In addition, because the average size of GS is 270 bp, the chances of
10 having an EcoRI site in the cDNA moiety were not high. In fact, only 7 clones out of the 160 analyzed had an EcoRI restriction site.

Membranes blotted with digested human genomic DNA were hybridized with radio-labeled GS probes and washed at high stringency. Since the 3'-terminal region of cDNA has, in general, a unique sequence which differs from that of protein encoding regions which tend to have conserved motifs, cross hybridization
15 with unrelated cDNA sequences will not occur under such stringency. Examples of the results of hybridization are shown in Figs. 13 and 14. Clones s503 and s632 (Figs. 13a and 13b; junk) respectively represent unique single band producers. As shown below, 67 clones belonged to this class. The positions of the GS sequence relative to the restriction sites were inferred from the band patterns. Clone s311 (Fig. 13c; GS000092) showed a single band with EcoRI -as well as (EcoRI + BamHI)-digested DNA, but two bands of
20 different sizes in other double digests. The double digestion thus helped resolve multiple GSs. Similar results were obtained with clone c13a08 (Fig. 13d; GS000055), in which there were 2 bands with EcoRI- or (EcoRI + BamHI)-digested DNAs, and 4 when digested with (EcoRI + BglII) or (BamHI + BglII). On the other hand, 4 hybridization bands appeared with clone s479 with EcoRI alone, but the number of bands decreased with (EcoRI + BglII) and (BamHI + BglII) (Fig. 14e; GS000180). These results indicate that
25 genomic DNAs should be digested in various ways to reveal the maximum number of hybridizing fragments. The results of the analysis showed that 41, 10, 7 and 19 clones contained 2, 3, 4 and 5 or more bands, respectively. Clones s14f01 and tw1-46 (Figs. 14f and 14g; GS000407 and junk, respectively) contained at least 10 bands in each lane. Since the EcoRI restriction site is not present in the two GS sequences, the multiplicity of bands is likely to represent the multiple copy number of these genes. Clone
30 kmb07 moved as a smear (Fig. 14h; junk), even after intensive high stringency washes, suggesting that this probe has a repetitious sequence which has not been hitherto identified.

(Chromosomal assignments)

35 A set of monochromosomal hybrid cells carrying a single human chromosome in a background of rodent chromosome was collected (Fig. 15). Thirteen cell lines were microcell hybrids established by Koi et al. (Koi, M., et al., Jpn. J. Cancer Res. 80, 413-418, 1989) and the others were obtained from NIGMS. The results of monitoring the human chromosomes in these cell lines by *in situ* hybridization using biotinylated total human DNA are also presented in Fig. 15.

40 The GSs were assigned to chromosomes using hybrid cell mapping panels. Three types of membranes were prepared, each having DNAs prepared from hybrid cells, and digested with EcoRI, (EcoRI + BamHI), or (BamHI + BglII). Among these three types of membranes, the one which should have yielded the maximum number of bands was used for each GS probe, according to the results of total genomic Southern blots. Examples of hybridization results are shown in Figs. 16 - 22. The numeral on each lane represents the
45 human chromosome numbers which is contained in the hybrid cell, and H stands for the total human chromosomes. Clone s14g02 (GS000152; Fig. 16) that showed a single hybridization band with the total human DNA digested with EcoRI (lane H), showed the corresponding band only with the hybrid cell line containing human chromosome 4. Thus, this GS lies in chromosome 4.

The clone s650 (GS000041; Fig. 17) was assigned to chromosome 12 which showed a characteristic
50 7.5kb band in the presence of an (EcoRI + BamHI)-digested membrane. However, with an EcoRI digested DNA, the clone could not be assigned, as the human-specific and the cross-reacting rodent DNA fragments overlapped. The single, but shorter fragment band (1.3kb) which appeared in lanes 3, 4, 9, 13 and 22 represents the homologous DNA sequence in Chinese hamster, and the 3.3kb band in other lanes represents the homologous DNA in the mouse.

55 Clone hm01e01 (GS000181; Fig. 18) exhibited two fragments when hybridized to total human DNA treated with EcoRI alone, and these corresponding bands appeared in lanes 1 and 2. Thus, the two members of this gene family are located on two chromosomes.

Fig. 19 shows that clone c13a08 (GS000055) exhibited 4 bands when hybridized to (BamHI + BglII)- or (EcoRI + BglII)-digested total human DNA, although only 2 bands appeared with EcoRI- or (EcoRI + BamHI)-digested human DNA. Therefore, the (BamHI + BglII)-digested DNA panel was used for this clone. Two bands (12.3kb and 7.5kb) appeared in lane 7, a 5.2kb band in lane 2, and a 3.2kb band in lane 17. Two bands (6.0kb and 3.8kb) that cross-reacted with Chinese hamster DNA appeared in lanes 3, 4, 9, 13 and 22, and a single band (3.5kb) that cross-reacted with mouse DNA appeared in other lanes.

Clone s479 (GS000180; Fig. 20) showed 4 EcoRI fragments with total human DNA. The hybridization to an EcoRI-digested DNA panel yielded in bands of 10.5kb in lanes 7 and 19, 8.5kb in lane 8, 7.8kb in lanes 11 and 12, and 3.5kb in lane 11. Thus, the human specific genes are dispersed among chromosomes 7, 8, 11, 12 and 19, among which the 10.5 and 7.8kb bands in the total DNA both consist of two overlapping fragments. As shown in lane H, the intensity of these overlapping fragments was higher than normal. The 3.5kb band in lane H, as well as in lane 11 was also intense, suggesting that it also represents overlapping fragments.

Clone s173 (GS000094) exhibited 5 bands in EcoRI-cleaved total DNA (Fig. 21). Four corresponding fragments included a 4.5kb fragment in lane 1. Another 4.5kb band was observed in lane 4, indicating that the corresponding band in lane H overlapped. In addition, an intense 3.1kb band was observed in lane 17.

Clone hm01g02 (junk; Fig. 22) exhibited many bands with total DNA, and with those from monochromosomal hybrids. This clone must represent a multiple and closely related family of genes. It also contains a sequence conserved in homologous rodent genes which also give rise to multiple bands. Since most of the human specific and rodent bands overlapped, the chromosomes could not be assigned. Other combinations of restriction enzymes did not resolve the overlap.

The results of the total genomic DNA analyses and the chromosome assignments of 160 GSs are summarized in Figs. 23 - 26. Through total genomic DNA analyses using 4 differently digested human DNAs, 67 clones were categorized into a single band group, 41 in a two band group, 10 in a three band group, 7 in a four band group and 19 in a group that yielded five or more bands. Nine clones did not show any hybridization band under fixed conditions.

Assignment of two band clones showed that the two genes lie in different chromosomes in 15 of them, whereas the gene represented by clone s317 originated from the same chromosome. The three band clones s308 (GS000412) and s401 (GS000224) showed that two of the fragments lie on the same chromosome, and clone hm05g02 (GS000209) and s17a10 (GS000294) showed bands in different chromosomes. Clones displaying four or more bands showed a relatively dispersed distribution among chromosomes. "junk" in Example 9 is the DNA segment cloned by the same method used for GS but is not numbered.

[Example 10 Cloning of gene using GS]

[10A. Cloning of a full length cDNA encoding a human ribosomal protein, homologue of yeast S28. Cloning of the full length cDNA by PCR using a primer comprising a partial sequence of a GS(1)]

Using a primer (5'-TGAAATTTATTACTACAGTGTTCACCA-3' (SEQ ID NO:7839)) that is a partial sequence of a DNA which is substantially the same as the complementary strand of HUMGS00500 and a primer (5'-TAATACGACTCACTATAGGG-3' (SEQ ID NO: 7840)) complementary to the vector (pSPORT) sequence that is located external to the 5' end of the cDNA, HepG2 cDNA library was amplified by the PCR and a full length cDNA clone encoding a human ribosomal protein, a homologue of yeast ribosomal protein S28 was isolated. (Hori et al., Nucl. Acids Res. 21: 4394, 1993).

[10B. A human ribosomal protein homologous to rat L9 ribosomal protein-Cloning of the full length cDNA by PCR using a primer comprising a partial sequence of a GS(2)]

Using a primer 5'-CTTCTTTCTGTAGCCAGGTAAGTCT-3' (SEQ ID NO: 7841) that is a partial sequence of a DNA which is substantially the same as the complementary strand of HUMGS00418 and a primer (SEQ ID NO: 7840) complementary to the vector (pSPORT) sequence that is located external to the 5' end of the cDNA, a full length cDNA clone encoding a human ribosomal protein homologous to rat L9 was isolated (Hori et al., Nucl. Acids Res. 21:4395, 1993).

[10C. A human protein homologous to bovine phosphatidylethanolamine-binding protein. Cloning of the full length cDNA by hybridization using a probe comprising a partial sequence of a GS]

By hybridization with the probe,

5' - GATCGTTCTTCATGGGGGTAAGAAAAGCTGGTCTGGAGTTGCTGAATG

TTGCATTAATTGTCCTGTTTGCTTGTAGTTGAATAAAAAATAGAAACCTGAAT

GAAGGAAA-3' (SEQ ID NO:7838),

that comprises a partial sequence of HUMGS00421, a full length cDNA clone encoding a human protein homologous to bovine phosphatidylethanolamine-binding protein was isolated (Hori et al., Gene 140:293, 1994).

[10D. Human mpl-ligand. Cloning of a cDNA coding for the human mpl-ligand using a GS]

This embodiment employs the 5' SLIC (single ligation to single stranded cDNA) method which is an improved version of the 5'RACE (rapid amplification of cDNA ends) method, and is described in Nucleic Acids Res., 19, 5227-5232 (1991).

① Reverse transcription of cDNA and attachment of anchor

The template was prepared using the reagents of the 5'-Amplifinder™ Kit (Toyobo, Inc.) in accordance with the protocol included therewith. Specifically, 2μg of human fetal liver poly A⁺RNA (Clontech Laboratories, Inc.) and 10 pmol of the primer PA-6, a primer corresponding to the 3' end of the gene signature (GS) sequence HUMGS02342 and consisting of the sequence 5'-TTTTCGGCGCTCCCATTTATTCCTT-3' (SEQ ID NO: 7842), were mixed together and then denatured by heating the mixture at 65°C for 5 min. The cDNA was synthesized by combining the denatured sample with AMW reverse transcriptase, RNase inhibitor, dNTPs, and a reaction buffer, and then heating the resultant mixture at 52°C for 30 min. EDTA was then added to the mixture to stop the reaction. Thereafter, the RNA was hydrolyzed by adding NaOH to the reaction mixture and heating the resultant mixture at 65°C for 30 min. The mixture was then neutralized with acetic acid. A suspension of glass beads (GENO-BIND™) and NaI were added to the neutralized solution and the cDNA was adsorbed onto the beads. The cDNA, adsorbed onto the beads, was washed with an aqueous solution of 80% EtOH, and then eluted in 50 μl of distilled water. Glycogen was added to the solution of purified cDNA, and the cDNA was precipitated with EtOH and resuspended in 6 μl of distilled water. The resultant suspension (2.5 μl) was added to a solution containing 4 pmol of AmpliFINDER Anchor (5'-CACGAATTCATCTGATTCTGGAACCTTCAGAGG NH₂-3') (SEQ ID NO: 7843) provided with the Kit, T4 RNA ligase, and a ligation (reaction) buffer. The reaction mixture was incubated at room temperature overnight, and the AmpliFINDER Anchor primer in the reaction mixture was thereby ligated to the 3' end of the cDNA. The ligated product was then used as a template for the subsequent PCR.

② Amplification by PCR

The primary PCR was carried out using the template produced in the procedure described above (①), the Anchor primer, 5'-CTGGTTCGGCCACCTCTGAAGGTTCCAGAATCGATAG-3' (SEQ ID NO: 7846) and the PA-5 primer consisting of the sequence 5'-CTCGCTCGCCCATCCTTATACAGGCTCAGTTTGTCT-3' (SEQ ID NO: 7844). Specifically, 1 μl of the template was mixed with Taq DNA polymerase (Takara Shuzo Inc., Code No. R001A), dNTPs, a PCR buffer, and 10 pmol each of the PA-5 primer and Anchor primer. The resultant reaction mixture was diluted with distilled water to a final volume of 50 μl and the PCR was performed in a DNA Thermal Cycler 480 (Perkin Elmer Cetus Corp.). The reaction mixture was subjected to 40 cycles of the PCR, wherein each cycle consisted of incubating the sample in sequence at 94°C for 1 min, 63°C for 1 min, and 72°C for 3 min and, in the last PCR cycle, at 72°C for an additional 8 min. The products of the PCR were resolved by electrophoresis in a 1% agarose gel and a broad band of

approximately 800 bp in length, representing a product of the PCR, was detected. The detected band was excised from the agarose gel and the DNA contained therein was recovered using a Sephaglas Bandprep Kit™ (Pharmacia Corp.) in accordance with the protocol included therewith. Specifically, the gel was dissolved in a solution of NaI and the resultant mixture was heated at 60 °C for 10 min. Sephaglas™ BP
 5 was added to the gel mixture and the DNA was adsorbed onto the glass beads contained therein. The glass beads, containing the adsorbed DNA, were then washed three times with a Wash Buffer provided with the Kit and eluted in 30 µl of TE buffer (10 mM Tris-HCl pH 8.0, 1mM EDTA).

One µl of the eluted DNA was used as a template in a secondary PCR. In order to enhance the specificity of the secondary PCR, the reaction was performed with PA-4 primer which consisted of the
 10 sequence 5'-CTCGCTCGCCCATGTATAGGGACAGCATTCTGAGAG-3' (SEQ ID NO: 7845) and was positioned within the template sequence internal to the PA-5 primer and the Anchor primer. Specifically, 1 µl of the template was mixed with 2.5 units of Taq DNA polymerase (Takara Shuzo Inc., Code No. R001A), dNTPs, a PCR buffer, and 10 pmol each of the PA-4 primer and Anchor primer. The resultant reaction mixture was diluted with distilled water to a final volume of 50 µl preheated at 94 °C for 6 min, and the
 15 secondary PCR was then performed under the same conditions described above (①) for the primary PCR. The products of the secondary PCR were resolved by electrophoresis in a 1% agarose gel and a broad band of approximately 800 bp in length, representing a product of the PCR, was detected. The detected band was excised from the agarose gel and the DNA contained therein was recovered and purified under the same conditions as described above (①) for the primary PCR.

20 ③ Subcloning into plasmid vector

The purified DNA product of the secondary PCR was subcloned into the plasmid vector pUC18 (pharmacia Corp.), using a SureClone™ Ligation Kit (Pharmacia Corp.) in accordance with the protocol
 25 included therewith. Specifically, the purified DNA was added to a solution containing Klenow polymerase, polynucleotide kinase and a reaction buffer, mixed and heated at 37 °C for 30 min in order to create blunt-ended termini and to phosphorylate the 5' terminus of the DNA molecules contained in the reaction mixture. The blunt-ended and phosphorylated DNA was combined with a solution containing 50 ng of a de-phosphorylated and Sma I-cleaved pUC18 vector provided with the Ligation Kit, T4 DNA ligase, DTT and a
 30 ligation reaction buffer, and the resultant mixture was warmed at 16 °C for 3 hr. One sixth volume of the reaction solution was employed to transform E. coli competent cells using standard methods. Specifically frozen E. coli competent cells (Wako Pure Chemical Industries, Ltd.) were thawed and mixed with the ligated DNA. The resultant mixture was incubated on ice for 20 min, heat-treated at 42 °C for 45 sec, and then incubated on ice for 2 min. A medium [Hi-Competence Broth (Wako Pure Chemical Industries, Ltd.)]
 35 was added to the mixture containing the transformed E. coli cells. The mixture was incubated for 37 °C for 1 hr and then spread onto agar plates containing 100 µg/ml Ampicillin, 40 µg/ml X-Gal (6-bromo-4-chloro-3-indolyl-β-D-galactoside), 0.1 mM IPTG (isopropyl-β-D-thiogalactopyranoside) and cultured overnight at 37 °C. White colonies were selected from the colonies which consequently appeared on the agar plates and analyzed by the PCR to determine the presence or absence of the DNA insert. Specifically, a sample of a
 40 selected colony was picked with a sterilized toothpick and used to inoculate a 50 µl reaction solution containing 1 unit of Taq DNA polymerase, dNTPs, PCR buffer, 200 µM each of the M13 P4-22 primer consisting of the sequence 5'-CCAGGGTTTCCCAGTCACGAC-3' (SEQ ID No: 7847) and M13 P5-22 primer consisting of the sequence 5'-TCACACAGGAAACAGCTATGAC-3' (SEQ ID No: 7848), wherein both primers are comprised of sequences complementary to the pUC18 vector. The resultant mixture was
 45 heated at 94 °C for 6 min and then subjected to 30 cycles of the PCR wherein each cycle consisted of incubating the sample in sequence, at 94 °C for 1 min, 55 °C for 1 min, and 72 °C for 2 min. The amplified insert was detected by electrophoresis of the PCR products on an agarose gel and thereby the clone pR02342-2, containing an insert, was selected.

50 ④ Sequencing of cDNA

The plasmid DNA was prepared using the QIAprep-Spin Kit (Funakoshi, Ltd.) in accordance with the standard alkali-SDS protocol included therewith. Specifically, E. coli cells transformed with the DNA of clone pR02342-2 were cultured overnight in Luria Broth medium containing 100 µg/ml Ampicillin. The cultured
 55 cells were then pelleted by centrifugation and resuspended in P1 solution provided in the Kit. The resultant cell suspension was mixed with the P2 alkali solution of the Kit, incubated at room temperature for 5 min, neutralized with N3 solution of the Kit, incubated on ice for an additional 5 min and then centrifuged. The supernatant obtained from the centrifuged solution was applied to a QIAprep-Spin column. The Spin column

was then washed in sequence with PB and then PE solution of the Kit and the DNA was eluted from the column with TE buffer. Sequencing of the eluted DNA was then carried out using the sequencing kit PRISM™ Terminator Mix (Applied Biosystem Corp). Approximately 1 µg of the purified DNA was mixed with a solution containing 3.3 pmol of either the M13 P4-22 primer or M13 P5-22 primer and 9.5 µl of PRISM™ Terminator Mix. The M13 P4-22 and M13 P5-22 primer were used to sequence both strands of the DNA insert of clone pR02342-2. The resultant mixture was diluted to a final volume of 20 µl with distilled water and subjected to 25 cycles of the PCR wherein each cycle consisted of incubating the sample in sequence at 96 °C for 30 sec, 50 °C for 15 sec, and 60 °C for 4 min. The excess primers and fluorescent dye present in the reaction mixture were removed by gel filtration using a MicroSpin™ S-200 HR column (Pharmacia Corp.) and the DNA products of the sequencing reaction were precipitated with EtOH. The precipitated DNA was resuspended, sequenced using an automated sequencer, "Model 373A" (Applied Biosystem Corp.), and thereafter analyzed to determine the nucleotide sequence.

The analysis of the nucleotide sequence revealed that the insert of clone pR02342-2, including the PA-4 primer, was 608 bp in length. The sequence of this insert was subjected to a search for homologous sequences entered in the Gen Bank data base, and a 100% match was found to a sequence in the cDNA which encodes the human mpl-ligand (Accession No. L 33410, Nature 369, 533-538, 1994). Further comparison of the insert of clone pR02342-2 with the cDNA sequence of the human mpl-ligand revealed that the cloned insert contained 81 bp of the 3' coding region of open reading frame. In addition, the insert of clone pR02342-2 contained an additional sequence extending beyond the 3' end of the human mpl-ligand cDNA sequence registered under Gen Bank Accession No. L 33410. These findings suggest that, using the GS HUMGS02342, the inventors of the present invention succeeded in cloning a cDNA clone pR02342-2, which could possibly have a different and more desirable property for expression than the human mpl-ligand cDNA represented by the sequence registered under Gen Bank Accession No. L 33410.

⑤ Cloning of the full-length cDNA encoding the human mpl-ligand

In order to find an optimal PCR primer, an appropriate computer program is used to search the sequence downstream of the coding region of the human mpl-ligand (clone pR02342-2) and thereby a primer PA-7 is designed and synthesized. A PCR similar to that described above in ② is performed using the template produced by the procedure described above in ①, the Anchor primer, and the PA-7 primer. Specifically, 1 µl of the template is mixed with 2.5 units of Taq DNA polymerase (Takara Shuzo Inc., Code No. R001A), dNTPs, a PCR buffer, and 10 pmol each of the PA-7 primer and Anchor primer. The resultant reaction mixture is diluted with distilled water to a final volume of 50 µl and the PCR is performed in a DNA Thermal Cycler 480 (Perkin Elmer Cetus Corp.) under conditions similar to that described above in ②. The products of the PCR are then resolved by electrophoresis on a 1% agarose gel and a band greater than 1300 bp in length, representing a product of the PCR, is recovered and cloned into a suitable vector in a manner similar to that described in ③. The cloned DNA is sequenced in a manner similar to that described in ④. The sequence is then compared to that of the human mpl-ligand cDNA registered under Gen Bank Accession No. L 33410 to confirm the presence of the full-length open reading frame.

Alternatively, using the Takara La PCR Kit (Takara Shuzo Inc., Code No. RR011) in accordance with the protocol included therewith, performing the 5'RACE procedure using primers similar to those described above in ②, a cDNA of approximately 2 Kb in length, corresponding to the human mpl-ligand, was isolated.

The tables of appearance frequencies for all GSs related to the present invention are followed by "Sequence Listing" for these GSs, wherein HUMGS numbers after the heading 'clone' represent GS numbers. In the sequence table, N in the base sequence stands for "A or C or G or T or U". However, since nucleic acids in the Sequence Listing are DNAs, "T or U" stands for T in this case.

By the present invention, it has become possible to provide DNA molecules which carry "the information for expression" in various cells and can be used for detecting and diagnosing the cellular abnormalities, recognizing and identifying cells and further efficiently cloning genes which are expressed in a tissue-specific manner, and furthermore cloned DNA molecules which can be used for the production of proteins useful as pharmaceutical products.

A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AN	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1	00001	00001	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
2	00002	00002	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
3	00003	00003	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
4	00004	00004	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
5	00005	00005	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	00006	00006	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
7	00007	00007	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
8	00008	00008	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9	00009	00009	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10	00010	00010	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11	00011	00011	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	00012	00012	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
13	00013	00013	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
14	00014	00014	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
15	00015	00015	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
16	00016	00016	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
17	00017	00017	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
18	00018	00018	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
19	00019	00019	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
20	00020	00020	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
21	00021	00021	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AI	AK	AM	AN	AS	AT	AY	BAC	BE	BF	BGBH	BI	BK
22	00023	00021	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	00026	00022	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	00028	00023	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	00029	00024	5	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	00030	00025	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	00031	00026	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	00033	00027	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	00034	00028	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	00036	00029	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	00037	00030	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	00038	00031	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	00039	00032	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	00040	00033	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	00041	00034	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	00042	00035	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	00043	00036	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	00044	00037	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	00045	00038	5	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	00046	00039	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	00047	00040	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	00048	00041	10	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	00049	00042	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
44	00050	00043	16	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
45	00051	00044	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
46	00053	00045	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	00055	00046	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	00056	00047	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	00057	00048	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	00060	00049	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	00061	00050	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
52	00062	00051	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
53	00064	00052	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
54	00065	00053	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	00066	00054	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
56	00067	00055	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	00068	00056	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 2

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
94	00105	00093	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
95	00106	00094	8	2	1	1	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
96	00107	00095	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
97	00108	00096	31	2	3	0	0	0	0	0	0	0	0	0	0	3	0	0	3	6	2	1	1	0	1	0	0	0	3	X63237	94.8	384	1	154
98	00109	00097	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	532	
99	00110	00098	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
100	00111	00099	38	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
101	00113	00100	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1352	
102	00114	00101	38	1	1	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
103	00115	00102	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
104	00116	00103	17	2	1	1	0	0	0	0	0	0	0	0	0	0	4	3	1	0	9	0	1	1	0	0	0	0	0	0	0	0	0	1918
105	00117	00104	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
106	00118	00105	7	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
107	00119	00106	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
108	00120	00107	5	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
109	00121	00108	4	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
110	00122	00109	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
111	00123	00110	14	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
112	00124	00111	6	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
113	00125	00112	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
114	00127	00113	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
115	00128	00114	6	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
116	00129	00115	11	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
117	00130	00116	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
118	00131	00117	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
119	00132	00118	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
120	00133	00119	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
121	00134	00120	24	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
122	00135	00121	81	5	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
123	00136	00122	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
124	00137	00123	10	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
125	00138	00124	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
126	00139	00125	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
127	00140	00126	13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
128	00141	00127	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
129	00142	00128	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
																																</		

Table 4

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AN	AO	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK				
130	00143	00129	5	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0			
131	00144	00130	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
132	00145	00131	2	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
133	00146	00132	8	1	2	2	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
134	00147	00133	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
135	00148	00134	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
136	00149	00135	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
137	00150	00136	17	2	0	0	0	0	0	0	1	0	0	0	0	1	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
138	00151	00137	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
139	00152	00138	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
140	00153	00139	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
141	00154	00140	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
142	00155	00141	81	1	0	3	8	0	3	0	2	2	3	4	5	1	0	15	4	1	2	0	0	0	4	7	11	0	411948	93.8	321	1	110	425	
143	00156	00142	20	2	1	0	1	0	0	0	0	0	0	0	1	1	0	1	0	0	3	0	0	0	1	0	8	0	423613	98.6	348	1	949	1296	
144	00157	00143	11	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
145	00158	00144	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
146	00159	00145	4	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
147	00160	00146	9	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
148	00161	00147	47	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
149	00162	00148	4	1	4	3	2	1	0	1	2	5	2	4	4	2	0	2	2	1	7	1	0	2	1	0	0	0	417887	98.7	312	1	149	460	
150	00163	00149	30	1	1	0	0	1	0	1	0	1	0	1	2	0	1	1	0	4	2	1	0	2	7	0	1	0	417886	95.7	305	1	210	512	
151	00164	00150	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
152	00165	00151	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
153	00166	00152	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
154	00167	00153	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
155	00168	00154	6	1	1	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
156	00169	00155	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
157	00170	00156	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
158	00171	00157	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
159	00172	00158	14	1	1	0	0	0	1	1	0	0	0	0	0	1	5	3	0	1	0	0	0	1	0	0	0	0	412623	98.7	299	1	879	1187	
160	00173	00159	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	426658	98.7	305	1	31	2490	
161	00174	00160	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
162	00175	00161	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
163	00176	00162	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	119739	98.7	293	1	36	329	
164	00177	00163	18	2	2	0	1	0	2	1	0	1	0	1	0	0	1	0	0	1	0	0	1	0	5	0	0	0	0	100295	100	295	1	1001	1634
165	00178	00164	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	BA	BC	BE	BF	BG	BH	BI	BK	
166	00179	00165	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
167	00180	00166	7	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
168	00181	00167	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
169	00182	00168	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
170	00183	00169	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
171	00184	00170	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
172	00185	00171	13	2	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
173	00186	00172	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
174	00187	00173	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
175	00188	00174	11	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
176	00189	00175	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
177	00190	00176	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
178	00191	00177	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
179	00192	00178	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
180	00193	00179	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
181	00194	00180	34	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
182	00195	00181	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
183	00196	00182	67	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
184	00197	00183	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
185	00198	00184	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
186	00199	00185	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
187	00200	00186	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
188	00201	00187	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
189	00202	00188	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
190	00203	00189	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
191	00204	00190	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
192	00205	00191	5	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
193	00206	00192	7	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
194	00207	00193	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
195	00209	00194	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
196	00210	00195	14	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
197	00211	00196	128	8	24	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
198	00212	00197	16	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
199	00213	00198	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200	00215	00199	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201	00216	00200	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 6

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK		
238	00254	00237	38	1	0	0	2	0	0	1	2	1	0	1	0	2	0	1	3	0	0	0	0	0	1	3	20	0	0	0	98.1	214	1	1152	1365
239	00255	00238	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
240	00256	00239	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
241	00257	00240	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
242	00258	00241	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
243	00259	00242	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
244	00260	00243	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
245	00261	00244	17	2	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
246	00262	00245	50	7	2	0	1	1	0	1	2	0	3	6	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
247	00263	00246	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
248	00264	00247	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
249	00265	00248	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
250	00266	00249	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
251	00267	00250	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
252	00268	00251	5	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
253	00269	00252	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
254	00270	00253	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
255	00271	00254	24	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
256	00272	00255	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
257	00273	00256	119	9	6	4	13	2	11	2	1	12	14	0	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
258	00274	00257	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
259	00275	00258	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
260	00276	00259	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
261	00277	00260	36	3	0	0	0	0	8	14	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
262	00278	00261	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
263	00279	00262	10	2	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
264	00280	00263	3	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
265	00281	00264	8	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
266	00282	00265	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
267	00283	00266	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
268	00284	00267	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
269	00285	00268	89	6	14	1	8	0	3	4	1	4	3	5	3	5	0	2	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
270	00286	00269	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
271	00287	00270	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
272	00288	00271	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
273	00289	00272	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 8

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK		
274	00290	00273	85	5	9	3	8	4	2	1	1	1	7	4	1	4	5	0	2	6	5	3	6	1	0	2	0	5	0	X66999	99.5	184	1	163	349
275	00291	00274	8	1	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	1	0	1	0	0	0	0	1	0	0	0	0	0	0	0	
276	00292	00275	49	4	12	1	0	2	1	1	4	6	4	0	0	2	0	0	5	4	0	1	0	1	0	1	0	0	M60854	100	181	1	338	538	
277	00293	00276	74	6	13	1	6	2	4	3	3	2	5	0	1	0	4	0	0	2	2	0	0	1	5	0	11	3	0	0	0	0	0	0	
278	00294	00277	5	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	
279	00295	00278	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
280	00296	00279	8	1	4	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	M86737	100	183	1	2641	2839	
281	00297	00280	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
282	00298	00281	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
283	00299	00282	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
284	00300	00283	24	2	1	0	0	2	0	1	0	0	1	2	0	3	1	4	2	0	1	1	0	0	1	0	0	0	M37104	98.3	179	1	294	471	
285	00301	00284	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
286	00302	00285	4	1	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
287	00303	00286	17	2	2	0	0	0	0	1	0	0	2	0	0	0	0	0	1	2	0	1	0	0	0	0	2	2	2	109260	96.176	1	1141	1322	
288	00304	00287	48	2	1	2	2	1	0	1	3	2	2	3	1	0	4	2	6	0	3	0	1	4	3	3	1	0	M26880	99.4	175	1	2088	2309	
289	00305	00288	46	1	6	0	2	2	3	1	2	1	4	4	2	2	0	3	0	0	1	0	0	2	1	2	0	0	0	0	0	0	0	0	
290	00306	00289	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
291	00307	00290	4	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
292	00308	00291	10	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Y00052	96.7	183	1	542	723	
293	00309	00292	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
294	00310	00293	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
295	00311	00294	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
296	00312	00295	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
297	00313	00296	17	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Y00472	96.8	63	1	767	839	
298	00314	00297	45	1	3	1	3	0	1	1	5	1	3	2	0	0	7	2	0	3	2	0	3	0	0	2	0	0	2	X06617	96.4	168	1	378	543
299	00315	00298	21	3	4	1	0	0	0	1	0	1	3	2	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
300	00316	00299	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
301	00317	00300	10	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
302	00320	00301	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
303	00322	00302	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
304	00323	00303	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
305	00325	00304	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
306	00327	00305	20	1	3	1	0	0	0	1	2	0	0	0	0	0	2	1	0	0	0	2	3	0	0	0	0	0	0	X03342	96.4	169	1	328	505
307	00328	00306	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
308	00329	00307	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
309	00330	00308	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		

Table 9

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
310	00331	00309	6	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
311	00332	00310	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
312	00333	00311	16	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
313	00334	00312	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
314	00335	00313	86	1	16	4	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
315	00336	00314	47	1	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
316	00337	00315	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
317	00338	00316	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
318	00339	00317	13	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
319	00340	00318	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
320	00341	00319	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
321	00342	00320	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
322	00343	00321	12	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
323	00344	00322	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
324	00346	00323	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
325	00347	00324	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
326	00348	00325	10	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
327	00349	00326	29	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
328	00350	00327	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
329	00351	00328	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
330	00352	00329	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
331	00353	00330	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
332	00354	00331	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
333	00355	00332	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
334	00356	00333	43	1	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
335	00357	00334	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
336	00358	00335	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
337	00359	00336	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
338	00360	00337	19	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
339	00361	00338	11	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
340	00362	00339	19	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
341	00363	00340	29	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
342	00364	00341	632	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
343	00365	00342	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
344	00366	00343	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
345	00367	00344	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 10

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A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
346	00368	00345	11	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
347	00369	00346	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
348	00370	00347	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
349	00372	00348	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
350	00373	00349	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
351	00374	00350	10	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
352	00375	00351	36	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
353	00376	00352	21	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
354	00377	00353	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
355	00378	00354	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
356	00379	00355	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
357	00380	00356	47	1	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
358	00381	00357	22	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
359	00382	00358	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
360	00383	00359	28	3	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
361	00384	00360	10	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
362	00385	00361	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
363	00386	00362	6	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
364	00387	00363	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
365	00388	00364	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
366	00389	00365	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
367	00390	00366	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
368	00391	00367	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
369	00392	00368	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
370	00393	00369	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
371	00394	00370	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
372	00395	00371	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
373	00396	00372	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
374	00397	00373	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
375	00398	00374	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
376	00399	00375	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
377	00400	00376	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
378	00401	00377	16	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
379	00402	00378	39	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
380	00403	00379	21	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
381	00404	00380	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 11

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	EA	GA	IA	KA	MA	QA	SA	TA	WA	YA	BA	BC	BE	BF	BGBH	BI	BK	
418	00442	00417	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
419	00443	00418	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
420	00444	00419	71	6	10	1	4	2	4	1	1	0	3	1	0	5	0	0	1	4	8	5	5	0	0	0	0	0	0	0	0	0	0	0
421	00445	00420	3	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
422	00446	00421	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
423	00447	00422	38	2	6	1	1	0	3	2	0	0	0	0	0	1	0	0	3	1	1	0	1	1	1	1	0	0	0	0	0	0	0	0
424	00448	00423	17	1	0	1	1	0	0	0	0	0	0	0	0	0	1	0	1	0	2	0	1	2	0	0	0	0	0	0	0	0	0	0
425	00450	00424	30	3	2	2	0	0	0	0	0	0	0	0	0	0	2	0	0	3	1	10	0	2	0	0	0	0	0	0	0	0	0	0
426	00451	00425	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
427	00453	00426	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
428	00454	00427	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
429	00455	00428	10	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
430	00456	00429	18	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
431	00457	00430	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
432	00458	00431	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
433	00459	00432	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
434	00460	00433	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
435	00461	00434	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
436	00462	00435	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
437	00463	00436	26	2	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
438	00464	00437	18	1	1	0	2	0	1	0	0	0	0	0	0	0	2	0	2	2	3	1	1	2	4	0	0	0	0	0	0	0	0	0
439	00465	00438	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
440	00466	00439	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
441	00467	00440	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
442	00468	00441	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
443	00469	00442	6	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
444	00470	00443	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
445	00471	00444	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
446	00473	00445	10	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
447	00474	00446	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
448	00475	00447	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
449	00477	00448	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
450	00478	00449	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
451	00479	00450	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
452	00480	00451	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
453	00481	00452	24	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 13

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
490	00545	00489	36	3	0	2	0	0	0	2	1	2	3	0	1	3	1	1	0	2	1	0	1	0	7	1M94314	93.4	439	1	75	556	
491	00546	00490	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
492	00547	00491	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
493	00548	00492	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
494	00549	00493	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
495	00551	00494	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
496	00552	00495	4	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
497	00553	00496	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
498	00554	00497	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
499	00555	00498	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
500	00556	00499	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
501	00557	00500	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
502	00558	00501	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
503	00560	00502	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
504	00561	00503	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
505	00562	00504	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
506	00564	00505	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
507	00565	00506	70	4	2	5	0	0	1	1	1	1	4	0	5	1	1	0	4	6	2	1	2	0	25	2M30684	96.4	415	1	519	929	
508	00567	00507	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
509	00568	00508	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
510	00569	00509	10	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
511	00571	00510	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
512	00572	00511	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
513	00573	00512	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
514	00574	00513	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
515	00575	00514	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
516	00576	00515	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
517	00577	00516	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
518	00578	00517	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
519	00579	00518	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
520	00580	00519	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
521	00581	00520	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
522	00582	00521	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
523	00583	00522	34	1	2	5	3	0	0	0	0	1	3	0	2	1	4	0	0	0	0	0	0	0	0							
524	00584	00523	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
525	00585	00524	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	EA	GA	IA	KA	MA	QA	SA	TA	WA	YA	BA	BC	BE	BF	BGBH	BI	BK		
526	00586	00525	6	1	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X07674	95.5	396	1	2559	2970
527	00589	00526	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
528	00590	00527	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
529	00591	00528	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
530	00592	00529	15	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
531	00593	00530	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
532	00594	00531	17	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
533	00595	00532	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
534	00596	00533	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
535	00597	00534	5	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
536	00598	00535	3	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
537	00599	00536	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
538	00600	00537	12	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
539	00601	00538	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
540	00602	00539	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
541	00603	00540	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
542	00604	00541	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
543	00606	00542	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
544	00607	00543	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
545	00608	00544	22	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
546	00609	00545	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
547	00610	00546	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
548	00611	00547	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
549	00612	00548	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
550	00614	00549	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
551	00615	00550	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
552	00616	00551	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
553	00617	00552	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
554	00618	00553	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
555	00619	00554	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
556	00620	00555	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
557	00621	00556	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
558	00622	00557	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
559	00623	00558	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
560	00624	00559	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
561	00625	00560	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AK	AM	AN	AO	AS	AT	AW	AY	BABC	BE	BF	BGBH	BI	BK
562	00626	00561	4		2	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
563	00627	00562	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
564	00628	00563	4		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
565	00629	00564	3		1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
566	00630	00565	3		1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
567	00631	00566	2		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
568	00632	00567	5		1	1	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0				
569	00633	00568	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
570	00634	00569	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
571	00635	00570	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
572	00636	00571	5		1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
573	00637	00572	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
574	00638	00573	3		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
575	00639	00574	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
576	00640	00575	10		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
577	00641	00576	8		2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
578	00642	00577	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
579	00643	00578	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
580	00644	00579	24		5	0	0	0	1	1	0	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
581	00645	00580	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
582	00646	00581	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
583	00647	00582	3		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
584	00648	00583	8		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
585	00649	00584	3		1	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
586	00650	00585	52		14	2	6	0	0	0	0	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
587	00651	00586	9		4	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
588	00652	00587	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
589	00653	00588	13		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
590	00654	00589	2		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
591	00656	00590	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
592	00657	00591	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
593	00658	00592	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
594	00659	00593	6		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
595	00661	00594	9		2	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
596	00662	00595	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0												

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634	00701	00633	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
635	00702	00634	2		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
636	00703	00635	17		4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.3	172	1	466	635
637	00704	00636	45		4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	217	1	506	722
638	00705	00637	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
639	00706	00638	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
640	00707	00639	10		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
641	00708	00640	32		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
642	00710	00641	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.3	209	1	887	1093
643	00711	00642	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
644	00712	00643	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
645	00713	00644	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
646	00714	00645	13		3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
647	00715	00646	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
648	00716	00647	48		5	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
649	00717	00648	6		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
650	00718	00649	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
651	00719	00650	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
652	00720	00651	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
653	00721	00652	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
654	00722	00653	11		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
655	00723	00654	10		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
656	00725	00655	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
657	00726	00656	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
658	00727	00657	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
659	00728	00658	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
660	00729	00659	7		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
661	00730	00660	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
662	00731	00661	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
663	00732	00662	47		6	3	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
664	00733	00663	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
665	00734	00664	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
666	00735	00665	11		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
667	00736	00666	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
668	00737	00667	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
669	00738	00668	6		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 19

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AN	AO	AS	AL	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
670	00739	00669	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
671	00740	00670	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
672	00741	00671	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
673	00742	00672	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
674	00743	00673	54	7	1	1	7	2	6	1	0	1	8	0	0	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
675	00745	00674	4	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
676	00746	00675	13	1	1	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
677	00747	00676	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
678	00748	00677	5	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
679	00749	00678	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
680	00750	00679	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
681	00751	00680	5	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
682	00752	00681	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
683	00753	00682	6	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
684	00754	00683	5	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
685	00755	00684	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
686	00757	00685	5	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
687	00758	00686	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
688	00759	00687	25	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
689	00760	00688	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
690	00761	00689	10	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
691	00762	00690	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
692	00763	00691	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
693	00764	00692	6	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
694	00765	00693	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
695	00766	00694	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
696	00768	00695	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
697	00769	00696	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
698	00770	00697	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
699	00771	00698	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
700	00772	00699	6	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
701	00773	00700	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
702	00774	00701	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
703	00775	00702	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
704	00777	00703	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
705	00778	00704	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 20

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
742	00816	00741	14		1	5	1	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0	1631
743	00817	00742	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1507
744	00818	00743	20		4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
745	00819	00744	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
746	00820	00745	18		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
747	00821	00746	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
748	00822	00747	3		1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
749	00823	00748	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
750	00824	00749	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
751	00825	00750	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
752	00826	00751	6		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
753	00827	00752	10		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
754	00828	00753	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
755	00829	00754	3		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
756	00830	00755	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
757	00831	00756	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
758	00832	00757	6		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
759	00833	00758	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
760	00834	00759	13		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
761	00835	00760	8		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
762	00836	00761	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
763	00837	00762	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
764	00838	00763	7		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
765	00840	00764	8		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
766	00841	00765	10		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
767	00842	00766	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
768	00843	00767	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
769	00844	00768	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
770	00845	00769	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
771	00846	00770	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
772	00847	00771	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
773	00848	00772	12		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
774	00849	00773	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
775	00850	00774	12		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
776	00851	00775	14		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
777	00852	00776	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 22

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
778	00853	00777	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	702		
779	00854	00778	8	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	591		
780	00855	00779	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
781	00856	00780	4	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
782	00857	00781	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
783	00858	00782	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
784	00859	00783	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
785	00860	00784	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
786	00861	00785	34	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
787	00862	00786	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
788	00863	00787	5	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
789	00864	00788	5	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
790	00865	00789	56	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
791	00866	00790	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
792	00867	00791	8	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
793	00868	00792	5	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
794	00869	00793	5	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
795	00870	00794	4	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
796	00871	00795	5	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
797	00872	00796	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
798	00873	00797	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
799	00874	00798	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
800	00875	00799	21	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
801	00876	00800	9	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
802	00877	00801	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
803	00878	00802	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
804	00879	00803	5	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
805	00880	00804	5	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
806	00882	00805	20	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
807	00883	00806	5	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
808	00884	00807	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
809	00885	00808	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
810	00886	00809	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
811	00887	00810	14	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
812	00889	00811	17	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
813	00890	00812	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			

Table 23

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AI	AK	AM	AN	AO	AP	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
814	00891	00813	5		1	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
815	00892	00814	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
816	00894	00815	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
817	00895	00816	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
818	00896	00817	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
819	00897	00818	10		2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
820	00898	00819	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
821	00900	00820	27		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
822	00903	00821	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
823	00904	00822	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
824	00905	00823	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
825	00906	00824	2		2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
826	00908	00825	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
827	00910	00826	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
828	00911	00827	9		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
829	00912	00828	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
830	00913	00829	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
831	00914	00830	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
832	00915	00831	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
833	00917	00832	45		3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
834	00918	00833	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
835	00919	00834	7		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
836	00920	00835	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
837	00922	00836	9		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
838	00924	00837	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
839	00925	00838	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
840	00926	00839	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
841	00929	00840	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
842	00930	00841	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
843	00931	00842	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
844	00932	00843	16		3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
845	00934	00844	34		3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
846	00935	00845	6		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
847	00936	00846	8		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
848	00937	00847	62		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
849	00938	00848	8		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 24

Table 25

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
922	01048	00921	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	1	0	0	96.9	382	1	708	1089	
923	01049	00922	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
924	01051	00923	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
925	01052	00924	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
926	01053	00925	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.3	380	24	3711	4221	
927	01054	00926	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
928	01055	00927	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
929	01057	00928	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
930	01061	00929	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
931	01062	00930	8		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
932	01063	00931	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
933	01064	00932	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
934	01065	00933	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
935	01066	00934	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
936	01067	00935	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
937	01068	00936	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
938	01069	00937	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
939	01070	00938	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
940	01071	00939	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
941	01072	00940	8		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
942	01073	00941	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
943	01074	00942	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
944	01075	00943	10		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
945	01076	00944	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
946	01077	00945	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
947	01078	00946	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
948	01079	00947	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
949	01080	00948	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
950	01081	00949	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
951	01082	00950	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
952	01083	00951	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
953	01084	00952	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
954	01085	00953	6		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
955	01086	00954	8		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
956	01087	00955	18		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
957	01088	00956	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 27

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AO	AS	AL	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
994	01130	00993	4																															
995	01131	00994	1																															
996	01132	00995	3																															
997	01133	00996	1																															
998	01134	00997	3																															
999	01135	00998	1																															
1000	01136	00999	1																															
1001	01137	01000	1																															
1002	01138	01001	6																															
1003	01139	01002	3																															
1004	01140	01003	5																															
1005	01141	01004	18																															
1006	01142	01005	1																															
1007	01143	01006	3																															
1008	01144	01007	1																															
1009	01145	01008	7																															
1010	01147	01009	1																															
1011	01148	01010	1																															
1012	01149	01011	2																															
1013	01150	01012	6																															
1014	01151	01013	4																															
1015	01152	01014	1																															
1016	01153	01015	3																															
1017	01154	01016	17																															
1018	01155	01017	3																															
1019	01156	01018	2																															
1020	01157	01019	9																															
1021	01158	01020	2																															
1022	01159	01021	1																															
1023	01160	01022	1																															
1024	01161	01023	2																															
1025	01162	01024	1																															
1026	01163	01025	16																															
1027	01164	01026	2																															
1028	01165	01027	3																															
1029	01167	01028	2																															

Table 29

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AN	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
1030	01168	01029	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1031	01169	01030	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1032	01170	01031	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1033	01171	01032	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1034	01172	01033	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1035	01173	01034	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1036	01174	01035	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1037	01175	01036	14		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1038	01176	01037	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1039	01177	01038	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1040	01178	01039	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1041	01179	01040	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1042	01180	01041	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1043	01181	01042	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1044	01182	01043	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1045	01183	01044	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1046	01184	01045	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1047	01186	01046	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1048	01187	01047	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1049	01188	01048	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1050	01189	01049	13		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1051	01191	01050	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1052	01192	01051	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1053	01193	01052	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1054	01194	01053	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1055	01195	01054	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1056	01196	01055	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1057	01197	01056	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1058	01198	01057	10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1059	01199	01058	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1060	01200	01059	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1061	01201	01060	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1062	01202	01061	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1063	01203	01062	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1064	01204	01063	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1065	01205	01064	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 30

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AE	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
1066	01207	01065	5		0	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1067	01208	01066	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1068	01209	01067	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1069	01210	01068	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1070	01211	01069	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1071	01212	01070	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1072	01213	01071	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1073	01214	01072	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1074	01215	01073	15		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1075	01216	01074	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1076	01217	01075	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1077	01218	01076	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1078	01219	01077	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1079	01220	01078	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1080	01221	01079	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1081	01222	01080	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1082	01223	01081	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1083	01224	01082	10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1084	01225	01083	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1084	01226	01084	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1085	01227	01085	15		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1087	01228	01086	12		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1088	01229	01087	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1089	01230	01088	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1090	01231	01089	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1091	01232	01090	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1092	01233	01091	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1093	01235	01092	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1094	01236	01093	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1095	01237	01094	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1096	01238	01095	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1097	01239	01096	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1098	01240	01097	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1099	01241	01098	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1100	01242	01099	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1101	01243	01100	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 31

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
1102	01244	01101	25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1103	01245	01102	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1104	01246	01103	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1105	01247	01104	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1106	01248	01105	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1107	01249	01106	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1108	01250	01107	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1109	01251	01108	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1110	01252	01109	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1111	01253	01110	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1112	01254	01111	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1113	01256	01112	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1114	01257	01113	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1115	01258	01114	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1116	01259	01115	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1117	01260	01116	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1118	01261	01117	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1119	01262	01118	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1120	01263	01119	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1121	01264	01120	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1122	01265	01121	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1123	01266	01122	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1124	01267	01123	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1125	01268	01124	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1126	01269	01125	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1127	01270	01126	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1128	01272	01127	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1129	01273	01128	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1130	01274	01129	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1131	01276	01130	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1132	01277	01131	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1133	01278	01132	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1134	01279	01133	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1135	01280	01134	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1136	01281	01135	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1137	01282	01136	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 32

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1138	01283	01137	9		0	2	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1139	01284	01138	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1140	01285	01139	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1141	01286	01140	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1142	01287	01141	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1143	01288	01142	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1144	01289	01143	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1145	01290	01144	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1146	01291	01145	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1147	01292	01146	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1148	01293	01147	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1149	01294	01148	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1150	01295	01149	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1151	01296	01150	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1152	01297	01151	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1153	01298	01152	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1154	01299	01153	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1155	01300	01154	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1156	01301	01155	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1157	01302	01156	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1158	01303	01157	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1159	01304	01158	10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1160	01305	01159	28		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1161	01306	01160	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1162	01307	01161	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1163	01308	01162	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1164	01309	01163	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1165	01310	01164	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1166	01311	01165	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1167	01312	01166	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1168	01313	01167	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1169	01314	01168	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1170	01315	01169	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1171	01316	01170	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1172	01317	01171	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1173	01318	01172	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 33

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1210	01355	01209	2			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1211	01356	01210	2			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1212	01357	01211	1			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1213	01358	01212	1			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1214	01359	01213	2			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1215	01360	01214	1			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1216	01361	01215	1			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1217	01362	01216	1			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1218	01363	01217	1			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1219	01364	01218	1			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1220	01365	01219	4			0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1221	01366	01220	1			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1222	01367	01221	21			0	3	1	0	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1223	01368	01222	1			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1224	01369	01223	5			0	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1225	01370	01224	1			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1226	01371	01225	5			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1227	01372	01226	7			0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1228	01373	01227	2			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1229	01374	01228	1			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1230	01375	01229	2			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1231	01377	01230	3			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1232	01378	01231	5			0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1233	01379	01232	1			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1234	01380	01233	1			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1235	01381	01234	1			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1236	01382	01235	5			0	1	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1237	01383	01236	3			0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1238	01384	01237	16			0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1239	01385	01238	1			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1240	01386	01239	3			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1241	01387	01240	1			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1242	01388	01241	3			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1243	01389	01242	1			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1244	01390	01243	5			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1245	01391	01244	2			0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 35

A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AK	AM	AO	AS	AW	AY	B	BE	BF	BG	BH	BI	BK
1246	01392	01245	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0X03342	90.7	161	1	67	505	
1247	01393	01246	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	---	---	---	---	---	
1248	01394	01247	12	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	---	---	---	---	---	
1249	01395	01248	7	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Z17227	100	152	1	1724	1875	
1250	01396	01249	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	---	---	---	---	---	
1251	01397	01250	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	---	---	---	---	---	
1252	01398	01251	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	---	---	---	---	---	
1253	01400	01252	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	---	---	---	---	---	
1254	01401	01253	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	---	---	---	---	---	
1255	01402	01254	7	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	---	---	---	---	---	
1256	01403	01255	6	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	---	---	---	---	---	
1257	01404	01256	16	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	---	---	---	---	---	
1258	01405	01257	4	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	---	---	---	---	---	
1259	01406	01258	7	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	---	---	---	---	---	
1260	01407	01259	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	---	---	---	---	---	
1261	01408	01260	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	---	---	---	---	---	
1262	01409	01261	5	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	---	---	---	---	---	
1263	01410	01262	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	---	---	---	---	---	
1264	01411	01263	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	---	---	---	---	---	
1265	01412	01264	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	---	---	---	---	---	
1266	01413	01265	0																											

Table 36

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	BA	GA	IA	KA	MA	QA	SA	LA	WA	YA	BA	BF	BG	BI	BK
1282	01430	01281	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.3	144	1	1470	1612
1283	01431	01282	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1284	01432	01283	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1285	01433	01284	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1286	01434	01285	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1287	01435	01286	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1288	01436	01287	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1289	01437	01288	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1290	01438	01289	3		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1291	01439	01290	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1292	01440	01291	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1293	01441	01292	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1294	01442	01293	4		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1295	01443	01294	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1296	01444	01295	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1297	01445	01296	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1298	01446	01297	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1299	01447	01298	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1300	01448	01299	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1301	01449	01300	10		0	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1302	01450	01301	4		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1303	01451	01302	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1304	01452	01303	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1305	01453	01304	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1306	01454	01305	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1307	01455	01306	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1308	01456	01307	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1309	01457	01308	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1310	01458	01309	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1311	01459	01310	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1312	01460	01311	2		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1313	01461	01312	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1314	01462	01313	6		0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1315	01463	01314	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1316	01464	01315	1		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1317	01466	01316	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 37

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK	
1318	01467	01317	4	0	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
1319	01468	01318	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
1320	01469	01319	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
1321	01470	01320	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
1322	01471	01321	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
1323	01472	01322	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
1324	01473	01323	9	0	2	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1325	01474	01324	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1326	01475	01325	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1327	01476	01326	19	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1328	01477	01327	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1329	01478	01328	5	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1330	01479	01329	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1331	01481	01330	3	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1332	01482	01331	2	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1333	01483	01332	9	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1334	01484	01333	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1335	01485	01334	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1336	01486	01335	3	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1337	01487	01336	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1338	01488	01337	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1339	01489	01338	5	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1340	01490	01339	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1341	01491	01340	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1342	01492	01341	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1343	01493	01342	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1344	01494	01343	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1345	01495	01344	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1346	01496	01345	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1347	01497	01346	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1348	01498	01347	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1349	01499	01348	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1350	01500	01349	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1351	01501	01350	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1352	01502	01351	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1353	01503	01352	9	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 38

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AO	AS	AW	B	BC	DE	BF	BG	BH	BI	BK
1354	01505	01353	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1355	01506	01354	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1356	01507	01355	5		0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	98.3	406	1	1923	2327	
1357	01508	01356	13		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	99.1	112	1	1617	1760	
1358	01509	01357	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1359	01510	01358	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1360	01511	01359	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1361	01512	01360	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1362	01513	01361	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1363	01514	01362	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1364	01515	01363	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1365	01516	01364	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.6	110	1	3448	4221	
1366	01517	01365	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1367	01518	01366	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1368	01519	01367	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1369	01520	01368	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1370	01521	01369	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1371	01522	01370	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1372	01523	01371	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1373	01524	01372	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.5	231	62	1	229	
1374	01525	01373	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1375	01526	01374	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1376	01527	01375	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1377	01528	01376	16		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1378	01529	01377	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1379	01530	01378	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1380	01531	01379	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1381	01532	01380	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1382	01533	01381	19		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.1	105	1	2333	2455	
1383	01534	01382	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1384	01535	01383	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1385	01537	01384	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1386	01538	01385	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1387	01539	01386	12		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1388	01540	01387	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1389	01541	01388	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 39

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AV	AW	AY	BABC	BE	BF	BG	BH	BI	BK
1390	01542	01389	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	006814	90.1	101	1	552	702	
1391	01543	01390	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1392	01544	01391	4		0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1393	01545	01392	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1394	01546	01393	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1395	01547	01394	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1396	01548	01395	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1397	01549	01396	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1398	01550	01397	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1399	01551	01398	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1400	01552	01399	10		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1401	01553	01400	5		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1402	01554	01401	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1403	01555	01402	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1404	01556	01403	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1405	01557	01404	5		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1406	01558	01405	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1407	01560	01406	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1408	01561	01407	2		0	0</																											

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	BA	GA	IA	KA	MA	QA	SA	LA	WA	YA	B	BC	BE	BF	BG	BH	BI	BK
1426	01579	01425	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1427	01580	01426	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1428	01581	01427	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1429	01582	01428	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1430	01583	01429	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1431	01584	01430	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1432	01585	01431	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1433	01586	01432	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1434	01587	01433	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1435	01588	01434	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1436	01589	01435	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1437	01590	01436	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1438	01591	01437	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1439	01592	01438	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1440	01593	01439	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1441	01594	01440	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1442	01595	01441	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1443	01596	01442	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1444	01597	01443	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1445	01598	01444	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1446	01599	01445	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1447	01600	01446	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1448	01601	01447	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1449	01602	01448	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1450	01603	01449	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1451	01604	01450	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1452	01605	01451	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1453	01606	01452	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1454	01607	01453	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1455	01608	01454	23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1456	01609	01455	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1457	01610	01456	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1458	01611	01457	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1459	01612	01458	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1460	01613	01459	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1461	01615	01460	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 41

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A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK		
1462	01616	01461	32	0	1	3	1	0	0	0	0	0	0	3	0	0	1	0	5	11	0	2	1	0	0	1	0	3	103558	98.2	55	1	588	642
1463	01617	01462	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1464	01618	01463	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1465	01619	01464	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1466	01620	01465	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1467	01621	01466	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1468	01622	01467	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1469	01623	01468	5	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1470	01624	01469	8	0	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1471	01625	01470	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1472	01626	01471	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1473	01627	01472	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1474	01628	01473	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1475	01629	01474	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1476	01630	01475	9	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1477	01632	01476	11	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1478	01633	01477	7	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1479	01642	01478	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1480	01671	01479	35	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1481	01673	01480	6	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1482	01686	01481	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1483	01687	01482	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1484	01688	01483	6	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1485	01689	01484	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1486	01691	01485	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1487	01692	01486	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1488	01693	01487	5	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1489	01694	01488	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1490	01695	01489	11	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1491	01696	01490	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1492	01697	01491	4	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1493	01698	01492	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1494	01699	01493	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1495	01700	01494	9	0	0	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1496	01701	01495	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1497	01702	01496	4	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 42

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1534	01746	01533	1				1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1535	01747	01534	1				1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1536	01748	01535	1				1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1537	01749	01536	2				2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1538	01750	01537	2				2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1539	01751	01538	1				1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1540	01752	01539	4				4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1541	01753	01540	1				1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1542	01754	01541	2				2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1543	01755	01542	2				2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1544	01756	01543	3				3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1545	01758	01544	1				1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1546	01759	01545	7				7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1547	01760	01546	3				3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1548	01761	01547	1				1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1549	01763	01548	1				1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1550	01764	01549	1				1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1551	01765	01550	1				1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1552	01766	01551	63				63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1553	01767	01552	3				3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1554	01768	01553	3				3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1555	01769	01554	1				1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1556	01770	01555	5				5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1557	01771	01556	1				1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1558	01772	01557	1				1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1559	01773	01558	2				2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1560	01774	01559	1				1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1561	01775	01560	2				2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1562	01776	01561	2				2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1563	01777	01562	3				3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1564	01778	01563	2				2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1565	01779	01564	1				1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1566	01780	01565	1				1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1567	01781	01566	1				1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1568	01782	01567	1				1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1569	01783	01568	3				3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 44

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1570	01784	01569	2										1																				
1571	01785	01570	1										0																				
1572	01786	01571	8										0																				
1573	01787	01572	1										0																				
1574	01788	01573	3										0																				
1575	01789	01574	1										0																				
1576	01790	01575	3										0																				
1577	01791	01576	34										0																				
1578	01792	01577	1										0																				
1579	01793	01578	1										0																				
1580	01794	01579	6										0																				
1581	01795	01580	1										0																				
1582	01796	01581	7										0																				
1583	01797	01582	1										0																				
1584	01798	01583	1										0																				
1585	01799	01584	2										0																				
1586	01800	01585	2										0																				
1587	01801	01586	2										0																				
1588	01802	01587	1										0																				
1589	01803	01588	4										0																				
1590	01804	01589	1										0																				
1591	01805	01590	1										0																				
1592	01806	01591	26										0																				
1593	01807	01592	1										0																				
1594	01808	01593	47										0																				
1595	01809	01594	19										0																				
1596	01810	01595	2										0																				
1597	01811	01596	39										0																				
1598	01812	01597	2										0																				
1599	01813	01598	3										0																				
1600	01814	01599	1										0																				
1601	01815	01600	1										0																				
1602	01816	01601	1										0																				
1603	01817	01602	1										0																				
1604	01818	01603	3										0																				
1605	01819	01604	6										0																				

Table 45

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1678	01893	01677	1																														
1679	01895	01678	7																														
1680	01896	01679	2																														
1681	01897	01680	1																														
1682	01898	01681	1																														
1683	01899	01682	14																														
1684	01900	01683	1																														
1685	01901	01684	1																														
1686	01902	01685	2																														
1687	01903	01686	2																														
1688	01904	01687	3																														
1689	01905	01688	3																														
1690	01906	01689	3																														
1691	01907	01690	1																														
1692	01908	01691	21																														
1693	01909	01692	4																														
1694	01910	01693	1																														
1695	01911	01694	10																														
1696	01912	01695	5																														
1697	01913	01696	2																														
1698	01914	01697	3																														
1699	01915	01698	1																														
1700	01916	01699	3																														
1701	01917	01700	1																														
1702	01918	01701	2																														
1703	01919	01702	111																														
1704	01920	01703	1																														
1705	01921	01704	1																														
1706	01922	01705	3																														
1707	01923	01706	2																														
1708	01924	01707	3																														
1709	01925	01708	1																														
1710	01926	01709	24																														
1711	01927	01710	3																														
1712	01928	01711	10																														
1713	01929	01712	19																														

Table 48

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	A	C	A	E	A	K	A	M	A	C	A	S	A	L	A	W	A	B	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ	BA	BB	BC	BD	BE	BF	BG	BH	BI	BJ	BK	BL	BM	BN	BO	BP	BQ	BR	BS	BT	BU	BV	BW	BX	BY	BZ	CA	CB	CC	CD	CE	CF	CG	CH	CI	CJ	CK	CL	CM	CN	CO	CP	CQ	CR	CS	CT	CU	CV	CW	CX	CY	CZ	DA	DB	DC	DD	DE	DF	DG	DH	DI	DJ	DK	DL	DM	DN	DO	DP	DQ	DR	DS	DT	DU	DV	DW	DX	DY	DZ	EA	EB	EC	ED	EE	EF	EG	EH	EI	EJ	EK	EL	EM	EN	EO	EP	EQ	ER	ES	ET	EU	EV	EW	EX	EY	EZ	FA	FB	FC	FD	FE	FF	FG	FH	FI	FJ	FK	FL	FM	FN	FO	FP	FQ	FR	FS	FT	FU	FV	FW	FX	FY	FZ	GA	GB	GC	GD	GE	GF	GG	GH	GI	GJ	GK	GL	GM	GN	GO	GP	GQ	GR	GS	GT	GU	GV	GW	GX	GY	GZ	HA	HB	HC	HD	HE	HF	HG	HH	HI	HJ	HK	HL	HM	HN	HO	HP	HQ	HR	HS	HT	HU	HV	HW	HX	HY	HZ	IA	IB	IC	ID	IE	IF	IG	IH	II	IJ	IK	IL	IM	IN	IO	IP	IQ	IR	IS	IT	IU	IV	IW	IX	IY	IZ	JA	JB	JC	JD	JE	JF	JG	JH	JI	IJ	JK	KL	KM	KN	KO	KP	KQ	KR	KS	KT	KU	KV	KW	KX	KY	KZ	LA	LB	LC	LD	LE	LF	LG	LH	LI	LJ	LK	LL	LM	LN	LO	LP	LQ	LR	LS	LT	LU	LV	LW	LX	LY	LZ	MA	MB	MC	MD	ME	MF	MG	MH	MI	MJ	MK	ML	MM	MN	MO	MP	MQ	MR	MS	MT	MU	MV	MW	MX	MY	MZ	NA	NB	NC	ND	NE	NF	NG	NH	NI	NJ	NK	NL	NM	NN	NO	NP	NQ	NR	NS	NT	NU	NV	NW	NX	NY	NZ	OA	OB	OC	OD	OE	OF	OG	OH	OI	OJ	OK	OL	OM	ON	OO	OP	OQ	OR	OS	OT	OU	OV	OW	OX	OY	OZ	PA	PB	PC	PD	PE	PF	PG	PH	PI	PJ	PK	PL	PM	PN	PO	PP	PQ	PR	PS	PT	PU	PV	PW	PX	PY	PZ	QA	QB	QC	QD	QE	QF	QG	QH	QI	QJ	QK	QL	QM	QN	QO	QP	QQ	QR	QS	QT	QU	QV	QW	QX	QY	QZ	RA	RB	RC	RD	RE	RF	RG	RH	RI	RJ	RK	RL	RM	RN	RO	RP	RQ	RR	RS	RT	RU	RV	RW	RX	RY	RZ	SA	SB	SC	SD	SE	SF	SG	SH	SI	SJ	SK	SL	SM	SN	SO	SP	SQ	SR	SS	ST	SU	SV	SW	SX	SY	SZ	TA	TB	TC	TD	TE	TF	TG	TH	TI	TJ	TK	TL	TM	TN	TO	TP	TQ	TR	TS	TT	TU	TV	TW	TX	TY	TZ	UA	UB	UC	UD	UE	UF	UG	UH	UI	UJ	UK	UL	UM	UN	UO	UP	UQ	UR	US	UT	UU	UV	UW	UX	UY	UZ	VA	VB	VC	VD	VE	VF	VG	VH	VI	VJ	VK	VL	VM	VN	VO	VP	VQ	VR	VS	VT	VU	VV	VW	VX	VY	VZ	WA	WB	WC	WD	WE	WF	WG	WH	WI	WJ	WK	WL	WM	WN	WO	WP	WQ	WR	WS	WT	WU	WV	WW	WX	WY	WZ	XA	XB	XC	XD	XE	XF	YG	YH	YI	YJ	YK	YL	YM	YN	YO	YP	YQ	YR	YS	YT	YU	YV	YW	YX	YY	YZ	ZA	ZB	ZC	ZD	ZE	ZF	ZG	ZH	ZI	ZJ	ZK	ZL	ZM	ZN	ZO	ZP	ZQ	ZR	ZS	ZT	ZU	ZV	ZW	ZX	ZY	ZZ	AA	AB
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[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	BAB	BC	BE	BF	BGBH	BI	BK
2002	02281	02001	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2003	02282	02002	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2004	02283	02003	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2005	02285	02004	10		0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2006	02287	02005	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2007	02288	02006	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2008	02289	02007	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2009	02290	02008	16		0	0	0	0	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2010	02291	02009	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2011	02292	02010	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2012	02293	02011	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2013	02294	02012	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2014	02295	02013	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2015	02296	02014	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2016	02297	02015	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2017	02298	02016	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2018	02299	02017	4		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2019	02300	02018	3		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2020	02301	02019	1		0	0	0	0	1	0	0	0	0																					

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AE	AF	AG	AH	AI	AK	AM	AN	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2218	02528	02217	2		0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2219	02529	02218	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2220	02531	02219	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
2221	02532	02220	3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2222	02534	02221	5		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	0						
2223	02535	02222	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2224	02537	02223	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2225	02538	02224	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2226	02540	02225	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2227	02542	02226	33		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2228	02543	02227	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2229	02544	02228	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2230	02545	02229	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2231	02546	02230	19		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2232	02547	02231	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2233	02548	02232	8		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2234	02549	02233	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2235	02551</																																				

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	CA	IA	KA	MA	QA	SA	TA	WA	YA	BA	BC	BE	BF	BG	BI	BK
2254	02573	02253	1																														
2255	02574	02254	2																														
2256	02575	02255	3																														
2257	02576	02256	2																														
2258	02577	02257	3																														
2259	02578	02258	1																														
2260	02580	02259	1																														
2261	02581	02260	4																														
2262	02582	02261	5																														
2263	02583	02262	2																														
2264	02585	02263	3																														
2265	02586	02264	5																														
2266	02588	02265	1																														
2267	02589	02266	2																														
2268	02590	02267	1																														
2269	02591	02268	2																														
2270	02592	02269	1																														
2271	02593	02270	2																														
2272	02612	02271	3																														
2273	02627	02272	1																														
2274	02628	02273	1																														
2275	02629	02274	1																														
2276	02630	02275	1																														
2277	02631	02276	1																														
2278	02632	02277	1																														
2279	02633	02278	1																														
2280	02634	02279	1																														
2281	02635	02280	5																														
2282	02637	02281	1																														
2283	02638	02282	3																														
2284	02639	02283	1																														
2285	02640	02284	9																														
2286	02641	02285	4																														
2287	02642	02286	3																														
2288	02643	02287	4																														
2289	02644	02288	1																														

Table 64

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AO	AS	AL	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2290	02645	02289	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2291	02646	02290	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2292	02648	02291	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2293	02650	02292	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2294	02651	02293	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2295	02652	02294	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2296	02653	02295	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2297	02654	02296	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2298	02656	02297	20		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2299	02657	02298	1		0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2300	02658	02299	6		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2301	02659	02300	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2302	02660	02301	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2303	02661	02302	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2304	02662	02303	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2305	02663	02304	4		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2306	02664	02305	5		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2307	02665	02306	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2308	02666	02307	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2309	02667	02308	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2310	02668	02309	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2311	02669	02310	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2312	02670	02311	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2313	02672	02312	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2314	02673	02313	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2315	02675	02314	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2316	02676	02315	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2317	02677	02316	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2318	02678	02317	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2319	02679	02318	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2320	02680	02319	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2321	02681	02320	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2322	02682	02321	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2323	02684	02322	13		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2324	02685	02323	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2325	02686	02324	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 65

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2362	02724	02361	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2363	02725	02362	2		0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2364	02727	02363	2		0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2365	02728	02364	6		0	0	0	0	0	0	3	0	1	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
2366	02729	02365	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2367	02730	02366	5		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2368	02731	02367	7		0	0	0	0	0	0	0	0	0	0	1	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2369	02732	02368	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2370	02733	02369	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2371	02734	02370	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2372	02735	02371	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2373	02736	02372	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2374	02737	02373	2		0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2375	02738	02374	5		0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2376	02739	02375	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2377	02740	02376	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2378	02741	02377	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2379	02742	02378	1		0	0	0	0	0</																									

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	CA	CAC	CA	AS	AL	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2398	02765	02397	1																																	
2399	02767	02398	9																																	
2400	02768	02399	5																																	
2401	02769	02400	7																																	
2402	02770	02401	3																																	
2403	02771	02402	2																																	
2404	02772	02403	2																																	
2405	02773	02404	2																																	
2406	02774	02405	3																																	
2407	02775	02406	1																																	
2408	02776	02407	2																																	
2409	02777	02408	1																																	
2410	02778	02409	1																																	
2411	02779	02410	1																																	
2412	02780	02411	1																																	
2413	02781	02412	1																																	
2414	02782	02413	3																																	
2415	02783	02414	5																																	
2416	02785	02415	2																																	
2417	02786	02416	2																																	
2418	02787	02417	1																																	
2419	02788	02418	1																																	
2420	02789	02419	3																																	
2421	02790	02420	1																																	
2422	02791	02421	3																																	
2423	02792	02422	4																																	
2424	02793	02423	9																																	
2425	02794	02424	1																																	
2426	02795	02425	7																																	
2427	02796	02426	5																																	
2428	02797	02427	3																																	
2429	02798	02428	1																																	
2430	02799	02429	3																																	
2431	02800	02430	1													</																				

Table 68

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK
2434	02803	02433	2								1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2435	02804	02434	5								2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2436	02805	02435	4								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2437	02806	02436	1								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2438	02807	02437	2								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2439	02808	02438	1								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2440	02809	02439	1								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2441	02810	02440	2								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2442	02811	02441	4								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2443	02812	02442	12								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2444	02813	02443	5								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2445	02814	02444	15								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2446	02815	02445	4								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2447	02816	02446	2								2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2448	02817	02447	2								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2449	02818	02448	5								2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2450	02819	02449	1								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2451	02820	02450	29								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2452	02821	02451	22								2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2453	02822	02452	1								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2454	02823	02453	5								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2455	02824	02454	2								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2456	02825	02455	1								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2457	02826	02456	1								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2458	02827	02457	1								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2459	02828	02458	1								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2460	02829	02459	1								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2461	02830	02460	1								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2462	02831	02461	3								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2463	02832	02462	2								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2464	02833	02463	7								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2465	02834	02464	1								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2466	02835	02465	4								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2467	02836	02466	3								3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2468	02837	02467	1								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2469	02838	02468	1								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 69

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AS	AW	AY	BAB	BC	BE	BF	BG	BH	BI	BK	
2650	03086	02649	5		0	0	0	0	0	0	0	1	0	3	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
2651	03087	02650	8		0	0	0	0	0	0	0	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	394	1			691	
2652	03088	02651	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2653	03089	02652	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2654	03090	02653	8		0	0	0	0	0	0	0	1	0	0	2	0	0	0	0	3	0	1	0	0	0	0	0	0	0					
2655	03091	02654	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2656	03092	02655	4		0	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0						
2657	03094	02656	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2658	03095	02657	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.1	279	1	159	1187	
2659	03096	02658	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2660	03097	02659	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2661	03098	02660	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
2662	03099	02661	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2663	03100	02662	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91	266	7	7860	8201	
2664	03101	02663	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2665	03102	02664	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2666	03103	02665	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2667	03104	02666	3		0	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2668	03105	02667	15		0	0	0	0	0	0	2																							

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2794	03257	02793	1										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2795	03258	02794	2										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2796	03259	02795	10										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2797	03261	02796	2										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2798	03263	02797	5										2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2799	03264	02798	1										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2800	03267	02799	3										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2801	03268	02800	5										3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2802	03271	02801	3										2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2803	03274	02802	7										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2804	03279	02803	8										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2805	03281	02804	2										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2806	03282	02805	2										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2807	03283	02806	1										2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2808	03284	02807	2										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2809	03286	02808	1										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2810	03289	02809	1										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2811	03294	02810	5										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2812	03296	02811	1										2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2813	03297	02812	4										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2814	03299	02813	1										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2815	03300	02814	1										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2816	03304	02815	1										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2817	03305	02816	15										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2818	03306	02817	2										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2819	03307	02818	1										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2820	03308	02819	2										2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2821	03310	02820	7										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2822	03311	02821	3										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2823	03312	02822	4										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2824	03313	02823	1										2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2825	03315	02824	1										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2826	03318	02825	1										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2827	03319	02826	1										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2828	03324	02827	2										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2829	03325	02828	1										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 79

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AN	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2830	03326	02829	1									1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2831	03331	02830	24									1	10	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2832	03332	02831	6									1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2833	03356	02832	2									1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2834	03374	02833	1									1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2835	03375	02834	1									1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2836	03376	02835	2									1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2837	03377	02836	4									1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2838	03378	02837	1									1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2839	03379	02838	3									1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2840	03380	02839	1									1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2841	03381	02840	3									2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2842	03382	02841	3									1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2843	03383	02842	1									1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2844	03384	02843	3									1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2845	03385	02844	1									1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2846	03386	02845	2									2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2847	03387	02846	1									1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2848	03388	02847	3									2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2849	03389	02848	1									1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2850	03390	02849	1			</																										

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK
3010	03552	03009	4																													
3011	03553	03010	2																													
3012	03554	03011	5																													
3013	03555	03012	1																													
3014	03556	03013	1																													
3015	03557	03014	1																													
3016	03558	03015	5																													
3017	03559	03016	1																													
3018	03560	03017	4																													
3019	03561	03018	1																													
3020	03562	03019	1																													
3021	03563	03020	1																													
3022	03564	03021	11																													
3023	03565	03022	1																													
3024	03566	03023	1																													
3025	03567	03024	3																													
3026	03568	03025	2																													
3027	03569	03026	1																													
3028	03570	03027	4																													
3029	03571	03028	1																													
3030	03572	03029	3																													
3031	03573	03030	9																													
3032	03574	03031	1																													
3033	03575	03032	17																													
3034	03576	03033	3																													
3035	03577	03034	5																													
3036	03578	03035	3																													
3037	03579	03036	1																													
3038	03580	03037	3																													
3039	03581	03038	1																													
3040	03582	03039	6																													
3041	03583	03040	4																													
3042	03584	03041	1																													
3043	03585	03042	1																													
3044	03586	03043	1																													
3045	03587	03044	2																													

Table 85

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Table 86

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AN	AO	AS	AW	AY	B	BC	DE	DF	BG	BH	BI	BK
3082	03625	03081	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3083	03626	03082	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3084	03627	03083	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3085	03628	03084	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3086	03629	03085	9		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3087	03631	03086	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3088	03632	03087	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3089	03633	03088	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3090	03634	03089	8		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3091	03635	03090	3		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3092	03636	03091	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3093	03637	03092	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3094	03638	03093	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3095	03639	03094	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3096	03640	03095	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3097	03641	03096	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3098	03642	03097	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3099	03643	03098	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3100	03644	03099	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3101	03645	03100	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3102	03646	03101	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3103	03647	03102	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3104	03648	03103	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3105	03649	03104	8		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3106	03650	03105	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3107	03651	03106	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3108	03652	03107	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3109	03653	03108	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3110	03654	03109	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3111	03655	03110	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3112	03659	03111	6		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3113	03661	03112	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3114	03679	03113	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3115	03680	03114	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3116	03681	03115	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3117	03682	03116	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 87

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AL	AW	AY	BA	BC	BE	BF	BG	BI	BK
3118	03683	03117	1																														
3119	03684	03118	2																														
3120	03685	03119	1																														
3121	03686	03120	1																														
3122	03688	03121	1																														
3123	03689	03122	5																														
3124	03690	03123	4																														
3125	03691	03124	3																														
3126	03693	03125	1																														
3127	03694	03126	10																														
3128	03695	03127	1																														
3129	03696	03128	1																														
3130	03697	03129	1																														
3131	03698	03130	13																														
3132	03699	03131	1																														
3133	03701	03132	1																														
3134	03702	03133	1																														
3135	03703	03134	2																														
3136	03704	03135	3																														
3137	03705	03136	3																														
3138	03707	03137	3																														
3139	03708	03138	4																														
3140	03709	03139	2																														
3141	03710	03140	4																														
3142	03711	03141	1																														
3143	03712	03142	3																														
3144	03713	03143	1																														
3145	03714	03144	2																														
3146	03715	03145	3																														
3147	03716	03146	4																														
3148	03717	03147	5																														
3149	03718	03148	1																														
3150	03719	03149	1																														
3151	03720	03150	2																														
3152	03721	03151	1																														
3153	03722	03152	1																														

Table 88

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3154	03723	03153	3	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
3155	03724	03154	3	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3156	03725	03155	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3157	03726	03156	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3158	03727	03157	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3159	03728	03158	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3160	03729	03159	3	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3161	03730	03160	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3162	03731	03161	3	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3163	03732	03162	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3164	03733	03163	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3165	03734	03164	7	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3166	03736	03165	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3167	03737	03166	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3168	03738	03167	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3169	03739	03168	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3170	03740	03169	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3171	03741	03170	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3172	03742	03171	3	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3173	03743	03172	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3174	03744	03173	4	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3175	03745	03174	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3176	03746	03175	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3177	03747	03176	2	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3178	03748	03177	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3179	03749	03178	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3180	03750	03179	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3181	03751	03180	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3182	03752	03181	8	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3183	03753	03182	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3184	03754	03183	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3185	03755	03184	6	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3186	03756	03185	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3187	03757	03186	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3188	03758	03187	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3189	03759	03188	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 89

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3190	03760	03189	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3191	03761	03190	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3192	03762	03191	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3193	03763	03192	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3194	03764	03193	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3195	03765	03194	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3196	03766	03195	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3197	03767	03196	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3198	03768	03197	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3199	03769	03198	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3200	03770	03199	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3201	03771	03200	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3202	03772	03201	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3203	03773	03202	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3204	03774	03203	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3205	03775	03204	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3206	03776	03205	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3207	03777	03206	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3208	03778	03207	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3209	03779	03208	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3210	03780	03209	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3211	03781	03210	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3212	03782	03211	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3213	03783	03212	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3214	03784	03213	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3215	03785	03214	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3216	03786	03215	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3217	03787	03216	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3218	03788	03217	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3219	03789	03218	6		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3220	03790	03219	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3221	03791	03220	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3222	03792	03221	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3223	03793	03222	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3224	03794	03223	5		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3225	03795	03224	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 90

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AK	AM	AN	AO	AP	AR	AS	AT	AW	AY	B	BC	BE	BF	BGBH	BI	BK
3226	03796	03225	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3227	03797	03226	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3228	03798	03227	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3229	03799	03228	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3230	03800	03229	1											2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3231	03801	03230	3											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3232	03802	03231	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3233	03803	03232	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3234	03804	03233	7											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3235	03805	03234	1											2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3236	03806	03235	3											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3237	03807	03236	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3238	03808	03237	3											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3239	03809	03238	2											2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3240	03810	03239	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3241	03811	03240	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3242	03812	03241	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3243	03813	03242	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3244	03814	03243	6											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3245	03815	03244	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3246	03816	03245	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3247	03817	03246	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3248	03818	03247	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3249	03819	03248	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3250	03820	03249	3											2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3251	03821	03250	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3252	03822	03251	5											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3253	03823	03252	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3254	03824	03253	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3255	03825	03254	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3256	03826	03255	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3257	03827	03256	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3258	03828	03257	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3259	03829	03258	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3260	03830	03259	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3261	03831	03260	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 91

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AO	AS	AL	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3262	03832	03261	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3263	03833	03262	2											2	0	0	0	0	0	0	0	0	0	0	0	0	0							
3264	03835	03263	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3265	03836	03264	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3266	03837	03265	13											5	0	0	0	0	0	0	0	0	0	0	0	0	0							
3267	03838	03266	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3268	03839	03267	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3269	03840	03268	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3270	03841	03269	3											3	0	0	0	0	0	0	0	0	0	0	0	0	0							
3271	03842	03270	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3272	03843	03271	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3273	03844	03272	50											25	0	0	0	0	0	0	0	0	0	0	0	0	0							
3274	03845	03273	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3275	03846	03274	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3276	03847	03275	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3277	03848	03276	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3278	03849	03277	3											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3279	03850	03278	2											2	0	0	0	0	0	0	0	0	0	0	0	0	0							
3280	03851	03279	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3281	03852	03280	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3282	03853	03281	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3283	03854	03282	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3284	03855	03283	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3285	03856	03284	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3286	03857	03285	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3287	03859	03286	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3288	03860	03287	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3289	03861	03288	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3290	03862	03289	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3291	03863	03290	3											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3292	03864	03291	6											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3293	03865	03292	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3294	03866	03293	3											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3295	03867	03294	20											2	0	0	0	0	0	0	0	0	0	0	0	0	0							
3296	03868	03295	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3297	03869	03296	7											1	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 92

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	B	BE	BF	BG	BH	BI	BK
3298	03870	03297	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3299	03871	03298	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3300	03872	03299	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3301	03873	03300	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3302	03874	03301	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3303	03875	03302	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3304	03876	03303	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3305	03877	03304	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3306	03878	03305	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3307	03879	03306	7		0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3308	03880	03307	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3309	03881	03308	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3310	03882	03309	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3311	03883	03310	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3312	03884	03311	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3313	03885	03312	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3314	03886	03313	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3315	03887	03314	2		0	0	0</																													

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
3442	04051	03441	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3443	04052	03442	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3444	04053	03443	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3445	04054	03444	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3446	04055	03445	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3447	04056	03446	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3448	04057	03447	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3449	04058	03448	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3450	04059	03449	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3451	04060	03450	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3452	04061	03451	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3453	04062	03452	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3454	04063	03453	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3455	04064	03454	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3456	04065	03455	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3457	04066	03456	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3458	04067	03457	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3459	04068	03458	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3460	04069	03459	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3461	04070	03460	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3462	04071	03461	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3463	04072	03462	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3464	04073	03463	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3465	04074	03464	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3466	04075	03465	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3467	04076	03466	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3468	04077	03467	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3469	04078	03468	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3470	04079	03469	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3471	04080	03470	10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3472	04081	03471	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3473	04082	03472	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3474	04083	03473	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3475	04084	03474	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3476	04086	03475	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3477	04087	03476	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3622	04273	03621	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3623	04274	03622	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3624	04275	03623	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3625	04276	03624	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3626	04278	03625	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3627	04279	03626	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3628	04280	03627	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3629	04281	03628	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3630	04282	03629	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3631	04284	03630	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3632	04285	03631	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3633	04286	03632	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3634	04287	03633	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3635	04288	03634	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3636	04289	03635	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3637	04290	03636	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3638	04291	03637	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3639	04292	03638	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3640	04293	03639	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3641	04294	03640	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3642	04295	03641	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3643	04296	03642	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3644	04297	03643	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3645	04298	03644	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3646	04299	03645	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3647	04300	03646	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3648	04302	03647	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3649	04303	03648	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3650	04304	03649	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3651	04305	03650	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3652	04306	03651	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3653	04307	03652	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3654	04308	03653	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3655	04309	03654	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3656	04310	03655	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3657	04311	03656	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 102

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3658	04312	03657	3		0	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0						
3659	04313	03658	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3660	04314	03659	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3661	04315	03660	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0						
3662	04316	03661	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3663	04317	03662	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3664	04318	03663	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3665	04319	03664	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3666	04320	03665	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3667	04321	03666	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3668	04322	03667	12		0	0	0	0	0	0	0	0	0	0	0	3	1	1	1	1	0	2	0	0	0	0	0	0	99.8	415	1	2379	2834
3669	04323	03668	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3670	04324	03669	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3671	04325	03670	2		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0						
3672	04326	03671	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3673	04327	03672	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3674	04328	03673	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3675	04329	03674	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3676	04330	03675	2		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0						
3677	0433																																

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	BA	GA	AK	MA	CA	AS	AL	AW	AY	BA	BC	BE	BF	BG	BI	BK
3766	04425	03765	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3767	04426	03766	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3768	04427	03767	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3769	04428	03768	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3770	04429	03769	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3771	04430	03770	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3772	04431	03771	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3773	04432	03772	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3774	04433	03773	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3775	04434	03774	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3776	04435	03775	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3777	04436	03776	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3778	04437	03777	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3779	04439	03778	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3780	04440	03779	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3781	04441	03780	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3782	04442	03781	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3783	04443	03782	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3784	04445	03783	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3785	04446	03784	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3786	04447	03785	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3787	04448	03786	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3788	04449	03787	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3789	04450	03788	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3790	04452	03789	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3791	04453	03790	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3792	04454	03791	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3793	04455	03792	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3794	04456	03793	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3795	04457	03794	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3796	04460	03795	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3797	04462	03796	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3798	04463	03797	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3799	04464	03798	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3800	04465	03799	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3801	04466	03800	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 106

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AS	AT	AV	AW	AY	B	BC	BE	BF	BGBH	BI	BK
3802	04467	03801	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3803	04468	03802	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3804	04469	03803	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3805	04470	03804	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3806	04471	03805	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3807	04472	03806	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3808	04473	03807	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3809	04474	03808	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3810	04476	03809	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3811	04478	03810	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3812	04482	03811	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3813	04483	03812	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3814	04484	03813	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3815	04485	03814	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3816	04486	03815	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3817	04487	03816	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3818	04488	03817	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3819	04489	03818	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3820	04491	03819	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3821	04492	03820	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3822	04493	03821	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3823	04494	03822	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3824	04495	03823	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3825	04496	03824	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3826	04497	03825	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3827	04498	03826	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3828	04499	03827	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3829	04500	03828	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3830	04501	03829	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3831	04502	03830	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3832	04503	03831	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3833	04504	03832	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3834	04506	03833	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3835	04507	03834	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3836	04509	03835	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3837	04510	03836	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 107

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AE	AG	AI	AK	AM	AO	AS	AT	AW	AY	BABC	BE	BF	BGBH	BI	OK
3838	04511	03837	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3839	04512	03838	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3840	04513	03839	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3841	04514	03840	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3842	04515	03841	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3843	04516	03842	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3844	04517	03843	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3845	04518	03844	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3846	04519	03845	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3847	04520	03846	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3848	04521	03847	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3849	04522	03848	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3850	04523	03849	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3851	04525	03850	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3852	04527	03851	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3853	04528	03852	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3854	04529	03853	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3855	04530	03854	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3856	04531	03855	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3857	04532	03856	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3858	04533	03857	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3859	04534	03858	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3860	04535	03859	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3861	04536	03860	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3862	04537	03861	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3863	04538	03862	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3864	04539	03863	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3865	04541	03864	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3866	04542	03865	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3867	04543	03866	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3868	04546	03867	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3869	04547	03868	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3870	04548	03869	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3871	04552	03870	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3872	04556	03871	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3873	04557	03872	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 108

[illegible]

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	DG	BH	BI	BK
4018	04745	04017	1																														
4019	04746	04018	1																														
4020	04747	04019	3																														
4021	04748	04020	1																														
4022	04750	04021	2																														
4023	04751	04022	1																														
4024	04752	04023	3																														
4025	04753	04024	3																														
4026	04754	04025	8																														
4027	04755	04026	2																														
4028	04756	04027	1																														
4029	04757	04028	5																														
4030	04758	04029	1																														
4031	04759	04030	1																														
4032	04760	04031	1																														
4033	04761	04032	2																														
4034	04762	04033	6																														
4035	04763	04034	4																														
4036	04764	04035	2																														
4037	04765	04036	1																														
4038	04766	04037	1																														
4039	04767	04038	2																														
4040	04768	04039	1																														
4041	04769	04040	1																														
4042	04770	04041	2																														
4043	04771	04042	1																														
4044	04772	04043	4																														
4045	04773	04044	2																														
4046	04774	04045	1																														
4047	04775	04046	1																														
4048	04776	04047	1																														
4049	04777	04048	2																														
4050	04778	04049	1																														
4051	04779	04050	3																														
4052	04780	04051	2																														
4053	04781	04052	1																														

Table 113

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
4162	04900	04161	1																													
4163	04902	04162	1																													
4164	04903	04163	1																													
4165	04904	04164	5																													
4166	04905	04165	5																													
4167	04907	04166	2																													
4168	04908	04167	2																													
4169	04909	04168	1																													
4170	04910	04169	1																													
4171	04912	04170	1																													
4172	04913	04171	4																													
4173	04914	04172	6																													
4174	04915	04173	2																													
4175	04916	04174	1																													
4176	04917	04175	3																													
4177	04918	04176	1																													
4178	04919	04177	1																													
4179	04920	04178	1																													
4180	04921	04179	1																													
4181	04922	04180	2																													
4182	04923	04181	1																													
4183	04924	04182	1																													
4184	04925	04183	1																													
4185	04926	04184	1																													
4186	04927	04185	1																													
4187	04928	04186	3																													
4188	04929	04187	1																													
4189	04930	04188	1																													
4190	04940	04189	1																													
4191	04945	04190	2																													
4192	04947	04191	1																													
4193	04948	04192	3																													
4194	04950	04193	1																													
4195	04965	04194	3																													
4196	04985	04195	2																													
4197	04986	04196	2																													

Table 117

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	FA	GA	IA	KA	MA	QA	SA	TA	WA	YA	BA	BC	BE	BF	BG	BH	BI	BK
4198	04987	04197	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4199	04988	04198	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4200	04989	04199	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4201	04990	04200	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4202	04991	04201	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4203	04992	04202	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4204	04993	04203	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4205	04994	04204	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4206	04997	04205	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4207	04998	04206	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4208	04999	04207	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4209	05001	04208	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4210	05002	04209	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4211	05003	04210	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4212	05004	04211	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4213	05005	04212	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4214	05006	04213	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4215	05007	04214	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4216	05008	04215	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4217	05009	04216	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4218	05010	04217	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4219	05011	04218	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4220	05013	04219	14		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4221	05014	04220	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4222	05016	04221	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4223	05018	04222	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4224	05019	04223	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4225	05021	04224	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4226	05023	04225	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4227	05024	04226	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4228	05025	04227	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4229	05026	04228	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4230	05027	04229	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4231	05028	04230	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4232	05029	04231	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4233	05030	04232	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 118

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
4234	05031	04233	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4235	05033	04234	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4236	05034	04235	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4237	05035	04236	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4238	05037	04237	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4239	05039	04238	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4240	05040	04239	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4241	05041	04240	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4242	05042	04241	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4243	05043	04242	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4244	05044	04243	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4245	05045	04244	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4246	05046	04245	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4247	05047	04246	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4248	05051	04247	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4249	05052	04248	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4250	05053	04249	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4251	05054	04250	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4252	05055	04251	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4253	05056	04252	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4254	05058	04253	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4255	05059	04254	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4256	05060	04255	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4257	05061	04256	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4258	05062	04257	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4259	05063	04258	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4260	05064	04259	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4261	05065	04260	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4262	05066	04261	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4263	05068	04262	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4264	05069	04263	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4265	05070	04264	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4266	05071	04265	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4267	05073	04266	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4268	05074	04267	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4269	05075	04268	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 119

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	AG	AI	AK	AM	AN	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4270	05076	04269	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4271	05077	04270	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4272	05079	04271	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4273	05080	04272	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4274	05081	04273	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4275	05082	04274	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4276	05083	04275	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4277	05085	04276	4	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4278	05086	04277	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4279	05087	04278	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4280	05088	04279	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4281	05089	04280	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4282	05090	04281	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4283	05092	04282	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4284	05094	04283	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4285	05095	04284	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4286	05096	04285	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4287	05099	04286	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4288	05100	04287	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4289	05102	04288	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4290	05103	04289	5	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4291	05104	04290	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4292	05105	04291	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4293	05106	04292	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4294	05107	04293	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4295	05108	04294	12	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4296	05109	04295	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4297	05110	04296	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4298	05111	04297	16	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4299	05112	04298	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4300	05113	04299	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4301	05114	04300	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4302	05115	04301	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4303	05116	04302	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4304	05117	04303	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4305	05118	04304	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 120

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
4342	05161	04341	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4343	05162	04342	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4344	05163	04343	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4345	05164	04344	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4346	05165	04345	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4347	05166	04346	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4348	05168	04347	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4349	05169	04348	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4350	05170	04349	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4351	05172	04350	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4352	05173	04351	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4353	05174	04352	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4354	05176	04353	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4355	05177	04354	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4356	05178	04355	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4357	05180	04356	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4358	05181	04357	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4359	05182	04358	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4360	05183	04359	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4361	05184	04360	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4362	05185	04361	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4363	05186	04362	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4364	05187	04363	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4365	05188	04364	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4366	05190	04365	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4367	05191	04366	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4368	05192	04367	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4369	05194	04368	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4370	05195	04369	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4371	05196	04370	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4372	05197	04371	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4373	05198	04372	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4374	05199	04373	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4375	05200	04374	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4376	05201	04375	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4377	05203	04376	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 122

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
4378	05204	04377	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4379	05205	04378	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4380	05206	04379	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4381	05207	04380	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4382	05208	04381	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4383	05209	04382	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4384	05210	04383	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4385	05211	04384	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4386	05212	04385	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4387	05213	04386	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4388	05214	04387	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4389	05215	04388	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4390	05216	04389	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4391	05217	04390	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4392	05218	04391	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4393	05219	04392	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4394	05220	04393	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4395	05221	04394	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4396	05222	04395	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4397	05224	04396	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4398	05227	04397	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4399	05228	04398	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4400	05229	04399	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4401	05230	04400	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4402	05231	04401	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4403	05232	04402	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4404	05233	04403	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4405	05234	04404	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4406	05235	04405	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4407	05236	04406	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4408	05237	04407	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4409	05238	04408	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4410	05239	04409	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4411	05240	04410	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4412	05241	04411	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4413	05242	04412	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 123

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK	
4414	05243	04413	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4415	05244	04414	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4416	05245	04415	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4417	05246	04416	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4418	05247	04417	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4419	05248	04418	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4420	05249	04419	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4421	05251	04420	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4422	05252	04421	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4423	05253	04422	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4424	05254	04423	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4425	05255	04424	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4426	05259	04425	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4427	05260	04426	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4428	05262	04427	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4429	05263	04428	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4430	05264	04429	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4431	05266	04430	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4432	05267	04431	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4433	05269	04432	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4434	05270	04433	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4435	05271	04434	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4436	05272	04435	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4437	05273	04436	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4438	05274	04437	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4439	05275	04438	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4440	05276	04439	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4441	05278	04440	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4442	05279	04441	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4443	05280	04442	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4444	05281	04443	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4445	05282	04444	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4446	05283	04445	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4447	05284	04446	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4448	05285	04447	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4449	05286	04448	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 124

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AT	AW	BA	BC	BE	BF	BG	BH	BI	BK
4450	05287	04449	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4451	05288	04450	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4452	05289	04451	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4453	05290	04452	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4454	05291	04453	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4455	05292	04454	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4456	05293	04455	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4457	05294	04456	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4458	05295	04457	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4459	05296	04458	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4460	05297	04459	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4461	05298	04460	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4462	05300	04461	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4463	05301	04462	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4464	05302	04463	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4465	05303	04464	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4466	05304	04465	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4467	05305	04466	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4468	05306	04467	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4469	05307	04468	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4470	05308	04469	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4471	05309	04470	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4472	05310	04471	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4473	05311	04472	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4474	05312	04473	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4475	05313	04474	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4476	05314	04475	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4477	05315	04476	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4478	05316	04477	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4479	05318	04478	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4480	05319	04479	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4481	05320	04480	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4482	05321	04481	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4483	05322	04482	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4484	05323	04483	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4485	05325	04484	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 125

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4558	05409	04557	1																														
4559	05410	04558	2																														
4560	05411	04559	4																														
4561	05412	04560	9																														
4562	05413	04561	1																														
4563	05414	04562	1																														
4564	05415	04563	3																														
4565	05416	04564	1																														
4566	05417	04565	5																														
4567	05418	04566	3																														
4568	05419	04567	2																														
4569	05420	04568	3																														
4570	05421	04569	1																														
4571	05422	04570	2																														
4572	05423	04571	3																														
4573	05424	04572	2																														
4574	05425	04573	1																														
4575	05427	04574	1																														
4576	05428	04575	2																														
4577	05429	04576	1																														
4578	05430	04577	1																														
4579	05431	04578	1																														
4580	05432	04579	2																														
4581	05433	04580	2																														
4582	05434	04581	4																														
4583	05435	04582	3																														
4584	05436	04583	1																														
4585	05437	04584	3																														
4586	05438	04585	3																														
4587	05439	04586	3																														
4588	05440	04587	1																														
4589	05441	04588	1																														
4590	05442	04589	1																														
4591	05443	04590	1																														
4592	05444	04591	1																														
4593	05445	04592	2																														

Table 128

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AO	AS	AT	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4702	05577	04701	4																									0	0	0	0	0	0	809
4703	05578	04702	1																									0	0	0	0	0	0	
4704	05579	04703	2																									0	0	0	0	0	0	
4705	05580	04704	2																									0	0	0	0	0	0	
4706	05581	04705	4																									0	0	0	0	0	0	
4707	05582	04706	1																									0	0	0	0	0	0	
4708	05583	04707	4																									0	0	0	0	0	0	
4709	05585	04708	1																									0	0	0	0	0	0	
4710	05586	04709	1																									0	0	0	0	0	0	
4711	05587	04710	4																									0	0	0	0	0	0	
4712	05588	04711	2																									0	0	0	0	0	0	
4713	05589	04712	1																									0	0	0	0	0	0	
4714	05590	04713	3																									0	0	0	0	0	0	
4715	05591	04714	1																									0	0	0	0	0	0	
4716	05593	04715	3																									0	0	0	0	0	0	
4717	05595	04716	2																									0	0	0	0	0	0	
4718	05598	04717	1																									0	0	0	0	0	0	
4719	05599	04718	1																									0	0	0	0	0	0	
4720	05600	04719	2																									0	0	0	0	0	0	
4721	05601	04720	1																									0	0	0	0	0	0	
4722	05602	04721	1																									0	0	0	0	0	0	
4723	05603	04722	1																									0	0	0	0	0	0	
4724	05604	04723	1																									0	0	0	0	0	0	
4725	05606	04724	1																									0	0	0	0	0	0	
4726	05607	04725	1																									0	0	0	0	0	0	
4727	05608	04726	1																									0	0	0	0	0	0	
4728	05610	04727	1																									0	0	0	0	0	0	
4729	05612	04728	2																									0	0	0	0	0	0	
4730	05613	04729	1																									0	0	0	0	0	0	
4731	05614	04730	2																									0	0	0	0	0	0	
4732	05615	04731	1																									0	0	0	0	0	0	
4733	05616	04732	1																									0	0	0	0	0	0	
4734	05618	04733	1																									0	0	0	0	0	0	
4735	05619	04734	1																									0	0	0	0	0	0	
4736	05621	04735	1																									0	0	0	0	0	0	
4737	05622	04736	1																									0	0	0	0	0	0	

Table 132

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AN	AO	AP	AQ	AS	AT	AV	AY	BAB	BC	BE	BF	BG	BH	BI	BK
4738	05623	04737	1																																	
4739	05624	04738	3																																	
4740	05625	04739	3																																	
4741	05627	04740	1																																	
4742	05628	04741	1																																	
4743	05629	04742	2																																	
4744	05630	04743	1																																	
4745	05631	04744	2																																	
4746	05632	04745	4																																	
4747	05634	04746	1																																	
4748	05635	04747	1																																	
4749	05636	04748	2																																	
4750	05637	04749	1																																	
4751	05639	04750	4																																	
4752	05640	04751	1																																	
4753	05642	04752	2																																	
4754	05643	04753	2																																	
4755	05644	04754	4																																	
4756	05645	04755	2																																	
4757	05646	04756	1																																	
4758	05647	04757	5																																	
4759	05648	04758	2																																	
4760	05649	04759	1																																	
4761	05650	04760	4																																	
4762	05651	04761	1																																	
4763	05652	04762	3																																	
4764	05653	04763	1																																	
4765	05654	04764	1																																	
4766	05655	04765	2																																	
4767	05656	04766	1																																	
4768	05657	04767	1																																	
4769	05658	04768	1																																	
4770	05659	04769	1																																	
4771	05660	04770	1																																	
4772	05661	04771	1																																	
4773	05662	04772	1																																	

Table 133

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK
4810	05718	04809	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4811	05719	04810	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4812	05720	04811	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4813	05721	04812	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4814	05722	04813	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4815	05723	04814	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4816	05724	04815	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4817	05725	04816	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4818	05726	04817	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4819	05727	04818	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4820	05729	04819	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4821	05730	04820	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4822	05731	04821	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4823	05732	04822	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4824	05733	04823	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4825	05734	04824	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4826	05735	04825	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4827	05736	04826	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4828	05738	04827	17		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4829	05741	04828	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4830	05742	04829	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4831	05743	04830	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4832	05747	04831	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4833	05748	04832	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4834	05749	04833	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4835	05751	04834	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4836	05752	04835	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4837	05754	04836	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4838	05755	04837	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4839	05756	04838	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4840	05757	04839	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4841	05758	04840	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4842	05759	04841	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4843	05763	04842	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4844	05765	04843	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4845	05767	04844	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 135

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
4882	05816	04881	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4883	05817	04882	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4884	05818	04883	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4885	05819	04884	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4886	05820	04885	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4887	05821	04886	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4888	05823	04887	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4889	05824	04888	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4890	05825	04889	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4891	05826	04890	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4892	05827	04891	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4893	05829	04892	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4894	05830	04893	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4895	05831	04894	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4896	05832	04895	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4897	05833	04896	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4898	05834	04897	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4899	05835	04898	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4900	05836	04899	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4901	05837	04900	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4902	05838	04901	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4903	05839	04902	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4904	05840	04903	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4905	05841	04904	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4906	05842	04905	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4907	05843	04906	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4908	05844	04907	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4909	05845	04908	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4910	05846	04909	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4911	05847	04910	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4912	05848	04911	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4913	05849	04912	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4914	05850	04913	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4915	05851	04914	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4916	05852	04915	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4917	05854	04916	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 137

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	TA	GA	IA	K	MA	QA	CA	SA	LA	WA	YA	B	BC	BE	BF	BGBH	BI	BK
4954	05899	04953	1																															
4955	05900	04954	2																															
4956	05902	04955	1																															
4957	05903	04956	1																															
4958	05907	04957	1																															
4959	05908	04958	1																															
4960	05912	04959	2																															
4961	05913	04960	1																															
4962	05914	04961	1																															
4963	05916	04962	1																															
4964	05917	04963	1																															
4965	05918	04964	1																															
4966	05919	04965	1																															
4967	05920	04966	1																															
4968	05921	04967	1																															
4969	05923	04968	1																															
4970	05925	04969	2																															
4971	05926	04970	1																															
4972	05927	04971	1																															
4973	05928	04972	1																															
4974	05932	04973	1																															
4975	05933	04974	1																															
4976	05934	04975	1																															
4977	05937	04976	1																															
4978	05938	04977	1																															
4979	05939	04978	1																															
4980	05940	04979	1																															
4981	05941	04980	1																															
4982	05942	04981	1																															
4983	05943	04982	2																															
4984	05946	04983	2																															
4985	05947	04984	1																															
4986	05948	04985	1																															
4987	05949	04986	1																															
4988	05951	04987	1																															
4989	05952	04988	1																															

Table 139

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
4990	05953	04989	1																								0	M37712	99.3	147	1	3717	3863
4991	05954	04990	2																								0						
4992	05955	04991	5																								0						
4993	05956	04992	1																								0						
4994	05957	04993	1																								0						
4995	05959	04994	3																								0						
4996	05960	04995	1																								0	M27319	98.5	65	1	735	799
4997	05961	04996	1																								0						
4998	05962	04997	1																								0						
4999	05963	04998	1																								0						
5000	05964	04999	1																								0						
5001	05966	05000	1																								0						
5002	05967	05001	1																								0						
5003	05968	05002	1																								0						
5004	05969	05003	1																								0						
5005	05970	05004	1																								0						
5006	05974	05005	1																								0						
5007	05975	05006	1																								0						
5008	05976	05007	1																								0						
5009	05978	05008	6																								0	M33197	94.8	305	1	495	1268
5010	05980	05009	1																								0						
5011	05981	05010	1																								0	M16447	91.2	330	1	1097	1550
5012	05982	05011	2																								0						
5013	05983	05012	1																								0						
5014	05984	05013	3																								0						
5015	05987	05014	2																								0						
5016	05988	05015	1																								0						
5017	05989	05016	1																								0						
5018	05991	05017	1																								0						
5019	05992	05018	1																								0						
5020	05993	05019	1																								0						
5021	05994	05020	1																								0						
5022	05996	05021	1																								0						
5023	05997	05022	1																								0						
5024	05998	05023	1																								0						
5025	05999	05024	1																								0						

Table 140

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	BABC	BE	BF	BGBH	BI	BK
5026	06000	05025	1																														
5027	06001	05026	1																														
5028	06004	05027	1																														
5029	06005	05028	1																														
5030	06008	05029	1																														
5031	06010	05030	1																														
5032	06011	05031	1																														
5033	06013	05032	3																														
5034	06014	05033	1																														
5035	06015	05034	1																														
5036	06016	05035	1																														
5037	06017	05036	2																														
5038	06018	05037	1																														
5039	06020	05038	1																														
5040	06021	05039	1																														
5041	06022	05040	1																														
5042	06023	05041	1																														
5043	06024	05042	2																														
5044	06025	05043	1																														
5045	06026	05044	4																														
5046	06027	05045	2																														
5047	06028	05046	2																														
5048	06030	05047	1																														
5049	06031	05048	1																														
5050	06032	05049	1																														
5051	06034	05050	1																														
5052	06035	05051	1																														
5053	06036	05052	2																														
5054	06038	05053	2																														
5055	06039	05054	1																														
5056	06040	05055	1																														
5057	06041	05056	3																														
5058	06042	05057	1																														
5059	06043	05058	1																														
5060	06044	05059	1																														
5061	06045	05060	1																														

Table 141

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
5062	06046	05061	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5063	06047	05062	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0					
5064	06048	05063	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5065	06049	05064	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5066	06050	05065	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5067	06051	05066	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5068	06052	05067	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5069	06053	05068	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0					
5070	06054	05069	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5071	06055	05070	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5072	06056	05071	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5073	06057	05072	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5074	06059	05073	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5075	06060	05074	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5076	06061	05075	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5077	06062	05076	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5078	06064	05077	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5079	06065	05078	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5080	06066	05079	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5081	06067	05080	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	EA	GA	IA	KA	MA	QA	CA	SA	LA	WA	YA	BA	BC	BE	BF	BGBH	BI	BK
5098	06086	05097	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5099	06087	05098	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5100	06089	05099	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5101	06090	05100	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5102	06091	05101	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5103	06092	05102	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5104	06093	05103	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5105	06094	05104	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5106	06095	05105	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5107	06097	05106	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5108	06098	05107	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5109	06100	05108	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5110	06101	05109	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5111	06102	05110	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5112	06103	05111	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5113	06104	05112	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5114	06105	05113	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5115	06107	05114	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5116	06108	05115	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5117	06109	05116	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5118	06110	05117	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5119	06111	05118	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5120	06112	05119	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5121	06113	05120	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5122	06114	05121	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5123	06115	05122	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5124	06116	05123	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5125	06117	05124	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5126	06118	05125	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5127	06119	05126	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5128	06122	05127	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5129	06123	05128	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5130	06125	05129	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5131	06126	05130	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5132	06127	05131	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5133	06128	05132	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 143

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	BA	CA	AK	KA	MA	CA	AS	AL	AW	AY	BA	BC	DE	BF	BGBH	BI	BK
5134	06129	05133	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5135	06130	05134	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5136	06131	05135	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5137	06133	05136	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5138	06136	05137	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5139	06137	05138	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5140	06138	05139	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5141	06139	05140	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5142	06141	05141	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5143	06142	05142	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5144	06144	05143	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5145	06145	05144	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5146	06146	05145	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5147	06148	05146	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5148	06150	05147	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5149	06151	05148	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5150	06152	05149	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5151	06153	05150	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5152	06154	05151	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5153	06155	05152	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5154	06156	05153	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5155	06157	05154	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5156	06158	05155	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5157	06159	05156	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5158	06160	05157	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5159	06161	05158	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5160	06163	05159	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5161	06164	05160	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5162	06165	05161	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5163	06166	05162	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5164	06167	05163	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5165	06168	05164	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5166	06169	05165	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5167	06170	05166	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5168	06171	05167	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
5169	06172	05168	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					

Table 144

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AL	AG	AI	AK	AN	AO	AS	AV	AY	B	BC	BE	BF	BG	BH	BI	BK
5170	06173	05169	1																														
5171	06174	05170	1																														
5172	06175	05171	1																														
5173	06176	05172	3																														
5174	06177	05173	1																														
5175	06179	05174	1																														
5176	06180	05175	1																														
5177	06181	05176	2																														
5178	06182	05177	1																														
5179	06183	05178	1																														
5180	06184	05179	1																														
5181	06185	05180	1																														
5182	06186	05181	4																														
5183	06187	05182	1																														
5184	06188	05183	1																														
5185	06189	05184	1																														
5186	06190	05185	1																														
5187	06191	05186	1																														
5188	06192	05187	1																														
5189	06195	05188	1																														
5190	06196	05189	1																														
5191	06197	05190	2																														
5192	06198	05191	1																														
5193	06199	05192	1																														
5194	06200	05193	1																														
5195	06201	05194	1																														
5196	06202	05195	1																														
5197	06203	05196	3																														
5198	06204	05197	3																														
5199	06205	05198	3																														
5200	06206	05199	1																														
5201	06207	05200	1																														
5202	06208	05201	1																														
5203	06209	05202	2																														
5204	06210	05203	1																														
5205	06211	05204	1																														

Table 145

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	RE	BF	BG	BH	BI	BK
5206	06213	05205	1																														
5207	06215	05206	1																														
5208	06216	05207	1																														
5209	06217	05208	1																														
5210	06218	05209	1																														
5211	06219	05210	1																														
5212	06220	05211	2																														
5213	06221	05212	1																														
5214	06222	05213	2																														
5215	06224	05214	2																														
5216	06225	05215	1																														
5217	06226	05216	1																														
5218	06227	05217	1																														
5219	06228	05218	1																														
5220	06229	05219	1																														
5221	06230	05220	1																														
5222	06232	05221	1																														
5223	06233	05222	1																														
5224	06234	05223	1																														
5225	06235	05224	1																														
5226	06236	05225	1																														
5227	06237	05226	1																														
5228	06238	05227	3																														
5229	06240	05228	1																														
5230	06241	05229	1																														
5231	06243	05230	1																														
5232	06244	05231	1																														
5233	06246	05232	2																														
5234	06247	05233	2																														
5235	06248	05234	1																														
5236	06249	05235	2																														
5237	06250	05236	1																														
5238	06251	05237	1																														
5239	06253	05238	1																														
5240	06254	05239	1																														
5241	06255	05240	1																														

Table 146

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AE	AF	AG	AH	AI	AK	AM	AN	AO	AP	AW	AY	BAC	DE	BF	BGBH	BI	BK	
5242	06256	05241	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5243	06257	05242	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5244	06258	05243	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5245	06259	05244	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5246	06260	05245	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			98.5	68	1 1297	1364
5247	06261	05246	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5248	06262	05247	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5249	06264	05248	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5250	06267	05249	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5251	06268	05250	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5252	06269	05251	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5253	06270	05252	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5254	06271	05253	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5255	06272	05254	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5256	06273	05255	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5257	06274	05256	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5258	06275	05257	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5259	06277	05258	1	0</																																

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AP	AS	AT	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
5278	06299	05277	3																											0M74002	98.7	229	1	2508	2736	
5279	06300	05278	1																											0	98.9	176	1	1256	1766	
5280	06301	05279	2																											0						
5281	06302	05280	2																											0						
5282	06303	05281	1																											0						
5283	06304	05282	1																											0						
5284	06305	05283	1																											0						
5285	06306	05284	1																											0						
5286	06307	05285	2																											0						
5287	06308	05286	2																											0						
5288	06309	05287	1																											0						
5289	06310	05288	3																											0						
5290	06311	05289	1																											0						
5291	06313	05290	1																											0						
5292	06314	05291	1																											0						
5293	06315	05292	3																											0						
5294	06316	05293	1																											0						
5295	06317	05294	1																											0						
5296	06318	05295	2																											0						
5297	06319	05296	5																											0						
5298	06320	05297	1																											0						
5299	06321	05298	1																											0						
5300	06322	05299	1																											0						
5301	06323	05300	1																											0						
5302	06324	05301	1																											0						
5303	06325	05302	1																											0						
5304	06326	05303	1																											0						
5305	06327	05304	1																											0						
5306	06329	05305	1																											0						
5307	06330	05306	2																											0						
5308	06331	05307	1																											0						
5309	06332	05308	1																											0						
5310	06333	05309	1																											0						
5311	06334	05310	1																											0						
5312	06335	05311	1																											0						
5313	06337	05312	1																											0						

Table 148

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AE	AF	AG	AH	AI	BK
5350	06380	05349	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5351	06381	05350	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5352	06382	05351	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5353	06383	05352	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5354	06384	05353	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5355	06385	05354	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5356	06386	05355	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5357	06387	05356	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5358	06388	05357	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5359	06389	05358	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5360	06390	05359	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5361	06392	05360	26		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5362	06393	05361	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5363	06394	05362	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5364	06395	05363	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5365	06396	05364	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5366	06397	05365	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5367	06398	05366	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5368	06399	05367	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5369	06400	05368	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5370	06401	05369	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5371	06402	05370	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5372	06403	05371	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5373	06404	05372	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5374	06405	05373	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5375	06407	05374	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5376	06408	05375	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5377	06409	05376	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5378	06410	05377	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5379	06411	05378	15		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5380	06412	05379	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5381	06413	05380	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5382	06414	05381	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5383	06415	05382	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5384	06416	05383	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
5385	06417	05384	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		

Table 150

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5386	06418	05385	1																														
5387	06419	05386	2																														
5388	06420	05387	1																														
5389	06421	05388	2																														
5390	06422	05389	1																														
5391	06423	05390	1																														
5392	06424	05391	2																														
5393	06425	05392	1																														
5394	06426	05393	1																														
5395	06427	05394	1																														
5396	06428	05395	1																														
5397	06429	05396	1																														
5398	06430	05397	1																														
5399	06431	05398	1																														
5400	06432	05399	1																														
5401	06433	05400	1																														
5402	06434	05401	4																														
5403	06435	05402	2																														
5404	06436	05403	1																														
5405	06437	05404	1																														
5406	06438	05405	1																														
5407	06439	05406	3																														
5408	06440	05407	1																														
5409	06441	05408	1																														
5410	06442	05409	2																														
5411	06443	05410	2																														
5412	06444	05411	1																														
5413	06445	05412	1																														
5414	06446	05413	1																														
5415	06447	05414	3																														
5416	06448	05415	3																														
5417	06449	05416	4																														
5418	06450	05417	1																														
5419	06451	05418	1																														
5420	06452	05419	1																														
5421	06453	05420	1																														

Table 151

[illegible]

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AT	AW	AY	BA	BB	BC	BE	BF	BG	BH	BI	BK
5494	06532	05493	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5495	06533	05494	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5496	06536	05495	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5497	06537	05496	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5498	06538	05497	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5499	06539	05498	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5500	06540	05499	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5501	06541	05500	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5502	06542	05501	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5503	06544	05502	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5504	06545	05503	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5505	06546	05504	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5506	06547	05505	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5507	06548	05506	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5508	06549	05507	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5509	06550	05508	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5510	06551	05509	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5511	06552	05510	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5512	06553	05511	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5513	06555	05512	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5514	06556	05513	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5515	06557	05514	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5516	06558	05515	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5517	06559	05516	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5518	06560	05517	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5519	06561	05518	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5520	06563	05519	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5521	06564	05520	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5522	06565	05521	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5523	06566	05522	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5524	06567	05523	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5525	06569	05524	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5526	06571	05525	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5527	06572	05526	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5528	06573	05527	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5529	06574	05528	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 154

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5566	06615	05565	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5567	06616	05566	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5568	06617	05567	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5569	06618	05568	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5570	06619	05569	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5571	06620	05570	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5572	06621	05571	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5573	06623	05572	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5574	06624	05573	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5575	06625	05574	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5576	06626	05575	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5577	06627	05576	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5578	06628	05577	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5579	06630	05578	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5580	06631	05579	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5581	06632	05580	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5582	06633	05581	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5583	06634	05582	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5584	06635	05583	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5585	06636	05584	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5586	06637	05585	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5587	06638	05586	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5588	06639	05587	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5589	06640	05588	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5590	06641	05589	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5591	06642	05590	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5592	06643	05591	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5593	06645	05592	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5594	06646	05593	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5595	06647	05594	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5596	06649	05595	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5597	06650	05596	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5598	06651	05597	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5599	06652	05598	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5600	06653	05599	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5601	06654	05600	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 156

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5602	06656	05601	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5603	06659	05602	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5604	06660	05603	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5605	06661	05604	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5606	06662	05605	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5607	06664	05606	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5608	06666	05607	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5609	06667	05608	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5610	06668	05609	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5611	06669	05610	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5612	06670	05611	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5613	06672	05612	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5614	06673	05613	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5615	06674	05614	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5616	06675	05615	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5617	06676	05616	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5618	06677	05617	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5619	06678	05618	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5620	06679	05619	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5621	06680	05620	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5622	06681	05621	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5623	06682	05622	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5624	06683	05623	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5625	06684	05624	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5626	06685	05625	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5627	06686	05626	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5628	06687	05627	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5629	06688	05628	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5630	06689	05629	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5631	06690	05630	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5632	06691	05631	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5633	06692	05632	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5634	06693	05633	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5635	06694	05634	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5636	06696	05635	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5637	06697	05636	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 157

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AP	AQ	AS	AT	AW	AY	BABC	BE	BF	BG	BH	BI	BK
5710	06778	05709	1																																	
5711	06780	05710	4																																	
5712	06781	05711	2																																	
5713	06783	05712	1																																	
5714	06784	05713	1																																	
5715	06785	05714	1																																	
5716	06786	05715	1																																	
5717	06787	05716	3																																	
5718	06788	05717	1																																	
5719	06789	05718	1																																	
5720	06790	05719	1																																	
5721	06791	05720	1																																	
5722	06792	05721	2																																	
5723	06794	05722	1																																	
5724	06795	05723	1																																	
5725	06796	05724	1																																	
5726	06797	05725	1																																	
5727	06798	05726	1																																	
5728	06800	05727	1																																	
5729	06801	05728	1																																	
5730	06802	05729	1																																	
5731	06803	05730	1																																	
5732	06804	05731	1																																	
5733	06805	05732	1																																	
5734	06806	05733	1																																	
5735	06807	05734	1																																	
5736	06808	05735	1																																	
5737	06809	05736	1																																	
5738	06810	05737	2																																	
5739	06811	05738	1																																	
5740	06812	05739	1																																	
5741	06813	05740	2																																	
5742	06815	05741	2																																	
5743	06816	05742	1																																	
5744	06817	05743	2																																	
5745	06818	05744	1																																	

Table 160

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5782	06859	05781	2																														
5783	06863	05782	1																														
5784	06864	05783	1																														
5785	06865	05784	1																														
5786	06866	05785	1																														
5787	06869	05786	4																														
5788	06870	05787	1																														
5789	06871	05788	1																														
5790	06872	05789	1																														
5791	06873	05790	1																														
5792	06874	05791	1																														
5793	06875	05792	1																														
5794	06876	05793	1																														
5795	06878	05794	1																														
5796	06879	05795	1																														
5797	06880	05796	1																														
5798	06882	05797	2																														
5799	06883	05798	1																														
5800	06884	05799	1																														
5801	06885	05800	2																														
5802	06886	05801	1																														
5803	06888	05802	1																														
5804	06889	05803	1																														
5805	06890	05804	1																														
5806	06891	05805	1																														
5807	06893	05806	1																														
5808	06894	05807	1																														
5809	06895	05808	1																														
5810	06896	05809	1																														
5811	06897	05810	1																														
5812	06898	05811	1																														
5813	06899	05812	1																														
5814	06900	05813	1																														
5815	06901	05814	1																														
5816	06902	05815	1																														
5817	06903	05816	1																														

Table 162

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5854	06952	05853	1																														
5855	06953	05854	1																														
5856	06954	05855	2																														
5857	06955	05856	1																														
5858	06956	05857	1																														
5859	06957	05858	2																														
5860	06959	05859	1																														
5861	06960	05860	1																														
5862	06961	05861	1																														
5863	06963	05862	1																														
5864	06964	05863	1																														
5865	06965	05864	2																														
5866	06966	05865	1																														
5867	06967	05866	2																														
5868	06969	05867	1																														
5869	06971	05868	3																														
5870	06972	05869	2																														
5871	06973	05870	1																														
5872	06975	05871	1																														
5873	06977	05872	2																														
5874	06978	05873	2																														
5875	06979	05874	1																														
5876	06981	05875	2																														
5877	06982	05876	2																														
5878	06983	05877	1																														
5879	06984	05878	1																														
5880	06985	05879	2																														
5881	06986	05880	1																														
5882	06987	05881	1																														
5883	06988	05882	1																														
5884	06989	05883	1																														
5885	06990	05884	1																														
5886	06991	05885	1																														
5887	06992	05886	1																														
5888	06993	05887	1																														
5889	06994	05888	5																														

Table 164

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AE	AF	AG	AH	AI	AK	AM	AN	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5926	07034	05925	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5927	07035	05926	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5928	07036	05927	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5929	07037	05928	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5930	07038	05929	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5931	07039	05930	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5932	07040	05931	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5933	07041	05932	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5934	07043	05933	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5935	07044	05934	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5936	07046	05935	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5937	07047	05936	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5938	07048	05937	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5939	07049	05938	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5940	07050	05939	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5941	07053	05940	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5942	07054	05941	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5943	07055	05942	1		0	0</																															

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AV	AW	AY	BABC	BE	BF	BG	BH	BI	BK
5962	0709	05961	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5963	0700	05962	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5964	0701	05963	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5965	0702	05964	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5966	0703	05965	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0						
5967	0704	05966	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5968	0705	05967	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5969	0706	05968	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5970	0707	05969	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5971	0708	05970	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5972	0709	05971	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5973	0701	05972	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5974	0703	05973	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5975	0704	05974	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5976	0705	05975	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5977	0706	05976	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5978	0707	05977	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5979	0708	05978	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5980	0709	05979	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5981	0710	05980	1		0	0	0	0																									

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BAB	BE	BF	BGBH	BI	BK
6034	07158	06033	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6035	07160	06034	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6036	07161	06035	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6037	07162	06036	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6038	07163	06037	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6039	07164	06038	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6040	07165	06039	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6041	07166	06040	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6042	07167	06041	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6043	07169	06042	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6044	07170	06043	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6045	07171	06044	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6046	07173	06045	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6047	07174	06046	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6048	07175	06047	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6049	07178	06048	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6050	07179	06049	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6051	07180	06050	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6052	07181	06051	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6053	07182	06052	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6054	07183	06053	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6055	07185	06054	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6056	07186	06055	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6057	07187	06056	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6058	07188	06057	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6059	07192	06058	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6060	07193	06059	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6061	07194	06060	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6062	07195	06061	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6063	07196	06062	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6064	07199	06063	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6065	07200	06064	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6066	07201	06065	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6067	07202	06066	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6068	07204	06067	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6069	07206	06068	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 169

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	GA	IA	KA	MA	QA	SA	TA	WA	YA	B	BC	BE	BF	BG	BH	BI	BK
6070	07209	06069	1																														
6071	07210	06070	2																														
6072	07211	06071	1																														
6073	07212	06072	1																														
6074	07213	06073	1																														
6075	07214	06074	1																														
6076	07215	06075	1																														
6077	07216	06076	2																														
6078	07217	06077	1																														
6079	07218	06078	2																														
6080	07219	06079	2																														
6081	07220	06080	1																														
6082	07221	06081	1																														
6083	07222	06082	1																														
6084	07223	06083	1																														
6085	07224	06084	1																														
6086	07225	06085	1																														
6087	07226	06086	1																														
6088	07227	06087	1																														
6089	07228	06088	1																														
6090	07229	06089	1																														
6091	07230	06090	1																														
6092	07231	06091	1																														
6093	07232	06092	1																														
6094	07233	06093	1																														
6095	07234	06094	1																														
6096	07241	06095	1																														
6097	07243	06096	1																														
6098	07244	06097	1																														
6099	07245	06098	1																														
6100	07246	06099	1																														
6101	07249	06100	1																														
6102	07250	06101	1																														
6103	07251	06102	1																														
6104	07253	06103	1																														
6105	07257	06104	1																														

Table 170

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
6106	07259	06105	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6107	07261	06106	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6108	07263	06107	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6109	07264	06108	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6110	07265	06109	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6111	07266	06110	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6112	07267	06111	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6113	07268	06112	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6114	07269	06113	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6115	07270	06114	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6116	07272	06115	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6117	07274	06116	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6118	07275	06117	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6119	07276	06118	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6120	07277	06119	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6121	07278	06120	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6122	07279	06121	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6123	07280	06122	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6124	07281	06123	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6125	07282	06124	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6126	07283	06125	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6127	07284	06126	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6128	07285	06127	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6129	07286	06128	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6130	07287	06129	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6131	07288	06130	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6132	07289	06131	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6133	07290	06132	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6134	07291	06133	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6135	07292	06134	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6136	07293	06135	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6137	07294	06136	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6138	07295	06137	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6139	07296	06138	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6140	07297	06139	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6141	07298	06140	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 171

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
6142	07299	06141	1																															
6143	07300	06142	1																															
6144	07301	06143	1																															
6145	07302	06144	2																															
6146	07303	06145	1																															
6147	07304	06146	1																															
6148	07305	06147	2																															
6149	07306	06148	1																															
6150	07307	06149	1																															
6151	07308	06150	1																															
6152	07309	06151	5																															
6153	07311	06152	1																															
6154	07312	06153	1																															
6155	07313	06154	1																															
6156	07315	06155	1																															
6157	07316	06156	1																															
6158	07317	06157	2																															
6159	07318	06158	1																															
6160	07319	06159	1																															
6161	07320	06160	2																															
6162	07321	06161	1																															
6163	07322	06162	1																															
6164	07323	06163	1																															
6165	07324	06164	1																															
6166	07325	06165	1																															
6167	07326	06166	1																															
6168	07327	06167	1																															
6169	07328	06168	2																															
6170	07329	06169	2																															
6171	07330	06170	1																															
6172	07331	06171	1																															
6173	07332	06172	2																															
6174	07333	06173	2																															
6175	07334	06174	1																															
6176	07335	06175	1																															
6177	07336	06176	1																															

Table 172

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
6178	07337	06177	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6179	07338	06178	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6180	07339	06179	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6181	07340	06180	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6182	07341	06181	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6183	07342	06182	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6184	07343	06183	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6185	07344	06184	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6186	07345	06185	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6187	07346	06186	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6188	07348	06187	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6189	07349	06188	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6190	07350	06189	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6191	07351	06190	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6192	07352	06191	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6193	07353	06192	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6194	07354	06193	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6195	07355	06194	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6196	07356	06195	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6197	07357	06196	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6198	07358	06197	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6199	07359	06198	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6200	07360	06199	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6201	07361	06200	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6202	07362	06201	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6203	07363	06202	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6204	07364	06203	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6205	07365	06204	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6206	07366	06205	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6207	07367	06206	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6208	07368	06207	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6209	07369	06208	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6210	07370	06209	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6211	07371	06210	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6212	07372	06211	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6213	07373	06212	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 173

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
6214	07374	06213	1																														
6215	07375	06214	2																														
6216	07376	06215	1																														
6217	07377	06216	4																														
6218	07378	06217	1																														
6219	07379	06218	1																														
6220	07380	06219	1																														
6221	07381	06220	1																														
6222	07382	06221	1																														
6223	07383	06222	1																														
6224	07384	06223	1																														
6225	07385	06224	1																														
6226	07386	06225	1																														
6227	07387	06226	1																														
6228	07388	06227	3																														
6229	07389	06228	1																														
6230	07390	06229	1																														
6231	07391	06230	1																														
6232	07392	06231	2																														
6233	07393	06232	1																														
6234	07394	06233	1																														
6235	07395	06234	1																														
6236	07396	06235	1																														
6237	07397	06236	1																														
6238	07398	06237	1																														
6239	07399	06238	1																														
6240	07400	06239	1																														
6241	07401	06240	1																														
6242	07402	06241	1																														
6243	07403	06242	1																														
6244	07404	06243	2																														
6245	07405	06244	1																														
6246	07406	06245	1																														
6247	07407	06246	1																														
6248	07408	06247	1																														
6249	07409	06248	1																														

Table 174

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
6250	07410	06249	1																														
6251	07411	06250	1																														
6252	07412	06251	2																														
6253	07413	06252	3																														
6254	07414	06253	1																														
6255	07415	06254	1																														
6256	07416	06255	1																														
6257	07417	06256	2																														
6258	07418	06257	1																														
6259	07419	06258	1																														
6260	07420	06259	1																														
6261	07421	06260	1																														
6262	07422	06261	2																														
6263	07423	06262	1																														
6264	07424	06263	1																														
6265	07425	06264	1																														
6266	07426	06265	1																														
6267	07427	06266	1																														
6268	07429	06267	1																														
6269	07430	06268	3																														
6270	07431	06269	1																														
6271	07432	06270	1																														
6272	07433	06271	2																														
6273	07434	06272	1																														
6274	07435	06273	1																														
6275	07436	06274	1																														
6276	07437	06275	1																														
6277	07438	06276	1																														
6278	07439	06277	1																														
6279	07440	06278	1																														
6280	07441	06279	1																														
6281	07442	06280	1																														
6282	07443	06281	2																														
6283	07444	06282	1																														
6284	07445	06283	1																														
6285	07446	06284	1																														

Table 175

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AL	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
5	6322	07484	06321	1																													
10	6323	07485	06322	1																													
15	6324	07486	06323	1																													
20	6325	07487	06324	1																													
25	6326	07488	06325	1																													
30	6327	07489	06326	2																													
35	6328	07490	06327	1																													
40	6329	07491	06328	1																													
45	6330	07492	06329	1																													
50	6331	07493	06330	1																													
	6332	07494	06331	1																													
	6333	07495	06332	1																													
	6334	07496	06333	2																													
	6335	07497	06334	1																													
	6336	07498	06335	1																													
	6337	07499	06336	1																													
	6338	07500	06337	1																													
	6339	07501	06338	1																													
	6340	07502	06339	1																													
	6341	07503	06340	1																													
	6342	07504	06341	1																													
	6343	07505	06342	1																													
	6344	07506	06343	2																													
	6345	07507	06344	1																													
	6346	07508	06345	1																													
	6347	07509	06346	1																													
	6348	07510	06347	1																													
	6349	07511	06348	1																													
	6350	07512	06349	1																													
	6351	07513	06350	1																													
	6352	07514	06351	1																													
	6353	07515	06352	1																													
	6354	07516	06353	1																													
	6355	07517	06354	1																													
	6356	07518	06355	1																													
	6357	07520	06356	1																													

Table 177

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AK	AM	AQ	AS	AV	AW	BA	BC	BE	BF	BG	BH	BI	BK
6358	07521	06357	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6359	07522	06358	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6360	07523	06359	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6361	07524	06360	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6362	07525	06361	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6363	07526	06362	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6364	07527	06363	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6365	07528	06364	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6366	07529	06365	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6367	07530	06366	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6368	07531	06367	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6369	07532	06368	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6370	07533	06369	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6371	07534	06370	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6372	07535	06371	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6373	07536	06372	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6374	07537	06373	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6375	07538	06374	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6376	07539	06375	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6377	07540	06376	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6378	07541	06377	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6379	07543	06378	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6380	07544	06379	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6381	07545	06380	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6382	07546	06381	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6383	07547	06382	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6384	07548	06383	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6385	07549	06384	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6386	07550	06385	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6387	07551	06386	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6388	07552	06387	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6389	07553	06388	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6390	07554	06389	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6391	07555	06390	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6392	07556	06391	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6393	07557	06392	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 178

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AQ	AS	AL	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
6394	07558	06393	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6395	07559	06394	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6396	07560	06395	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6397	07561	06396	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6398	07562	06397	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6399	07563	06398	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6400	07564	06399	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6401	07565	06400	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6402	07567	06401	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6403	07568	06402	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6404	07569	06403	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6405	07570	06404	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6406	07571	06405	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6407	07572	06406	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6408	07573	06407	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6409	07574	06408	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6410	07575	06409	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6411	07576	06410	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6412	07577	06411	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6413	07578	06412	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6414	07579	06413	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6415	07580	06414	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6416	07581	06415	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6417	07582	06416	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6418	07583	06417	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6419	07584	06418	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6420	07585	06419	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6421	07586	06420	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6422	07587	06421	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6423	07588	06422	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6424	07589	06423	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6425	07590	06424	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6426	07591	06425	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6427	07592	06426	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6428	07593	06427	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6429	07594	06428	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 179

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
5	6754	07971	06753	2																													
	6755	07973	06754	1																													
	6756	07974	06755	1																													
	6757	07975	06756	1																													
	6758	07976	06757	1																													
	6759	07977	06758	1																													
	6760	07981	06759	1																													
	6761	07986	06760	5																													
	6762	07987	06761	1																													
	6763	07988	06762	1																													
	6764	07989	06763	1																													
	6765	07990	06764	1																													
	6766	07991	06765	1																													
	6767	07992	06766	1																													
	6768	07994	06767	1																													
	6769	07995	06768	1																													
	6770	07997	06769	1																													
	6771	07998	06770	1																													
	6772	07999	06771	1																													
	6773	08000	06772	1																													
	6774	08001	06773	1																													
	6775	08002	06774	1																													
	6776	08003	06775	1																													
	6777	08004	06776	4																													
	6778	08005	06777	1																													
	6779	08006	06778	1																													
	6780	08007	06779	1																													
	6781	08008	06780	1																													
	6782	08009	06781	5																													
	6783	08010	06782	2																													
	6784	08011	06783	2																													
	6785	08012	06784	1																													
	6786	08013	06785	2																													
	6787	08014	06786	1																													
	6788	08015	06787	1																													
	6789	08016	06788	1																													

Table 189

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BAB	BE	BF	BG	BH	BI	BK		
6790	08017	06789	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	228407	92.7	300	1	236	852	
6791	08018	06790	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6792	08019	06791	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6793	08020	06792	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6794	08021	06793	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6795	08022	06794	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6796	08023	06795	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6797	08024	06796	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6798	08025	06797	27		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6799	08026	06798	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6800	08027	06799	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0						
6801	08028	06800	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6802	08029	06801	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6803	08030	06802	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0						
6804	08031	06803	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6805	08032	06804	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6806	08033	06805	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6807	08034	06806	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6808	08036	06807	1		0	0	0</																											

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AN	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
6826	08054	06825	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6827	08055	06826	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6828	08056	06827	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6829	08057	06828	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6830	08058	06829	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6831	08059	06830	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6832	08060	06831	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6833	08061	06832	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6834	08062	06833	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6835	08063	06834	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6836	08064	06835	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6837	08065	06836	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6838	08066	06837	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6839	08067	06838	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6840	08068	06839	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6841	08069	06840	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6842	08070	06841	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6843	08071	06842	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6844	08073	06843	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6845	08074	06844	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6846	08075	06845	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6847	08076	06846	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6848	08077	06847	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6849	08078	06848	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6850	08079	06849	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6851	08080	06850	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6852	08081	06851	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6853	08082	06852	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6854	08083	06853	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6855	08084	06854	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6856	08085	06855	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6857	08086	06856	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6858	08087	06857	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6859	08088	06858	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6860	08089	06859	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6861	08090	06860	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 191

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
6862	08091	06861	1																										0	0	97 8 225	1	1597	1821
6863	08092	06862	1																										0	0				
6864	08093	06863	1																										0	0				
6865	08094	06864	1																										0	0				
6866	08095	06865	4																										0	0				
6867	08096	06866	1																										0	0				
6868	08097	06867	1																										0	0				
6869	08098	06868	1																										0	0				
6870	08099	06869	1																										0	0				
6871	08100	06870	1																										0	0				
6872	08101	06871	1																										0	0				
6873	08102	06872	1																										0	0				
6874	08103	06873	2																										0	0				
6875	08104	06874	1																										0	0				
6876	08105	06875	2																										0	0	100 165	1	1582	1746
6877	08107	06876	1																										0	0				
6878	08108	06877	1																										0	0				
6879	08109	06878	1																										0	0				
6880	08110	06879	1																										0	0				
6881	08111	06880	1																										0	0				
6882	08112	06881	1																										0	0				
6883	08113	06882	1																										0	0				
6884	08114	06883	3																										0	0	92 8 166	1	1197	1360
6885	08115	06884	1																										0	0				
6886	08116	06885	2																										0	0				
6887	08117	06886	2																										0	0				
6888	08118	06887	3																										0	0				
6889	08119	06888	1																										0	0				
6890	08120	06889	1																										0	0				
6891	08121	06890	1																										0	0	99 5 221	1	4183	4403
6892	08122	06891	5																										0	0				
6893	08123	06892	1																										0	0				
6894	08124	06893	2																										0	0				
6895	08125	06894	1																										0	0				
6896	08126	06895	1																															

Table 192

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	CA	AK	AM	QA	CA	AS	AL	AW	AY	D	BC	BE	BF	BG	BH	BI	BK
6898	08128	06397	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6899	08129	06398	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6900	08130	06399	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6901	08131	06900	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6902	08132	06901	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6903	08133	06902	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6904	08134	06903	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		X57500	98.9	90	1	2021	2969
6905	08135	06904	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0		0					
6906	08136	06905	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6907	08137	06906	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6908	08138	06907	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6909	08139	06908	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6910	08140	06909	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6911	08141	06910	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6912	08142	06911	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6913	08143	06912	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6914	08144	06913	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6915	08145	06914	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6916	08146	06915	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0		D10923	97.7	298	1	1454	2051
6917	08147	06916	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		X59303	98.5	68	1	4016	4107
6918	08148	06917	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6919	08149	06918	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6920	08150	06919	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6921	08151	06920	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6922	08153	06921	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6923	08154	06922	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6924	08155	06923	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6925	08156	06924	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6926	08157	06925	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6927	08158	06926	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6928	08159	06927	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6929	08160	06928	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6930	08161	06929	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6931	08162	06930	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6932	08163	06931	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					
6933	08164	06932	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0					

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AK	AM	AO	AS	AV	AY	B	BC	BE	BF	BG	BI	BK
6970	08204	06969	1																											
6971	08205	06970	1																											
6972	08206	06971	1																											
6973	08207	06972	1																											
6974	08208	06973	1																											
6975	08209	06974	1																											
6976	08210	06975	1																											
6977	08211	06976	1																											
6978	08212	06977	1																											
6979	08213	06978	1																											
6980	08214	06979	1																											
6981	08215	06980	1																											
6982	08216	06981	1																											
6983	08217	06982	1																											
6984	08218	06983	1																											
6985	08219	06984	1																											
6986	08220	06985	1																											
6987	08221	06986	1																											
6988	08222	06987	1																											
6989	08223	06988	1																											
6990	08224	06989	2																											
6991	08225	06990	1																											
6992	08226	06991	1																											
6993	08227	06992	1																											
6994	08228	06993	1																											
6995	08229	06994	1																											
6996	08230	06995	1																											
6997	08232	06996	1																											
6998	08233	06997	1																											
6999	08234	06998	1																											
7000	08235	06999	3																											
7001	08236	07000	1																											
7002	08237	07001	2																											
7003	08238	07002	1																											
7004	08239	07003	1																											
7005	08240	07004	1																											

Table 195

Table 196

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AJ	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7042	08277	07041	1																														
7043	08278	07042	2																														
7044	08279	07043	4																														
7045	08280	07044																															
7046	08281	07045	1																								0457892	97.1	172	1	1145	1316	
7047	08282	07046																															
7048	08283	07047	1																														
7049	08284	07048	1																														
7050	08285	07049	1																														
7051	08286	07050	1																														
7052	08287	07051	1																														
7053	08288	07052	1																														
7054	08289	07053	1																														
7055	08290	07054	1																														
7056	08291	07055	1																														
7057	08292	07056	1																														
7058	08293	07057	1																														
7059	08294	07058	1																														
7060	08295	07059	1																														
7061	08296	07060	1																														
7062	08297	07061	2																														
7063	08298	07062	1																														
7064	08299	07063	1																														
7065	08300	07064	1																														
7066	08301	07065	1																														
7067	08302	07066	1																														
7068	08303	07067	1																														
7069	08304	07068	1																														
7070	08305	07069	1																														
7071	08306	07070	1																														
7072	08307	07071	1																														
7073	08308	07072	1																														
7074	08309	07073	1																														
7075	08310	07074	1																														
7076	08311	07075	1																														
7077	08312	07076	1																														

Table 197

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AJ	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7078	08313	07077	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7079	08314	07078	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7080	08315	07079	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7081	08316	07080	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7082	08317	07081	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7083	08318	07082	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7084	08319	07083	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7085	08320	07084	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7086	08321	07085	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7087	08322	07086	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7088	08323	07087	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7089	08324	07088	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7090	08325	07089	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7091	08326	07090	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7092	08327	07091	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7093	08328	07092	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7094	08329	07093	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7095	08330	07094	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7096	08331	07095	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7097	08332	07096	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7098	08333	07097	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7099	08334	07098	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7100	08335	07099	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7101	08336	07100	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7102	08337	07101	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7103	08338	07102	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7104	08339	07103	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7105	08340	07104	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7106	08341	07105	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7107	08342	07106	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7108	08343	07107	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7109	08344	07108	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7110	08345	07109	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7111	08346	07110	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7112	08347	07111	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7113	08348	07112	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 198

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AJ	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7150	08386	07149	1																					1	0							
7151	08387	07150	2																					1	0							
7152	08388	07151	1																					1	0							
7153	08389	07152	4																					3	1	0						
7154	08390	07153	1																					1	0							
7155	08391	07154	2																					2	1	0						
7156	08392	07155	1																					1	0							
7157	08393	07156	1																					1	0							
7158	08394	07157	1																					1	0							
7159	08395	07158	4																					4	1	0						
7160	08396	07159	2																					1	0							
7161	08397	07160	1																					1	0							
7162	08398	07161	1																					1	0							
7163	08399	07162	1																					1	0							
7164	08400	07163	1																					1	0							
7165	08402	07164	1																					1	0							
7166	08403	07165	1																					1	0							
7167	08404	07166	2																					2	1	0						
7168	08405	07167	1																					1	0							
7169	08406	07168	1																					1	0							
7170	08407	07169	1																					1	0							
7171	08408	07170	1																					1	0							
7172	08409	07171	1																					1	0							
7173	08410	07172	1																					1	0							
7174	08411	07173	1																					1	0							
7175	08412	07174	2																					2	1	0						
7176	08413	07175	1																					1	0							
7177	08414	07176	1																					1	0							
7178	08415	07177	1																					1	0							
7179	08416	07178	1																					1	0							
7180	08417	07179	1																					1	0							
7181	08418	07180	1																					1	0							
7182	08419	07181	1																					1	0							
7183	08420	07182	2																					2	1	0						
7184	08421	07183	1																					1	0							
7185	08422	07184	1																					1	0							

Table 200

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AO	AS	AT	AV	AW	AX	AY	B	C	D	E	F	G	H	I	BK
7186	08423	07185	1																																		
7187	08424	07186	3																																		
7188	08425	07187	1																																		
7189	08426	07188	1																																		
7190	08427	07189	1																																		
7191	08428	07190	1																																		
7192	08429	07191	1																																		
7193	08430	07192	1																																		
7194	08431	07193	1																																		
7195	08432	07194	2																																		
7196	08434	07195	1																																		
7197	08435	07196	2																																		
7198	08436	07197	1																																		
7199	08437	07198	1																																		
7200	08438	07199	4																																		
7201	08439	07200	1																																		
7202	08440	07201	1																																		
7203	08441	07202	1																																		
7204	08442	07203	1																																		
7205	08443	07204	1																																		
7206	08444	07205	2																																		
7207	08445	07206	1																																		
7208	08446	07207	1																																		
7209	08447	07208	1																																		
7210	08448	07209	1																																		
7211	08449	07210	1																																		
7212	08450	07211	1																																		
7213	08451	07212	1																																		
7214	08452	07213	1																																		
7215	08453	07214	1																																		
7216	08454	07215	1																																		
7217	08455	07216	1																																		
7218	08456	07217	1																																		
7219	08457	07218	1																																		
7220	08458	07219	2																																		
7221	08459	07220	1																																		

Table 201

Table 202

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7222	08460	07221	2																							0							
7223	08461	07222	1																							0							
7224	08462	07223	1																							0							
7225	08463	07224	1																							0							
7226	08464	07225	1																							0							
7227	08465	07226	1																							0							
7228	08466	07227	1																							0							
7229	08467	07228	1																							0							
7230	08468	07229	1																							0							
7231	08469	07230	1																							0							
7232	08470	07231	2																							0							
7233	08471	07232	1																							0							
7234	08472	07233	1																							0							
7235	08473	07234	1																							0							
7236	08474	07235	1																							0							
7237	08475	07236	1																							0							
7238	08476	07237	1																							0							
7239	08477	07238	2																							0							
7240	08478	07239	1																							0							
7241	08479	07240	1																							0							
7242	08480	07241	1																							0							
7243	08481	07242	1																							0							
7244	08482	07243	1																							0							
7245	08483	07244	1																							0							
7246	08484	07245	1																							0							
7247	08485	07246	1																							0							
7248	08486	07247	1																							0							
7249	08487	07248	1																							0							
7250	08488	07249	1																							0							
7251	08489	07250	1																							0							
7252	08490	07251	1																							0							
7253	08491	07252	1																							0							
7254	08492	07253	1																							0							
7255	08493	07254	1																							0							
7256	08494	07255	1																							0							
7257	08495	07256	1																							0							

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7258	08496	07257	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7259	08497	07258	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7260	08498	07259	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7261	08499	07260	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7262	08500	07261	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7263	08501	07262	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7264	08502	07263	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7265	08503	07264	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7266	08504	07265	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7267	08505	07266	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7268	08506	07267	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7269	08507	07268	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7270	08508	07269	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7271	08509	07270	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7272	08510	07271	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7273	08511	07272	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7274	08512	07273	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7275	08513	07274	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7276	08514	07275	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7277	08515	07276	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7278	08516	07277	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7279	08517	07278	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7280	08518	07279	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7281	08519	07280	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7282	08520	07281	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7283	08521	07282	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7284	08522	07283	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7285	08523	07284	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7286	08524	07285	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7287	08525	07286	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7288	08526	07287	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7289	08527	07288	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7290	08528	07289	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7291	08529	07290	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7292	08530	07291	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7293	08531	07292	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 203

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7294	08532	07293	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7295	08533	07294	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7296	08534	07295	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7297	08535	07296	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7298	08536	07297	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7299	08537	07298	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7300	08538	07299	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7301	08539	07300	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7302	08540	07301	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7303	08541	07302	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7304	08542	07303	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7305	08543	07304	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7306	08544	07305	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7307	08545	07306	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7308	08546	07307	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7309	08547	07308	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7310	08548	07309	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7311	08549	07310	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7312	08550	07311	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7313	08551	07312	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7314	08552	07313	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7315	08553	07314	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7316	08554	07315	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7317	08555	07316	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7318	08556	07317	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7319	08557	07318	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7320	08558	07319	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7321	08559	07320	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7322	08560	07321	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7323	08561	07322	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7324	08563	07323	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7325	08564	07324	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7326	08565	07325	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7327	08566	07326	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7328	08567	07327	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7329	08568	07328	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 204

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7366	08606	07365	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7367	08607	07366	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7368	08608	07367	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7369	08609	07368	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7370	08610	07369	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7371	08611	07370	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7372	08612	07371	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7373	08613	07372	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7374	08614	07373	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7375	08615	07374	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7376	08616	07375	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7377	08617	07376	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7378	08618	07377	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7379	08619	07378	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7380	08620	07379	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7381	08621	07380	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7382	08622	07381	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7383	08623	07382	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7384	08624	07383	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7385	08625	07384	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7386	08626	07385	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7387	08627	07386	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7388	08628	07387	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7389	08629	07388	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7390	08630	07389	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7391	08631	07390	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7392	08632	07391	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7393	08633	07392	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7394	08634	07393	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7395	08635	07394	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7396	08636	07395	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7397	08637	07396	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7398	08638	07397	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7399	08639	07398	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7400	08640	07399	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7401	08641	07400	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 206

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	CA	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7402	08642	07401	1																														
7403	08643	07402	1																														
7404	08644	07403	1																														
7405	08645	07404	1																														
7406	08646	07405	1																														
7407	08647	07406	1																														
7408	08648	07407	1																														
7409	08649	07408	1																														
7410	08650	07409	1																														
7411	08651	07410	1																														
7412	08652	07411	1																														
7413	08653	07412	1																														
7414	08654	07413	1																														
7415	08655	07414	1																														
7416	08656	07415	1																														
7417	08657	07416	1																														
7418	08658	07417	1																														
7419	08659	07418	1																														
7420	08660	07419	1																														
7421	08661	07420	1																														
7422	08662	07421	1																														
7423	08663	07422	1																														
7424	08664	07423	2																														
7425	08665	07424	1																														
7426	08666	07425	1																														
7427	08667	07426	1																														
7428	08668	07427	1																														
7429	08669	07428	1																														
7430	08670	07429	1																														
7431	08671	07430	1																														
7432	08673	07431	1																														
7433	08674	07432	2																														
7434	08675	07433	1																														
7435	08676	07434	1																														
7436	08677	07435	1																														
7437	08678	07436	1																														

Table 207

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7474	08715	07473	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7475	08716	07474	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7476	08717	07475	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7477	08718	07476	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7478	08719	07477	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7479	08720	07478	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7480	08721	07479	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7481	08722	07480	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7482	08723	07481	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7483	08724	07482	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7484	08725	07483	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7485	08726	07484	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7486	08727	07485	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7487	08728	07486	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7488	08729	07487	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7489	08730	07488	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7490	08731	07489	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7491	08732	07490	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7492	08733	07491	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7493	08734	07492	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7494	08735	07493	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7495	08736	07494	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7496	08737	07495	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7497	08738	07496	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7498	08739	07497	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7499	08740	07498	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7500	08741	07499	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7501	08742	07500	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7502	08743	07501	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7503	08744	07502	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7504	08745	07503	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7505	08746	07504	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7506	08747	07505	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7507	08748	07506	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7508	08749	07507	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7509	08750	07508	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

97.3 335 1 471 952
91.7 338 1 5220 8201
94 336 1 1501 2399

0M32886
0X63547
0X70649

Table 209

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AN	AO	AS	AL	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7510	08751	07509	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7511	08752	07510	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7512	08753	07511	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7513	08754	07512	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7514	08755	07513	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7515	08756	07514	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7516	08757	07515	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7517	08758	07516	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7518	08759	07517	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7519	08760	07518	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7520	08761	07519	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7521	08762	07520	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7522	08763	07521	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7523	08764	07522	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7524	08765	07523	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7525	08766	07524	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7526	08768	07525	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7527	08769	07526	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7528	08770	07527	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7529	08771	07528	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7530	08772	07529	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7531	08773	07530	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7532	08774	07531	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7533	08775	07532	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7534	08777	07533	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7535	08778	07534	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7536	08779	07535	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7537	08780	07536	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7538	08781	07537	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7539	08782	07538	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7540	08783	07539	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7541	08785	07540	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7542	08786	07541	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7543	08787	07542	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7544	08788	07543	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7545	08789	07544	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 210

[illegible]

Table 212

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7582	08827	07581	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7583	08828	07582	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7584	08829	07583	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7585	08830	07584	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0						
7586	08831	07585	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7587	08832	07586	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7588	08833	07587	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7589	08834	07588	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7590	08835	07589	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7591	08836	07590	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7592	08837	07591	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7593	08838	07592	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7594	08839	07593	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7595	08840	07594	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7596	08841	07595	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7597	08842	07596	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7598	08843	07597	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7599	08844	07598	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7600	08845	07599	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7601	08846	07600	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7602	08848	07601	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7603	08849	07602	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7604	08850	07603	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7605	08851	07604	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7606	08852	07605	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7607	08853	07606	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7608	08854	07607	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7609	08855	07608	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0						
7610	08856	07609	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7611	08857	07610	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7612	08858	07611	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0						
7613	08859	07612	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7614	08860	07613	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7615	08861	07614	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7616	08862	07615	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7617	08863	07616	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AK	AM	AN	AO	AP	AQ	AS	AT	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7618	08864	07617	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7619	08865	07618	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7620	08866	07619	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7621	08867	07620	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7622	08868	07621	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7623	08869	07622	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7624	08870	07623	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7625	08871	07624	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7626	08872	07625	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7627	08873	07626	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7628	08874	07627	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7629	08875	07628	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7630	08876	07629	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7631	08877	07630	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7632	08878	07631	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7633	08879	07632	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7634	08880	07633	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7635	08881	07634	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7636	08882	07635	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7637	08883	07636	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7638	08884	07637	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7639	08885	07638	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7640	08886	07639	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7641	08887	07640	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7642	08888	07641	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7643	08889	07642	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7644	08890	07643	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7645	08891	07644	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7646	08892	07645	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7647	08893	07646	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7648	08894	07647	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7649	08895	07648	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7650	08896	07649	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7651	08897	07650	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7652	08898	07651	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7653	08899	07652	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 213

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	BA	BC	DE	BF	BG	BH	BI	BK
7690	08939	07689	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7691	08940	07690	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7692	08941	07691	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7693	08942	07692	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7694	08943	07693	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7695	08944	07694	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7696	08945	07695	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7697	08946	07696	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7698	08947	07697	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7699	08948	07698	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7700	08949	07699	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7701	08950	07700	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7702	08951	07701	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7703	08952	07702	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7704	08953	07703	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7705	08954	07704	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7706	08955	07705	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7707	08956	07706	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7708	08957	07707	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7709	08958	07708	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7710	08959	07709	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7711	08960	07710	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7712	08961	07711	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7713	08962	07712	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7714	08963	07713	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7715	08964	07714	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7716	08965	07715	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7717	08966	07716	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7718	08967	07717	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7719	08968	07718	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7720	08969	07719	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7721	08970	07720	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7722	08971	07721	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7723	08972	07722	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7724	08973	07723	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7725	08974	07724	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 215

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7726	08975	07725	1																															
7727	08976	07726	1																															
7728	08977	07727	1																															
7729	08978	07728	1																															
7730	08979	07729	1																															
7731	08980	07730	1																															
7732	08981	07731	1																															
7733	08982	07732	1																															
7734	08983	07733	1																															
7735	08984	07734	1																															
7736	08985	07735	1																															
7737	08986	07736	1																															
7738	08987	07737	1																															
7739	08988	07738	2																															
7740	08989	07739	1																															
7741	08990	07740	1																															
7742	08991	07741	1																															
7743	08992	07742	1																															
7744	08993	07743	1																															
7745	08994	07744	1																															
7746	08995	07745	1																															
7747	08996	07746	1																															
7748	08997	07747	1																															
7749	08998	07748	1																															
7750	08999	07749	1																															
7751	09000	07750	1																															
7752	09001	07751	1																															
7753	09002	07752	1																															
7754	09003	07753	1																															
7755	09004	07754	1																															
7756	09005	07755	1																															
7757	09006	07756	1																															
7758	09007	07757	1																															
7759	09008	07758	1																															
7760	09009	07759	1																															
7761	09010	07760	1																															

Table 216

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7762	09011	07761	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7763	09012	07762	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7764	09013	07763	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7765	09014	07764	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7766	09015	07765	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7767	09016	07766	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7768	09017	07767	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7769	09018	07768	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7770	09019	07769	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7771	09020	07770	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7772	09021	07771	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7773	09022	07772	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7774	09023	07773	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7775	09024	07774	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7776	09025	07775	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7777	09026	07776	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7778	09027	07777	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7779	09028	07778	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7780	09029	07779	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7781	09030	07780	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7782	09031	07781	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7783	09032	07782	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7784	09033	07783	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7785	09034	07784	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7786	09035	07785	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7787	09036	07786	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7788	09037	07787	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7789	09038	07788	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7790	09039	07789	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7791	09040	07790	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7792	09041	07791	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7793	09042	07792	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7794	09043	07793	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7795	09044	07794	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7796	09045	07795	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7797	09046	07796	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 217

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7798	09047	07797	1																							0	0	1	95	261	1	103	1163
7799	09048	07798	1																							0	0						
7800	09049	07799	1																							0	0						
7801	09050	07800	3																							0	0						
7802	09051	07801	8																							0	0						
7803	09052	07802	1																							0	0						
7804	09053	07803	1																							0	0						
7805	09054	07804	1																							0	0						
7806	09055	07805	1																							0	0						
7807	09056	07806	1																							0	0						
7808	09057	07807	1																							0	0						
7809	09058	07808	1																							0	0						
7810	09059	07809	1																							0	0						
7811	09060	07810	1																							0	0						
7812	09061	07811	1																							0	0						
7813	09062	07812	1																							0	0						
7814	09063	07813	1																							0	0						
7815	09064	07814	1																							0	0						
7816	09065	07815	1																							0	0						
7817	09066	07816	1																							0	0						
7818	09067	07817	1																							0	0						
7819	09068	07818	1																							0	0						
7820	09069	07819	1																							0	0						
7821	09070	07820	1																							0	0						
7822	09071	07821	1																							0	0						
7823	09072	07822	1																							0	0						
7824	09073	07823	3																							0	0						
7825	09074	07824	1																							0	0						
7826	09075	07825	2																							0	0						
7827	09076	07826	1																							0	0						
7828	09077	07827	1																							0	0						
7829	09078	07828	1																							0	0						
7830	09079	07829	1																							0	0						
7831	09080	07830	2																							0	0						
7832	09081	07831	1																							0	0						
7833	09082	07832	1																							0	0						

Table 218

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AQ	AS	AL	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7834	09083	07833	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7835	09084	07834	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7836	09085	07835	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	XS5976	92 287	1	3066	3419
7837	09086	07836	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7838	09087	07837	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						

Table 219

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT:

(A) NAME: CHUGAI PHARMACEUTICAL CO., LTD.
(B) STREET: 41-8, Takada 3-chrome, Toshima-ku
(C) CITY: Tokyo
(E) COUNTRY: JAPAN
(F) ZIP: 171

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(ii) TITLE OF INVENTION: GENE SIGNATURE

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(iii) NUMBER OF SEQUENCES: 7848

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.5 in., DS, 1.44 MB
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/ MS-DOS
(D) SOFTWARE: MS-DOS

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(v) CURRENT APPLICATION DATA

(A) APPLICATION NUMBER: EP 95900295.7

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(vi) PRIOR APPLICATION DATA

(A) APPLICATION NUMBER: PCT/JP94/01916
(B) FILING DATE: 11. November 1994

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SEQ ID NO:1

SEQUENCE LENGTH:704

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00001

SEQUENCE DESCRIPTION:

GATCTTCAAA CAAGCATCAG CGTTTTCCAG GGCTTCCCAG AGGTCTGTGC GACTAGCCCC 60
 TGTCTATCAA AAGTTATTAG AGAGGATGAA GCATTAGCTT GAAGCACTAC AGGAGGAATG 120
 CACCACGGCA GCTCTCCGCC AATTTCTCTC AGATTTCAC AGAGACTGTT TGAATGTTTT 180
 CAAAACCAAG TATCACACTT TAATGTACAT GGGCCGCACC ATAATGAGAT GTGAGCCTTG 240
 TGCATGTGGG GGAGGAGGGA GAGAGATGTA CTTTTAAAT CATGTTCCCC CTAAACATGG 300
 CTGTTAACC ACTTGCATGC AGAACTTGG GATGTCATT GCCTGACATT CACTTTCCAG 360
 GAGAGGACCC TATCCCCAA TGTGGAATTG ACTTGCCTAT GGCCAAGGTC CCTTGGNAAA 420
 GGGAGCTTCA GTATTGTGG GGGCNTCATA AAACCATGGN TTCAAGNCAA TCCAGCCTCA 480
 TNGGGNNGT CCTGGGNACA GTTTTTGGT AAAGGCCCTT GGCCAGNTG GGGGGAATGG 540
 GCCTCCTTT TAAGNTTTGG GNTGGAATNG TCTNGCAAAT TGGGGCTCCC ATTCNCGGG 600
 GGTITGGGG TTTTNGGG CTTNCCNGG NNGGAAGGN TGGGTTGGG GGNTNGGTTN 660
 CCNTTGGNG GGCCTGGGN TTTGATTNA CCCGGGNCCT NGGN 704

SEQ ID NO:2

SEQUENCE LENGTH:659

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00002

SEQUENCE DESCRIPTION:

GATCTTTAAA ATACACACTC AAATCAAGAA ACTTAAGGT ACCTTTNTTC CCAAATTTCA 60
 TACCTATCAT CTAAAGTAGG GACTTCTGTC TTCACAACAN ATTATNACCT TACAGAAGTT 120
 TGAATTATCC GGTCTGGGTTT TATTGTTTAA AATCATTCT GCATCAGCTG CTGAAACAAC 180
 AAATAGGAAT TGTTTTATG GAGGCTTTGC ATAGATTCCC TGAGCAGGAT TTTAATCTTT 240
 TNCTAACTGG ACTGGTTCAA ATGTTGTNCT CTTCTTTAAA GGGATGGCAA GATGTGGGCA 300
 GTGATGTCAC TTAGGGCAGG GACAGGATAA GAGGGNTAG GGAGAGAAGA TAGCAGGGCA 360
 TGGCTGGGAA CCCAAGTCCA AGCATACCAA CACGGAGCAG GCTACTGTCA AGCTCCCTC 420
 GGAGCGGNG CTGGTTCACA GCCAGCTGGC ACCAGNTTT NTNGNGGAAG NCTTTTCAA 480
 ACAGTCTCAG GNAATCCAAT NTGCAAAGAC TTGCTTNTAG NAAAACCCAG NAGTTGAAAG 540
 GCTCCCAAGN ATTTAAGGG NACTTNCCAA AACGGGCCCC CNGGNNCCTT TTGGGTTNG 600
 GGGNTCAAAA CCCCGGAGG GTTTGGGAAG NTTTTAATTG GNTTTAAAN ATNNNTNTN 659

SEQ ID NO:3

SEQUENCE LENGTH:625

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00003

SEQUENCE DESCRIPTION:

GATCTAACTG GGTACCTGAG ATATTTNACA GCTGGACCTA GTTTCACAAT CTGTTGTCTC 60

CAGCTCTGCA TATGCTGGC CAGGGGGCTT CTAGGAAGTA GGTTCATCT ATCAAATGTC 120
 TCCTCTGACT TCCTTTTGAA ACTTACTGCT CTCTGTTTT ATTTTGTTC GTTTGAAGCT 180
 CAGAGGGAGA TGGGCAATTG ACAGGGATGC AATCCAGGGT GGGATTCTT GAGGAAGTTA 240
 CAAATAAGCT TGTACAACA TCAAGATAGA TGGAAATGGA AGGATGCTAC CAGGAGAGTA 300
 CTTACATAGT GCTCAGGAGT TTCTCTTCTT AAAATGTTA CTGCTGAAAG ATGAGCAGGA 360
 CCAGGGCGTT ATAGGCAGAG CCCTAGCCGA GAAACCTGCT GGCCTCTGCC TGTTCATT 420
 TCCCACTTTT GGTGTGTGTG GCATTACTTT CAGAATTTGC ACTTTCCTGC TTGTCATGAC 480
 TTTTGTGCA CACTTGCCAT GACGGGTGTT TCTGNGAACC ATGGAAGTTT TGCGGTAGTG 540
 CCTCCAGGGG CAGGGGGNAA GGAGNGGTG TACTGTCATT TNGTNCAAT AAATCCNGCC 600
 TATTGTTAAT NAACCACTCT TTTGN 625

SEQ ID NO:4

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00004

SEQUENCE DESCRIPTION:

GATCTGCCAG GCTGGGGTGT TTTCGGTATC TGCTGTTTAC AGGTCTCCAC TGTAAATCCGA 60
 ATACTTTGCC AGTGCACTAA TCTCTTTGGA GATAAAATTC ATTAGTGTGT TACTAAATGT 120
 NAATTTTNTT TTGCGGAAAA TACAGTACCG TGTCTGANTT AATTATTAAT ATTNAAAAA 180
 CTTCAATCCT TAACCTCTCC TCATTGCTT TGCCACAGC CTATTCAGTT CCTTTGTTG 240
 GCAGGNTTCT GCAAAA 256

SEQ ID NO:5

SEQUENCE LENGTH:616

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00005

SEQUENCE DESCRIPTION:

GATCAAGCTC AAGAATAAGC TGAAATATGG CCAGACTATC AGGCCCATTT NTCTCCCTG 60
 CACCGAGGGA ACAACTCGAG CTTTGAGGCT TCCTCCACT ACCACTGCC AGCAACAAAA 120
 GGAAGAGCTG CTCCCTGCAC AGGATATCAA AGCTCTGTTT GTGCTGAGG AGGAGAAAAA 180
 GCTGACTCGG AAGGAGGTCT ACATCAAGAA TGGGGATAAG AAAGGCAGCT GTGAGAGAGA 240
 TGCTCAATAT GCCCAGGCT ATGACAAAGT CAAGGACATC TCAGAGGTGG TCACCCCTCG 300
 GTTCCTTTGT ACTGGAGGAG TGAGTCCCTA TGCTGACCCC AATACTTGA GAGGTGATTC 360
 TGGCGGCCCC TTGATAGTTC ACAAGAGAAG TCGTTTCATT CAAAGTTGGT GTAATCAGCT 420
 GGGGGAGTAA GTGGGATGTN TGCAAAAACC AGAAGGCGGC AAAAGCAGGT ACCTGNTTCA 480
 NGGCCCGAAC TTTCACATCA NCTNTTCAA GGTNTNCCT GGNTGAGNG GAACNTCCAN 540
 GTTGGGGGTT TTGGGTTTTT TTAAGGGGTT CNTGTTNGCA AGGGGGTTGG GNTTNNTTA 600
 NNCCTGTTNN GNACCN 616

SEQ ID NO:6

SEQUENCE LENGTH:615

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00006

SEQUENCE DESCRIPTION:

5 GATCTCTGCT ATTTTANCCC CCCAAATAAG TTATTGTCC TTAAAGGTTG GTTACNNATA 60
 ATACCCCTCA GTAAGATTCC AGTATTAATT TCTGGGCAGT TTGTTCTCTG TATACAATTG 120
 CAAATGATAA GCATTTTGT GAGTGACCAC CTTTGCAATA TGTTTGTAA TTNTTCATGT 180
 TGGGTTCTTT CTGAAATGTA CATCTTTACA TAAAAACCTC ACATTCTACT TGATTTACAC 240
 TTCCTAGTCT ACATTACATG TGGTTGAAGG TTTTATACAT TCTATATGCT TTTACTAAAT 300
 10 ATACAAGATT TACTACTAGA AATTGGGAGA AAGAACAATA ACACATGTAC TTGTGATTG 360
 TTCATGTTAT ATTAACCT TGAGATTGT GTATTATGT AGGGGGGGGT ATTGNCCAGG 420
 NCTGNTGGTT TTTGCTCCN TGGGGCTATT NTAATAAANC NGGGGTATNG GGTGNTGGC 480
 CTNGGTTTGG GCCTAAANTT GGATATATNT GGGGTTCTT NGNTTTTACC AAAATNGNTT 540
 15 TTGGTTGGTA GGGTTNTTAT TGGACCCNNT CCTGGGCCTG GGATAATNTG GCNGNTTCCC 600
 NGGANAAAAAN NCCCN 615

SEQ ID NO:7

SEQUENCE LENGTH:608

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00007

SEQUENCE DESCRIPTION:

25 GATCAAACCA AAGGAAAAGT GTTGCTAGAG AAAATTGGGG AAAAGGTGAA AAAGAAAAA 60
 TGGTAGTAAT TGAGCAGAAA AAAATTAATT TATATATGTA TTGATTGGCA ACCAGATTTA 120
 TCTAAGTAGA ACTGAATTGG CTAGGAAAAA AGAAAACTG CATGTTAATC ATTTTCCTAA 180
 GCTGTCCTTT TGAGGCTTAG TCAGTTTATT GGGAAAATGT TTAGGATTAT TCCTTGCTAT 240
 TAGTACTCAT TTTATGTATG TTACCCTTCA GTAAGTTCTC CCCATTTTAG TTTTCTAGGC 300
 30 TGAAAGGATT CTTTCTACA TTATACATGT GTGTTGTAT ATTTGGCTTT TGCTATATAC 360
 TTTACCTTCA TTGTTAAATT TTTGTATTGT ATAGTTNCTT TGGNGGTATC TTAACCCCT 420
 ATTTTGTAAA ACCAACCTTG GCTTTGNTAA NCATTGGGC CGCTGGGTA NGTCCGGACC 480
 TNNCCTTNC CCCNAGGGCC TGCAGGAGN GCCGNTNN CCGGGGNGTT GGNCCGNNG 540
 35 CTTTCCCGAT TTTTNGGGT TGGTCCTTN GGTNCCGGC NTCTGTANGG GGTNCNCTT 600
 TNNNCCN 608

SEQ ID NO:8

SEQUENCE LENGTH:606

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00008

SEQUENCE DESCRIPTION:

45 GATCGCTTCC TAGAAATAAG CAACACCTCT CCCAAAAAGC AGCCCAACAG GCAGGGGCCA 60
 GCAGCCAGC CATCACTCAT CTTNAGGAA ATNAGTTGGT AGCCTCTGTG CACTGTTTGG 120
 TGGCCACATC ANNGGTGATG TCCTGTTTAC ATACCTGCTT GTATTAAAG CCCTCAGTCT 180
 GTCCTGTTGT GTGGGGCGAA GTGATGGACT CTGCCAGGTG GACATGCTGT GGGTGGATGT 240
 TCCCGGCGTG TGCCGGCCTG AATGGACAGG GGTCACTTCA CAAGCATGTC AGGGAAAAATC 300
 50 ACTGTCACAC AATCCAATG GATTTTGTG TCTTTTGAA AAAAAAAT TCTTAGCGT 360
 AAACCATGNA TTTTTTCA ATGTAGNCCC TTGGGGANTG AANTGAAAT TTGGGCTTCT 420

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TCANATNCGN AAAATNAAAT TTTTACCCCT GAGGGGGGGA GCCCCTTTCT GAAAGAAGGT 480
 NTGGGCCAAA AGCCCTTTTA ATGNTTGCTG GCCNTTGNTG GTTTNANNG TCCANTTTGC 540
 TTGGGGCGAA NGCCGNNNTG ANAAAGGTGG GTTTCNCTGG NGGNTTTAAG GNGGTGGTTT 600
 GNTTTN 606

SEQ ID NO:9

SEQUENCE LENGTH:606

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00009

SEQUENCE DESCRIPTION:

GATCTTCANN NGTTAAGCAC TTGCTCTNAA GATTAAAATT CCTTTTCTTT TTAAGGTAA 60
 GGGTGTGTAC GTATGGCAGT GATGTCTATG TTGAGATTAA CTTATGTATT GAGGAAAATT 120
 TGAAGTTTAT TTTTTCGATG AATAAGGCTG TCAAATNATT TAGTATAGAT TAATGACATC 180
 TTTTITAGAA ATATTAAAGT GAGTATTCCT CATTATGTCA TCATTTCTGA TAATTAGAGT 240
 GCTAATTGA ATGTTAGATA ATGNTCCAC ATCTATACCT ATTTCTTTCT AGGGCACTTC 300
 TGACCCCTGGG GCTTGGGGAT GGCCTTTAGG CACAAGTAGT GTCTGTGTTA AGTTCATAA 360
 ATGTGTATTT AATGAGAAAC ATTCCNATGT AAAAATGTGT GTATGTGAAC GTATGCNNAC 420
 ATTGTTATTG TGCACCNGTA CATTGTGAAG AAGTAGTTTN GAAATTTTGT AANGCACAAAC 480
 CCTTAANGNG GTGTGGAGTT ATTAAANTGN TGTAGGCNCA AATGTAATGT TTAGCCTATA 540
 AAAGGCCCTC CTATTGTCCN TNGGCAAGGC TTTGNCNCTT GNAANTAAAN CCCGTNTTTG 600
 TTTAAA 606

SEQ ID NO:10

SEQUENCE LENGTH:606

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00010

SEQUENCE DESCRIPTION:

GATCAGGGGA GACCCCAACT GCCAGATATA TTTTAATGTA CAAAACGTAA ACCAGATGAA 60
 ATAATGTTCT GTCACGTGAA ATATTAAAGT ATATAGTATA TTTATACTCT AGAACATGCA 120
 CATTATATA TATATGTATA TGTATATATA TATAGTAACT ACTTTTATA CTCCATACAT 180
 AACTTGATAT AGGAAGCTGT TTATTATTC ACTGTAAGTT TATTTTTTCT ACACAGTAAA 240
 ACTTGACTA TGTTAATACC TTGTCCTATG TCAATTTGTA TATCATGAAA CACTTCTCAT 300
 CATATTGTAT GTAAGTAATT GCATTTCTGC TCTTCCAAAG CTCCTGCGTC TGTTTTTAAA 360
 GAGCATGGAA AAATACTGCC TAGGAAAATG CAAAATGGAA ATAGGAGAGA GTAGGTTTTC 420
 CAGCTTAGTT TTGAGGGGGG CCGGTTACCT TGTATATTCC CCCATTCACT TTTGGTGTCC 480
 ATGTGTAGGG GAAGGTAAAG GGGTGGTTCC ATAATCAAGT TCCCGTGGG GTGTNCCCCC 540
 TGTTAAATGT CCCTGGTTTG GTGTTACCCG GGCTTTATGG GGNCCTTTCA TTATTTCCGG 600
 TNGGGN 606

SEQ ID NO:11

SEQUENCE LENGTH:598

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00011

SEQUENCE DESCRIPTION:

5 GATCAACAAA AGATAAACAA ATTTGCACGG AATACAAGTA GAATCACAGA GCTGAAGGAA 60
 GAAATAGAAG TAAAAAAGAA ACAACTCCAA AACCTAGAAG ATGCTTGTA TGACATCATG 120
 CTTGCAGATG ATGATTGCTT AATGATACCT TATCAAATTG GTGATGTCTT CATTAGCCAT 180
 TCTCAAGAAG AAACGCAGAA ATGTTAGAAG AAGCAAAGAA AAATTGCAA GAAGAAATTG 240
 ACGCCTTAGA ATCCAGAGTG GAATCAATTC AGCGAGTGTT AGCANGATTT GAAAGTTCAG 300
 10 TTGTATGCAA AATTCTGGGAG CAACATAAAC CTTGAAGCTN GATGAAAGTT AAACATTTTA 360
 TAATACTTTT TTTATTTGNT TTAATAANCT TGATTATTG TTTAANATGG TAATTTTTC 420
 TTCTTCANAT GGCNNNGGT NAGCAANCT TTCTTTTTT AAAAAATTT CCANTTGT 480
 AATGGGGAAC TTTGCCNTT TTCNCATGG CNTGNTNATT NATTTNTNT TTTAAAGGG 540
 15 GGGCCAGTTT TCCCCNNGG TTTTTGNCT TNCGGTTNT TNCAGGNTN GGGGGTCN 598

SEQ ID NO:12

SEQUENCE LENGTH:597

SEQUENCE TYPE:nucleic acid

20 TOPOLOGY:linear

CLONE:HUMGS00012

SEQUENCE DESCRIPTION:

25 GATCGACAGA CCTGAAGCCA TCAGTGAAGA GAGGTTGCGA GAGATGTTG GTTTATATGG 60
 TCAGACAACA GGAAAGGGGA GTATATCTCT GAAAGAACTG AATGCCCGAC CTTAGAAGT 120
 TTTCATGTGT AGTGTGCTCA AAAGACAAGG TTACGGAGAA GGCTTCGCT GGATGCACA 180
 GTACATTGAT TAACACAAAC TCACATTGGT TCCAGGTCTC AACGTTGAG CTTACTCAGA 240
 GATTTGATTG CTCAACATGC ATAATTGAA TTCAATAGAC TTTTGCTNGG TTATAAACA 300
 30 GATGTTTTT AGATTATTA TATTAANTCA ACTTAATTG ANTNGAAT NGAAANCTGA 360
 TTCAAGTAAG NTTGAGTAT CACANTGTTA GCTTTCCTAA TTCCATAAAN GTACCTGGG 420
 TTTTTCNAG NTTTATAAAT CTGGCCATCA NCCCCNGCG CCTTTNGTA AAGGGGCACC 480
 TTTTCNGCA GGCCATTGG NAGCNCITTT TTAACCACCT TGGGNTTTT AACCTTTT 540
 TNAAGGGNCN NCNTGGTTAA NTTTTTNTT GGGCCTTNC NGGGCCTGGT NTTAAN 597

35 SEQ ID NO:13

SEQUENCE LENGTH:593

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS00014

SEQUENCE DESCRIPTION:

45 GATCTTCCAA AGCACTATTT GTTGTAATA CTTTTCTAAA TGTAGTGCCT TTAAAGGAAA 60
 AATGAACACA GGGAAAGTAC TTTGCTACAA ATAATGTTG TGTGTTAAGT ATTCATATTA 120
 AATACATGCC TTCTATATGG AACATGGCAG AAAGACTGAA AAATAACAGT AATTAATTGT 180
 GTAATTCAGA ATTCATACCA ATCAGTGTG AACTCAAAC ATTGCAAAAG TGGGTGGCAA 240
 TATTCAGTGC TTAACACTTT TCTAGCGTTG GTACATCTGA GAAATGAGTG CTCAGGTGGA 300
 TTTTATCCTC GCAAGCATGT TGTATAAGA ATTGTGGGTG TGCCTATCAT ACCANTGT 360
 50 TTCTGTATCT TGA AAAAGTA TTCTCCACAT TTTANATGGT TTTATATNG GGGATTCCTT 420
 TAATGCCCC TTGGNCAAT TTATATATAT GGGCCCCATN GTTNCNTTT NAATTTTNG 480
 GTTTTNGGT GTAAGGGNCN TGCNCNTATG GTGGGGCCCT CCCAAAANTG GGANCANGNT 540

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TTNCCTNNG GACNCCNNT TGGTTGTTNA GGGGGGCCAA TTTTCNTNC CCN 593

SEQ ID NO:14

SEQUENCE LENGTH:574

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00015

SEQUENCE DESCRIPTION:

GATCGTNCCTG CAGTGGGAGC GTGTGACTGC GGAAGTTGTG AAGCCACGGG AAACCTGGAG 60
 CCTAGAGCAG CAGCTCAGCG CTTCTATGGG AAGCGGTCTC GAGCAGAAGC CCCACTGAAG 120
 TGTCCCTTGG CAGACACCCA CATGAACTCT TCCGAGAAAC TCCAGTTCTA TAAAGAGAAA 180
 GCCCCAGATT GCCATGGGCC AGTNTTGAAA CACGAAGCTA TCTCAAGCCA GGAGTCAAAG 240
 AAGAGCAAGA AGAGACCTTT TGAGGAGTCA GAGACAGAAC AGAATAACTC TTCACAACCT 300
 TCAAAGCAGA AATATGTATG TTTGCTGTG GAAGACTGGG GACTTGTTAA ATTCCTATTG 360
 ATTAAGTAGA TACAAGTTGA CCTTCTCTG GCCCCCAGCT CTAGTGTTG AGTAAAGGGA 420
 GACTNAGGGT GGGTTTACTT TTTTNGGTTT GNATTTANCC TATTGGCATT TAGNCATAGG 480
 TAAGGCGGTN TTTTCNNCT TTTNTGGNT TTGGGNGGGG GATTNTNTNN GGGGNNNAA 540
 AAAANTNCC ANGGGNTTTT TCCAAANCA NGGN 574

SEQ ID NO:15

SEQUENCE LENGTH:573

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00016

SEQUENCE DESCRIPTION:

GATCAGCCCA GAGGAATGCT GAGAAATCAC CTGGAGGAGG GAGCAGAAAG AGAAGGTTTT 60
 TAAGGAGGGG CTTCTGAATA CTTGGGAGAT ACGGAACGGA CCAAGGACCA CACTCCAGGG 120
 TGCATTGCTT GCTCCCTGGG GCACCACTTC TGGATTACAG TGTGCCAGGT CCTTTGGAGG 180
 CCCTACCCCT TCCCCATTCA TTGCCACCAG TGAGAAATNG GGGTGCCCT GTGTAAAGAA 240
 ACCTACCAAA GGTTTACATT TGCACCTTAG CCTCAATAGC TACGAACCCT AGAGAAGCAG 300
 CTAGCTGGAG CTCATGTGCA ACTCCTGATT CTCAGGAGAA AGATGGATT TAACCNAAAA 360
 TTATGAGTNA GCTGTTAACT CTAATAATGTA CTTNGGGAGA TAGGGCCAAG NGAGAGGTCA 420
 TGGGCCAACT TAAGTGTAT CCNGTAGGAA AGNNCAGGTA NCACTGGNT TTTTTTNN 480
 GGGTTGCTNT TNCCTNTNC TAAANGGATT TGNTANTTCC NTGGGGNTNG NATTTAAATT 540
 GGGTTNTAAA AAGNTTNGAC GTGANA AAAA TTN 573

SEQ ID NO:16

SEQUENCE LENGTH:567

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00017

SEQUENCE DESCRIPTION:

GATCAAAACA GTCTACCAG CACCATATCC ACATTCTAGC CCATGGAAAG GGTAAAGAAA 60
 AGAAAGTGA AGATATTAGT TTCCATTAA GGAAGTGACA TGGAGNTAAT ATAAGTCACC 120
 TGTGTTTACA TTCCACTGGC AAAAATTCAG TCACAGGAAT GTACTTAGCT GCAGAGGAGG 180

CTAGGATATG CCCTCCAAAA ACTCAGGGGG GATGTCCTAC TTGTAAAAGG AAGAAATGAA 240
 AANTGGACAC TGAGAGGAAA TCAGCAGTCT CAGAGGTAAT ATACTTACAC AAGTTTTTTA 300
 AAAACCATAA AATGATGCAG AATGAAGTTT CCACTCTATT CACCATCTAT CCAGTCCTCA 360
 TGCCTCCCAN CANGNGGTAA ATNCTTTATT ATTGTGTCAT GGTATCTTTC CAGGGTTTTT 420
 CTAAGCAATT TTGCAACNGN TTTTAATTAT GTATCCTNAT TTCCTACNTT ACCCCNTTTT 480
 TGTCCATGNA NNGNANANTN TCCTGNGGNN TAACCTTCNT GTNTCTTTT TTCCCTNAT 540
 ATTTTTTGGC GGTNCCNTNN NTTTGGN 567

SEQ ID NO:17

SEQUENCE LENGTH:552

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00018

SEQUENCE DESCRIPTION:

GATCTTACCC GTGACAAAAT GTGTCCATG GTCAAAAAT GGCAGACAAT GATTGANGCT 60
 CACGTTGATG TCAAGACTAC CGATGGTTAC TTGCTTCGTC TGTNCTGTGT TGGTTTTACT 120
 AAAAAACGCA ACAATCAGAT ACGGAAGACC TCTTATGCTC AGCACCAACA GGTCCGCCAA 180
 ATCCGGAAGA AGATGATGGA AATCATGACC CGAGANNNGC AGACAAATGN CTTGAAAGAA 240
 GTGGTCAATA AATTGATTCC AGACAGCATT GGAAGAGACA TAGAAAAGGC TTGCCAATCT 300
 ATTTATCCTC TCCATGGNTG TCTTCGTTAG AAAAGTAAAA ATGCTGAAGA AGCCCAAGTT 360
 TGAATTGGGA AAGCTCATGG AGCTTCATGG TGAAGGCAGT AGTCTGGAA AAAGCCACTT 420
 GGGGNCNGG ACAGGTGCTT AAAGGTTGAA CCGNGCTNGA TTGGTTNTGA ACCCACCAGT 480
 CCCAGGAATT CTTGTTTAAA GTTCCAGNCN TTCAATTAGT TGGCAAATTA AAAANGTGCT 540
 TTTTTGNGGA AA 552

SEQ ID NO:18

SEQUENCE LENGTH:581

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00019

SEQUENCE DESCRIPTION:

GATCGCCGTT CTGGTAAAAA GCTGGAAGAT GGCCCTAAAT TCTTGAAGTC TGGTGATGCT 60
 GCCATTGTTG ATATGTTTCC TGGCAAGCCC ATGTGTGTTG AGAGCTTCTC AGACTATCCA 120
 CCTTTGGGTC GCTTTGCTGT TCGTGATATN AGACAGACAG TTGCGGTGGG TGTATCAAA 180
 GCAGTGGACA AGAAGGCTGC TGGAGCTGGC AAGGTCACCA AGTCTNCCCA GAAAGCTCAG 240
 AAGGCTAAAT CGAATATTAT CCCTAATACC TGCCACCCCA CTCTTAATCA GTGGTGGAAG 300
 AACGGGTCTC AGAACTGTTT GTTTCAATTG GCCATTTAAG TTTTAGTAGT AAAAGACTGG 360
 TTTAATGATA ACAATGCATC GTAAAACCTT CANGAAGGNN AANGGAGGAA TGNTTTTGTG 420
 GGCCCACTTT GGGTTTTNCT TTTTNCGGT GTNGGCAGTT TTTAAGGTTN TTAAGTTTTT 480
 TNAATAATNCA GGACCTTTTT TAANTGGNAA CCAACTTTGG CCCAAAAATT TTGTACCAG 540
 ATTTTTTNGG GCCCCTTTA AAAANGTNTT NATNGGGAA A 581

SEQ ID NO:19

SEQUENCE LENGTH:556

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00020

SEQUENCE DESCRIPTION:

5 GATCAGCAGG GTTCTTTGTA AATAGTATTT TGAGACACTA AGATGTTTCT ACTGCTACGG 60
 AATGTATTTT AAACACATAT CGTTTCTTTT TCTTGGAAAA AAAGTTGATT AGGACCACAG 120
 NNNNGGTTTA GAAAGGGTAA TATTTTGAAG TACTACAAGG TTTAGACAGT CCATGAAATC 180
 GACCTGTTTA ATAATTTACC ATCCTGAAAG TCCAGAATTA AAATATGGAA GCAAGAACTA 240
 10 TATAATTGAT TAGGATGCTT GGTAGGTTTT TTTCATTGTT CAAATATTCA TTGCACAGTG 300
 GATTGTTTTG ATTAGTTAGT ATGCTTTTTT TTTAATTAAT TCAGTCTTCT GTTAATTTTT 360
 AAGNTTTGGT TAGTGCCACA AGGAATTTNA CTTNITGATT TGTATAATNG GAACCTGACC 420
 TNGGGATTNG TAGCGGGGNT TTGAAGGGTG GGGACCTNCC CNCAAAATAA GGGGGAGGTT 480
 TCCAAANNTT CCNCTGGCCG NCCNNNNATC CCAGGTAAAG GGGGTNGAAA TANTNNGGGN 540
 15 NCCCCCAGG GGAAAN 555

SEQ ID NO:20

SEQUENCE LENGTH:555

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00021

SEQUENCE DESCRIPTION:

25 GATCTGGTAC GAGTGTGTGA AAACATCCCC ATTGTGTTGT GTGGCAACAA AGNGGATATT 60
 AAGGACAGGA ANATGAAGGC GAAATCCATT GTCTTCCACC GAAAGAAGAA TCTTCAGTAC 120
 TACGACATTT CTGCCAAAAG TAACTACAAC TTTGAAAAGC CCTTCTCTG GCTTNCTAGG 180
 AAGCTCATTG GAGACCCTAA CTTGGAATTT GTTGCCATGC CTGCTCTCGC CCCACCAGAA 240
 GTTGTCTATG ACCCAGCTTT GGCAGCACAG TATGAGCACG ACTTAGAGGT TGCTCAGACA 300
 30 ACTGCTCTCC CGGATGAGGA TGATGACCTG TGAGAATGAA GCTGGAGCCC AGCGTCAAGA 360
 AGTCTAGTTT TATAGGGAAG TTGTCTGTG ATGTCAGCGG TNCAGCGTGT GTNCCACNTC 420
 ATTATTATCT AGCTAAGCGG ACATGTNTTC ATCTGTGGGN TCTTAAGGAG NTGAGTNGNN 480
 TNGGNGTAT NTGGANTTAA AAATAACTTC ATTNNTNGGC CNNATATTIA NGTNNTTNG 540
 CCCGNTTNNT CCCTN 555

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SEQ ID NO:21

SEQUENCE LENGTH:544

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00023

SEQUENCE DESCRIPTION:

45 GATCGATACA TGCAAAATTA ATGTAGTAAC TCACTTTTCC ATATATTTTN AATGTATATT 60
 TCTATTTATG AATACCAATT TATAAAAAAT AATTACACAG AAAAAATGG AATAGGAAAA 120
 ATTATGCATC TAGCACATTT AAAGTGTGCA AATATGAAAA TTTTTCGAGG ATTACATTTT 180
 NNNNTAGGC TGCATATTTT AACTGGCTTT AAAACTGTAA CACATCACAT AAAAGTACTT 240
 TACCCGGTAT GTATTGCATT ATATCATTGC AATAATTATT GGAGTCTAGA TATCGAGCCA 300
 TCCCAGGTGT TGGGCGGGGG GAGGGTTGTG GCAAGTTGTC TTTTCAATTT NGNGNGTTTT 360
 50 CCTGTNGCTC CAGGGCAAGT ACCGGGTTGG AAAGCTGCCT GTAAGCGTTG GCACCTTCAT 420
 AGNGTAGTGT TTNGGTGNCT TTTTNTTCG GTTCTTGTA AATTNGGTNCG GTNGGTGGTG 480

55

TTCAGATGNT TTTTNCNCT NGTTCAGCAA CTTNCCNNT NNCTTGCTT GATAGGGNAC 540
NTCN 544

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SEQ ID NO:22
SEQUENCE LENGTH:538
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

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CLONE:HUMGS00026

SEQUENCE DESCRIPTION:

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GATCTCTATC CAGTTGGACA CTTAATTGCT TTCTTCATTC AGAAAGATAG TCATGTTACAC 60
TGGTATATTT GGTCACTCTT AGAACCTGTC CTTACATAT GTTTTTTATG GGACCCATGA 120
ATGGTTAGCC TTTCTGTACT ATTGTAGAAG GAAATAAATA GGCCTAAAAA GACCATTGTA 180
GTAAATAAGT TCAAGGGGAA CTTGGGACCA GAAACCACTG GTATGTACAA AAAAGCTGGC 240
AATTTGAATA ACCTCAAGTT TGACAATAAT TTTTAAATTT GAACAGTTAT GATAAATTTT 300
AGTAGTTTTA TACACTAGAT GTGCCTAGAT GGTTCCTCAAG GCTTATAGGA CTGGCTCACA 360
GTTCAACATT TCTAGTGGCT TTTCTTGCCT TTGGGTCTGG GGGGCTGGGG GCAATGGGCT 420
TTTTTCCTTG GGTGCGCAAT CGGTTTCTCT GGTGGGTGAG TTTCCAATCC TTNGGGGGGT 480
CNTTGTGNTN TTNNCNGCCC NGNNNGGTNN GTCCNGGGTG TTNGCCGGGN NCNTTTTN 538

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SEQ ID NO:23
SEQUENCE LENGTH:535
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00028

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SEQUENCE DESCRIPTION:

30

GATCCTGGAA TATGTCGAGG TTATATTACC AGGTATTTTT ATAACAATCN GACAAAACAG 60
TGTGAACGTT TCAAGTATGG TGGATGCTG GGCAATATGA ACAATTTTNA GACTACTGGAA 120
GAATGCAAGA NCATTTGTNA AGATGGTCCG AATGGTTTCC AGGTGGATAA TTATGGAACC 180
CAGCTCAATG CTGTGAATAA CTCCTGACT CCGCAATCAA CCAAGGTTCC CAGCCTTTTT 240
GAATTTTACG GTCCTCATG GTGTCTCACT CCAGCAGACA GAGGATTGTG TCGTGCCAAT 300
NNGAACAGAT TCTACTACAA TTCAGTCATT GGGAAATGCC GCCCATTTAA GTACAGTGGA 360
TGTGGGGGGA AATGAAAACA ATTTTACTTC CAAACAAGGA ATGTCTGAGG GGCATGTAAA 420
AAAGGGTTTC ATCCAAAGGA TTTCANAAGG GNGGCTNATT TAAAACCANA NGGAANNNGN 480
AGGAGGCNGG NNGTGAATTT GNNTTTTGGN GGAANTTTTT GNTTNAANNT TNTGN 535

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SEQ ID NO:24
SEQUENCE LENGTH:528
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

45

CLONE:HUMGS00029

SEQUENCE DESCRIPTION:

50

GATCTACACT TGGATGGATG CAACTTTGAA AGAACTGACA AGTTTAGTAA AAGAAGTCTA 60
CCCAGAAGCT AGAAAGAAGG GCACTCACTT CAATTTTNC ATCGTTTTTA CAGATGTTAA 120
AAGACCTGGC TATCGAGTTA AGGAGATTGG CAGCACCATG TCTGGCAGAA AGGGGACTGA 180
TGATTCCATG ACCCTGCAGT CGCAGAAGTT CCAGATAGGA GATTACTTGG ACATAGCAAT 240

55

TACCCTTCCA AATCGGGCAC CACCTCCTTC AGGGCGCATG AGACCATATT AAATTCTATT 300
 TACTATTGTG TGAATTTATT TTTCCGTCAG TTATGTAAAA TAAACATACT CTNCCTTCCT 360
 CCCCTGGATT TATTGCCATT TAAGGCTTTT AAAATTCTAA TCAANNTTTG TNANTGCAAT 420
 CATCTGTTTN GGGNGTTNNG TTTTGGGATG TGCTTTTGN NTGGNTTNCG GNTTAGNCTT 480
 GGNTTGTTTT AATGGCCNTT CNNGTNANAT TTGGNGGNA NGNGCTTN 528

SEQ ID NO:25

SEQUENCE LENGTH:528

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00030

SEQUENCE DESCRIPTION:

GATCAAGGTA TAATGGAAAA ATATACCTAT TCTGAAGTA GTTTATTATN GTTTTCAAAT 60
 TGATTATAC CATTATTAAC CTGATGTGGT CTGCTTAAAA AATGAATATA TCAGTATTTA 120
 GAAATAAATT GCAAAGGTGG GAATATATAC TTAAATAATT TGTCTTAAGT AAATTAGCAT 180
 TTGGTAGTCT GANATGGTGA CAGATTACTT GTTAAAATTG TGAAANCTCT GTTGTGTCCT 240
 CTCTNCCTAC ATTTGTCCCT GAGAGTNCCT CACGATTACT AGGTTCTTGA TTCCCTTATA 300
 TGGCAATCAG GCAGAGGCGT TCCTTAAGCA TTAGAGAGTT CTGAAGCTTA AGATTGTTT 360
 TGTTTGGATG AANGTCCTTA GTACAGTTGA AAANCAGAGC ATTAAGNCT ANTCANTTTG 420
 TTTTGNCTC ACCAGTCATT TTAATNNG TNGGAATNCT TNTTNCTCA GTGCTTAAAN 480
 NTTTCNNTT TTTCAANCTG NNGGGGGTTN GGATTAAACC AGGCCNCTN 528

SEQ ID NO:26

SEQUENCE LENGTH:527

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00031

SEQUENCE DESCRIPTION:

GATCAGAATG CCCCTCCACT CATGAGACTC TTCATTTTGT CCACTTTGAC AGGAAAAGTG 60
 GGAATGTATG CAGAGCTCTC AAAAGAAACA AAAAAGGCCA AAACGGTGCC TTCAGCCACA 120
 TCCTCTGAAT TGGCCCTGAC TTGGACTAAA TGCACTAATG CAAAATCCCT TGACAAAAGC 180
 GCATAGGTTA TTTCAAACCA GCATTGTTTT TTATGTAACC TGTTTACCG CATCTTCTCA 240
 GCAGCTTCTG ACCACTGCTC AATTTTCTCC TTTACAGCCA TTGTTCTGGT GGACAAATAA 300
 CCTAGGTACT CCAATCCTG GCAGGAAAAA TATACAGCAT TATGAANCAG CACTCANGTA 360
 ATCCTAAAAT GGATTTCCAA AGCTGGTTAC ACATGGCCCT GGNAANGTCN TATTGANTTT 420
 ANANGGGCTT TCTTCNTTTC AGGAGTTTNG GTCAACGGTG GCAAATCCNT GGGGTNNTTA 480
 ANTGGNNNGG TTNNTTAANT TNGNTANTT TCNTNGGGGC CANAGGN 527

SEQ ID NO:27

SEQUENCE LENGTH:520

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00033

SEQUENCE DESCRIPTION:

GATCAAAATG GTTGGTGAAC CTCCACATGT CCAGTTCTGT TGCCAAACTT TCCATTCAGA 60

GTATTTGGTG GAGTTTGAAT TTGAGCAAAC TAAATGCCTT CATCTTAGGT AGAAAGGGCC 120
 TGAATCTTCC ATTTTATATT CAAACCTCAT TGTTATTGG CCTAAGTAAA AAGTCAGATT 180
 TCATTTCCAT TTACCTGAGT TCGCTTTAAA GAGCTTTTCA AAGAGAGCTT TATAGACACC 240
 CACAATTGTC CCCAATCTCT TCATGATGTT GCATTAATAG TTGTTTTTGT CCCTTTCTTG 300
 GAAATGTTAA TGCCAAAGNT TGCCTGAACA TTNGGGCGGG TTTTCTTAAA TTTGAANGTN 360
 TAAAANTTTT NTAANGGGGG AATTNCCAAA NGGGTATTTA AAAGGGTTNG TTTAACCAG 420
 GTATTGTNGT GGGGGGATGG TCCAATAATC CTCCNGGGGG AGGGCTTTCA AGGGAAATCC 480
 CNTTTTNGGG GAAATAAAAA NNGGGTTAAA ANNNNTTTTN 520

SEQ ID NO:28

SEQUENCE LENGTH:514

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00034

SEQUENCE DESCRIPTION:

GATCAGCGAG GCCGACAAGA AGAAGGTGCT GGACAAGTGT CAAGAGGTCA TCTCGTGGCT 60
 GGACGCCAAC ACCTTGGCCG AGAAGGACGA GTTTAAGCAC AAGAGGAAGG AGCTGGAGCA 120
 GGTGTGTAAC CCCATCATCA GCGGACTGTA CCAGGGTGCC GGTGGTCCCG GGCCTGGGGG 180
 CTTCGGGGCT CAGGGTCCCA AGGNAGGGTC TGGGTCAGGC CCCACCATTG AGGAGGTAGA 240
 TTAGGGGCTT TTCCAAGATT GCTGTTTTTN TTTTGGAGCT TCAAGACTTT GCATTTCTTA 300
 GTATTTCTGT TTGTNAGTTC TCAATTTTCT GTGTTGCAA TGTTGAAATT TTTTGGTGGA 360
 AGTACTGAAC TTGCTTTTTT TCCGGTTTCT ACATGCAAGA GATGAATTTA TACTGCCATC 420
 TTACCGGCTA TTTCTTCTTT TTTAATTCCA CTAACTCAG GCCATTTTTT AAAGTTGGGT 480
 ACTTGCAAAG TAAAATAAAC TTTAAAAATT CAAA 514

SEQ ID NO:29

SEQUENCE LENGTH:513

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00036

SEQUENCE DESCRIPTION:

GATCATCATT CTTCTGACTC TAGATGGGAC ACTTGACAGT GACTTGAAAC ATTTGCATAT 60
 TCAGGAATGC ATGAGATTTC AAGAGAGCCT ACAGTATGAA ATCATTTTCA CAAAATAAGC 120
 AGCTTGCTTC TGAATGCTG TCTTTCCAG TAGCTACTCA CCTGCCTCTG GTGGCTGGGA 180
 TTCAGATGCC AAAAACTGT CAGTATCTAT AGACCAGGTC TGTGCCACCT CCTCTCTCCT 240
 CTGTGCTCAG TGAGGAGGCA GTAAATGAAG TTACAGGCTA GCACAATACC TAACTCATGT 300
 TTCCAGTAC ACCTGTTGGA TATTNCTGT NCCTTTTAAT GGTTCCTAAG GGANTTAGGT 360
 TNTTGNCTG TTTCCAGNGG TTTCCAGGTT TTCTTTGGGT NCTTTTNA TTTTNAANTT 420
 CCNAGGGGGG GGGNNTTTG GGNAAAGGGG GGGCAAAGGG GNTTTTTTTT TTNTTGGGCC 480
 NNGNTTTTTG GGGGGAAANC CTTTNNGGTN NCN 513

SEQ ID NO:30

SEQUENCE LENGTH:512

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00037

SEQUENCE DESCRIPTION:

5 GATCTAAATT GTTACATTTT ACCATTTTCAT TCCGAAGTTG GTTTTACTTT ATTAAATGAA 60
 GATTTAGTTT TCATATCGTA TACATAGCTG TATAGATTTC AAAATNAGGT TGTTAATTTG 120
 TGTCACTTAC TATTTTTGTG TTGGTAATGC TTAAATGCA TACTTAAAAA TGAAGTACTG 180
 TTATCTAAGC TACTGTGTTT AGAAAAATGTT AAGAATGAGC AGAAATTTT ATAGAAAAGT 240
 ATAACCGGAA GANGAGAGAA GATACTGCCA ATAGGCCCTC AANCTTAAAA NAGAAAAACC 300
 10 TTTGCCAGTT TTANGGACAT ATTTTGATTC TTTCNGTATT CTTAACACCT TTTTAAACAA 360
 NGTTCITGAT AGTACCCACT ATTATTGGGT TTGTTTATG CCATTATTG ATTCTTGGAT 420
 ATTCAAGCAT TTNCAATGTG GCATATTNG NTTCCNNTN NCCTTNCNTT TTTTNGGNCN 480
 NCNTTACCCT TTCCNTTGA AAGNCANTN GN 512

SEQ ID NO:31

SEQUENCE LENGTH:510

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00038

SEQUENCE DESCRIPTION:

20 GATCAGCCAG GCACAGAATC TCCAGAACAA CCTAGAGAGT GAATGCTAAT TTGTAGAGCG 60
 AACTTCCATT TGGCCCATNA TTTGTAATG TGTAAGTCT CCAAGTGCCA GANTGCTTAC 120
 ACGTTAAAGC AGCACCTTTC CATTTGCCCA CATATTCTTC TTGCACACCC CTTCCATTAC 180
 25 TGCTGAATAG GACATTGCAT GGGGAAGAGTA CAGAGGTGGC AGANTGANGC TAGAGTGGGC 240
 AGGNCATAAG ACTGAGCCCC AGAGTGCTCC CAGCAACCGC CACGTACANG GTCTGNAATG 300
 NCANGGGCAN GNGTGAGATT GGAANCTGTG TGTGAANGGT AAGCCCTTGC AGTNTTCTG 360
 CCTCCCTTTC TTCTGCCTT TCACCCCNCT TANTTGTNTG GTTNTTGGTT TGCCCGTTCT 420
 30 TCTCTTGGTG GNTGCNCATT TGTANATGG TGTTAGGGGT GTGGGGNTGA GGTTCCTCCC 480
 TTTGATGTGG GNTTNTCCN TTGGGTTTAN 510

SEQ ID NO:32

SEQUENCE LENGTH:507

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00039

SEQUENCE DESCRIPTION:

40 GATCGTGAAG CCCAATGGCG AGAAGCCGGA CGAGTTCGAG TCCGGCATCT CNCAGGCTCT 60
 TCTGGAGCTG GAGATGAACT CGGACCTCAA GGCTCAGCTC AGGGAGCTGA ATATTACGGC 120
 AGCTAAGGAA ATTNAAGTTG GTGGTGGTCG GAAAGCTATC ATAATCTTTG TNCCCGTTCC 180
 TCAACTGAAA TCTTCCAGA AAATCCAAGT CCGGCTAGTA CGCGAATTGG AGAAAAAGTT 240
 45 CAGTGGGAAG CATGTCGTCT TTATCGCTCA GAGGAGAATT CTGCCTAAGC CAACTCGAAA 300
 AAGCCGTACA AAAAATAAGC AAAAGNGTCC CAGGAGCCGT ACTCTGACAG CTGTGCACGA 360
 TGCCATCCTT GAGGGACTTG GTCTTCCNA AGCGGAAATT NTNGGCAAGA GGANTCCNGN 420
 GTCAAACTTT GNTTGGCANG NCGGGCTCAT AAANGGTTCA TTTTGGNNCA ANNGACNAGN 480
 AGGNCCAATT NTGGGNCAAA NAGGNTN 507

SEQ ID NO:33

SEQUENCE LENGTH:508

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00040

SEQUENCE DESCRIPTION:

GATCAGAAAC TCACCCTAAA TCTNAACGGG TGCCGCTATA ATTNGTNACA TCTGGCAAGA 60
 TTTCCTTTA TGTATATATT TAAACAATCC GCTTGGACAC GAACAAAGCC ACACTTCTAA 120
 CTGCTTCTGG CGAACTGATT TAATTTTNA TTTTNTNCAA TAAAGATATT CTTAGATACT 180
 GAAAGAAATA GTTAATGAGT TTNCATTTGT CCTTGAGAAA ATTTGGCTCA AGTCCATTTG 240
 GCTGTAGTGT CAACGATGTT TCCAGTAGTG TTTAGGATTT GGTGTCTTCA AAGGTAGTTG 300
 ATTAAACCAA GTGTGTCTTT AATATCTTGT ATCAGAATAA CTTTGTATGT TACCAACTTA 360
 AATTGCTAGA ATAAGGGTAA ATTGGATACA CAACTGCTGA TTTTAAATTT AGGANCTTTG 420
 ACCNNATTTT GGGGTTTTCA AANCCGTTT TGGNTGCTNT GTATCCTTAT GCTGTTTGGT 480
 TNATTTCCAN TAAAAANTTC ACNCGNGN 508

SEQ ID NO:34

SEQUENCE LENGTH:505

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00041

SEQUENCE DESCRIPTION:

GATCTGTAAG TAACTTCACA TTAATAAATG AAATATTTTT TAATTTAAAG CTTACTCTGT 60
 CCATTTATCC ACAGGAAAGT GTTATTTTAA AAGNNAGGTT CATGTAGAGA AAAGCACACT 120
 TGTAGGATAA GTGAAATGGA TACTACATCT TTAACAGTA TTTCATTGCC TGTGTATGGA 180
 AAANCCATTT GAAGGTGACC TGTGTACATA ACTCTGTAAA ANCACTGAAA ANTTATACTA 240
 ACTTATTTAT GTTAAAGAT TTTTTTAAAT CTAGACAATA TACAAGCCAA AGTGGCATGT 300
 TTTGTGCATT TGTAATGCT GTGTTGGGTA GANTAGGTTT TCCCCTCTTT TGTTAAATAA 360
 TATGGCTATG CTTAAANGGT TGCATACTGG GGCCAAGTAT AATTTTNTG GTAATGTGTG 420
 GNAAGGATG NCCAGTTATT GGTACCNCCT TTANGNNATC CNNTAANGGG AACCTTCCCC 480
 TNGGTAAAA NCANGNNGTA NANNN 505

SEQ ID NO:35

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00042

SEQUENCE DESCRIPTION:

GATCTGAAAA GAGCTGTTTT GGATGAATGC AGTATAAAAT GTAAAANCCC TGCTAAATGA 60
 AA 62

SEQ ID NO:36

SEQUENCE LENGTH:503

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00043

SEQUENCE DESCRIPTION:

5 GATCGAAAGG CACTCCATGA GCTAAAACTG GAAGAGTGGA AAGGCAGACT ACAAGTTACT 60
 GAGCACCTCC CTGAGAAAAAT TGAAGTAGT TTACAGGAAG ATGAACCTGA GAATGNTGCT 120
 AAGAAAATTG AAGCACTGCT AAACCTTCCT AGAAACCCTT CAGTAATAGA TAAACAAGAC 180
 AAGGACTGAA AGTGCTCTGA ACTTGAACT CACTGGAGAG CTGAAGGGAG CTGCCATGTC 240
 CGATGAATGC CAACAGACAG GCCACTCTTT GGTGAGCCTG CTGACAAATT TAAGTGCTGG 300
 10 TACCTGTGGT GGCAGTGGCT TGCTCTTGTN TTNTTCTNGN CTNTTTAACT AAGAATGGGG 360
 CTGTTGTA CTCACTTTAC TNATCCNTAA ATNTAAATAC ATACTGATGN TTTGTATTAA 420
 TCGNTCCAAT ATATGNNTAC ATGNANTATA TCNACNCNCC TTNGATNTTT AAGCANGTAA 480
 ATAAAACCAT TNNGCAATGG AAA 503

SEQ ID NO:37

SEQUENCE LENGTH:497

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00044

SEQUENCE DESCRIPTION:

20 GATCGATAAA GAATTGGCTA GTGGTGAATA CTTTTGAAG GCAAATCAGA AGAAGCGGCA 60
 /GAAAATGGAA GCAATAAAGG CTAACAAGC AGAAGCCATC AGTAAGAGAC AAGAGGAAAG 120
 AAACAAAGCA TTTATTCCAC CTAAGGAAAA ACCAATTGTG AAACCTAAGG AAGCTTCTAC 180
 25 TGAAACTAAA ATTGATGTGG CCAGCATCAA GGAAGGGTT AAGAAAGCAA AGAATAAGAA 240
 ACTGGGAGCT CTTACAGCTG AAGAAATGCG ACTTAAGATG GAGGCAGATG AAANGAAAAAN 300
 GANGAAAAAN NAGTANCATA CCCAAANCTC CTTGNCTNGG ACCTATCTCC TTTTNGTAA 360
 AGGGGTTTTT TGGGGTTTTT AGGCCTTTAG GTTNCCCTTT TTTTNGGGGA AANTTTTNTT 420
 GGGGGGGTTT TTTNNCTTT TTTNGGGGGG GGNGGGGGTT TTNNTCCTTG GGNGGGGGTT 480
 30 TCTTTNNAAA AATTTTN 497

SEQ ID NO:38

SEQUENCE LENGTH:498

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00045

SEQUENCE DESCRIPTION:

40 GATCTTATGG ATGCTGAGCA TGTCTGCAC TGGTGCTAAT GTCTAATATA ATNTTATATT 60
 TACACACATA CGTGCTACCC AGAGATTAAT TTAGTCCATA TGAACCTATT ACCCATTGTT 120
 CATTGAGACA GCAACATACG CACTCCTAAA TCAGTGTGTT TAGACTTTTC AAGTATCTAA 180
 CTCATTTCCA AACATGTACC ATGTTTTATA AACCTCTTGA TTTCCAGCAA CATACTATAG 240
 AAAACACCTG CTACTCAAAA CACAACCTCT CAGTGTGATC CATTGCTGTC GTGAGAGACA 300
 45 ACATAGCAAT ATCTGGTATG TTGCAAGCT TTCAAGATAG CCTGAACCTA AAANGTTGGT 360
 GCATTAGTTG TATCTGATGG NTATAAATTT TGCCTCCTAG GTTCACTTTG GTGTCCAGGN 420
 GCTAAACCTG TGGANCTAA CTTTCCCTTN ATTGGGGGGG GAATAACCTG GAAAATAAAG 480
 GGTTTTTTTC CAGGGNTN 498

SEQ ID NO:39

SEQUENCE LENGTH:494

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00046

SEQUENCE DESCRIPTION:

GATCTGTGCT GTAGAAAAAC ATTAACCCTT GTTCAAAAAA GAAATGGATA ANCTTGGCCT 60
 TTCTAAGTGG TAAGAATGAC CTGTCACTAT AATATACTGT ATGTTTACAT TTNATTTAAA 120
 TTAAATCTCT TATGTATAGG GTGATAACCT TCCCAGAAA CAACAGTGAT TGCNATTGTT 180
 TTCTAGAAAC TNCCTTTAAAG TGCCACATTT GGCAGTACAA ATGAGTCTGA GTGTAATAGC 240
 CCAGAGATTT ATATATAGTT GAATGTCTAA NATGGTAAAA TGTGCCACTG TGTCAAGTTA 300
 CAGTGGCTTA TGTTCCTTGG AGTAATTCAN ATGANCTTCC TATTTTGTNT AGTAAATGGC 360
 CATTTAATAG NATTCCTTGG CCATTTGAGG CTCACTGGCA AATTTTAGGT GCNNGGGGNG 420
 GAANCCANTT TTTTANATGG NAATCCTTGG GTTTTNCN CCNTNNTNCC TGGNCCNTTC 480
 CCCCCAAAAN CCTN 494

SEQ ID NO:40

SEQUENCE LENGTH:244

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

/CLONE:HUMGS00047

SEQUENCE DESCRIPTION:

GATCAGTTGA CAGTGGCAAT TAAACTGTAA ATAACCTGCC CTGGGGGCCT TTTTAAAA 60
 AACAAAAACC AAAAAATTC CAAACCATA CTTGCTAAAA ATNCTGGTAA GTATGTGCTT 120
 TTNTGTGGGG GTGGGATTG GAAGGGGGGT TGGGTGGGC TGGATATCTT TGTAGATGTG 180
 GACCACCAAG GGGTTGTTGA AACTAATTG TATTAAATGT CTTTGATAA GCCTTCTGCT 240
 CAAA 244

SEQ ID NO:41

SEQUENCE LENGTH:283

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00048

SEQUENCE DESCRIPTION:

GATCACTGTA AATGAACCTC CCTGTTGGCC GCTCTGTGGA TGANACTTTA AGACTAGTTC 60
 AGGCCTTCCA GTTCACTGAC AAACATGGGG AAGTGTGCCC AGCTGGCTGG AAACCTGGCA 120
 GTGATACCAT CAAGCCTGAT GTCCAAAAGA GCAAAGAATA TTTCTCCAAG CAGAAGTGAG 180
 CGCTGGGCTG TTTTAGTGCC AGGCTGCGGT GGGCAGCCAT GAGAACAAA CCTCTTCTGT 240
 ATTTTTTTT NCCATTAGTA AANCACAAGA CTTAGATTC AAA 283

SEQ ID NO:42

SEQUENCE LENGTH:486

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00049

SEQUENCE DESCRIPTION:

GATCAGTTTT CNTTGTAACA CTGGGTTTAA TCTGAATGGC GCTGATTCTN CCAAGTGCAC 60

TGAGGAAGGA AAATGGAGCC CGGAGCTTCC TGTCTGTNCT CCCATCATCT GCCCTCCACC 120
 ATCCATACCT ACGTTTGCAA CACTTCGTGT TTATAAGCCA TCAGCTGGAA ACAATTCCT 180
 CTATCGGGAC ACAGCAGTTT TTNAATGTTT GCCACAACAT GCGATGTTTG GAAATNATAC 240
 AATTACCTGC ACGACACATG GAAATTGGAC TAANTTACCA GGAATGCAAG GGAAGTAAAA 300
 TGCCCATTC CATCAAGACC AGNCAATGGA TTTGTGGNAC TATCCTGCAA ANCCCAACAC 360
 TNTNTTCCA AAGGNTTAAA GGCCACATTT TGGGTGGCC ATTGGTNGG TTATTTNTCT 420
 TGGGAGTTGG GCCCGGANG GAANTTTGNN TGTGTTNCCN NAANCTTGGG GAACCCTTGG 480
 GTTTNN 486

SEQ ID NO:43
 SEQUENCE LENGTH:470
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00050

SEQUENCE DESCRIPTION:

GATCCACCAG CTGAGAATTC GTCCGCTCCC GAGGCTGAGC AGGGCGGGGC TGAGTAAATG 60
 CCGGCTTACC ATCTCTACCA TCATCCGTT TAGTCATCCA ACAAGAAGAA ATATGAAATT 120
 CCAGCAATAA GAAATGAACA AAAGATTGGA GCTGAAGACC TAAAGTGCTT GCTTTTGGC 180
 CGTTGACCAG ATAAATAGAA CTATCTGCAT TATCTATGCA GCATGGGGTT TTTATTATT 240
 TTACCTAAAG ACGTCTCTTT TTGGTAATAA CAAACGTGTT TTTAAAAA GCCTGNGTT 300
 TTCTCAATAC GCCTTTAAAG GTTTTAAAT TGTTCATAT CTGGTCAAGT TGAGATTTT 360
 AAGNCCTTCA TTTTAAATT GTAATAAAN GTTACCACC TTGGATTTT TCAANAAAG 420
 TCAACCAANC TGCAANGCAC CTGTTAATAA NGGGTCTTTA ANTAATTAAA 470

SEQ ID NO:44
 SEQUENCE LENGTH:479
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00051

SEQUENCE DESCRIPTION:

GATCTGTAAG TAACITCACA TTAATAAATG AAATATTTT TAATTTAAAG CTTACTCTGT 60
 CCATTTATCC ACAGGAAAGT GTTATTNTNA AAGGAAGGTT CATGTAGAGA AAAGCACACT 120
 TGTAGGATAA GTGAAATGGA TACTACATCT TTAANCAGTA TTTCATTGCC TGTGTATGGA 180
 AAANCCATTT GANGTGTACC TGTGTACATA ACTCTGTAAG ANCACTGAAA AATTATNCTA 240
 ACTTATTTAT GTTAANNAT TTTTAAAT CTAGACAATA TACAAGCCAA AGTGGCATGT 300
 TTTGTGCATT TGTAATNCT GTGTTGGGTA GAATAGGTTT TCCCTCTTT TTGTTAANTA 360
 ATATGGCTAT NCTTTAANGG GTTGCTACT GGGCCAGGTN TAATTTTTT TAATGGNGTG 420
 AAAGGGTGCC ATTTTTTGT CNCACTTNGG GGGTCTCANT GGGGGGNTT TNNCNGGGN 479

SEQ ID NO:45
 SEQUENCE LENGTH:477
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00053
 SEQUENCE DESCRIPTION:

5 GATCTCTAAG GAACTCCTGT TGCTAAATAT GAAGAGTATG GAACATTCAT ATAGTCTCTG 60
 TGAAGCATGG GGGGAGGGAA GACATTTCTT TTTCTTATAG GCTTTATGCT CAAATGTCAT 120
 AGTCTCCTTT CAAAGAATTG TGTGCAATT TAAATGCACC CAGCTTAAGT AGAAGACATT 180
 10 GAAGGATGCA TTAATTTTCA GGAACATTT TGAATTATGA AAAGATTCCC AATTGAAAAA 240
 NTTATTCAAC AAGTAAAAGC TAAGAAATTT CATTGAAATC ATAAGGCAGT TTAAGCATAA 300
 NTTGATAAAA ATAGCTGTGT ACTACTAATT AATAGAAAAT CATTCAACCA AGAGANGAGT 360
 CANGTGAATA TCGTTTGTGTT ATTTGCTAGT GAGTTTCTTT GTAACGTTGG ATTTTATTAA 420
 15 NTGGTTAATN TTTGGTTAGG TATGTCCTAT GTTANTNAAA ANTGGNCCAA NTTTAAA 477

SEQ ID NO:46

SEQUENCE LENGTH:476

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS00055

SEQUENCE DESCRIPTION:

20 GATCACCATT AGCAAATGGA AATNACATTT GAAAGCCATT AGACTTATAG GTGATGCAAG 60
 CATCTAAGAG AGAGGTAAAT CACACTATAG AGGCATAAGT GGTATCAGTT TTCATTTTCN 120
 TAATTGTTTA ANCTGTGTTT TATACCAGTN TTTGCAAGTA ATTGGGTGTT AGCTTGAGAT 180
 GGTAAAGGT GGTGTTGGGA GGGACTTCGT TGTAATGGTT TTCCTGTAAA ANATGTTTCC 240
 AACTCCNCTG AAATGTTGCT GAAAAGCATG GTGCTGGTAA CAGTTCAACA ATCCCGTGGC 300
 25 TGCTCATTCT TGGCCTACTT TTA CTCTCTCC ACTTGNNAGC AGGTTAGCGT TTGAAGGGTG 360
 GTATGGGAAA AGCCTNGCAT TGCCTGGGCC AAATTCCTTT TGGGGTTCN CTCCNTTCCC 420
 CNCTTCNCCN TNCCTTCCT TTCCCCCN TN ANGTCNNCC NCTTNCNTTA GGTTTN 476

SEQ ID NO:47

SEQUENCE LENGTH:472

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS00056

SEQUENCE DESCRIPTION:

35 GATCAAATCT GCACTGTGTC TACATATAGG AAAGGTCCTG GTGTGTGCTA ATGTTCCCAA 60
 TGCAGGACTT GAGGAAGAGC TCTGTTATAT GTTTCCATTT CTCTTTATCA AAGATAACCA 120
 AACCTTATGG CCCTTATAAC AATGGAGGCA CTGGCTGCCT CTTAATTTTC AATCATGGAC 180
 CTAAGAAGT ACTCTGAAGG GTCTCAACAA TGCCAGGTGG GGACAGATAT ACTCAGAGAT 240
 40 TATCCAGGTC TGCTCCAG CGAGCCTGGA GTACACCAGA CCCTCCTAGA GAAATCTGTT 300
 ATAATTTACC ACCCACTTAT CCACCTTTAA ACTTGGGGAA GGNNGCNTTT CAAATTAAAT 360
 TTAATCNTNG GGGGNTTTTA AACTTTAACC CTTTNCNT TN TNNGGGGTN GGNANTTGNC 420
 CCCNTTAAAG GGGGNCCCC TNCNNGGGG AATAAAACAA NTTNNTTTT TN 472

45 SEQ ID NO:48

SEQUENCE LENGTH:472

SEQUENCE TYPE:nucleic acid

50 TOPOLOGY:linear

CLONE:HUMGS00057

SEQUENCE DESCRIPTION:

55

5 GATCAAANCT GCACTGTGTC TACANATAGG AAAGGTCCTG GTGTGTGCTA ANGTTCCCAA 60
 TGCAGGACTT GAGGAAGAGC TCTGTTATAT GTTCCATT TCTTTATCA AAGATAACCA 120
 AACCTTATGG CCCNTATAAC AATGGAGGCA CTGGCTGCCT CTTAATTTTC AATCATGGAC 180
 CTAAGNNGT ACTCTGAAGG GTCTCAACAA TGCCAGGTGG GGACAGATAT ACTCAGAGAT 240
 TATCCAGGTC TGCCCTCCAG CGAGCCTGGA GTACACCAGA CCCTCCTAGA GAAATCTGTT 300
 NTANTTTAGC AACCCAGTTA TCCNCNTTAA NNCTGNGGAG AGTGGTCTTT ACATCTTAAT 360
 TTTATTCNTG TGGTGGTNT TACCTTTAAC CCGGTTTCTT ATTTTGGGT TTGTTATTGG 420
 10 CCCTTTTATG GGGTGGTCCC TNTTCCNGGT TGGNTTCCC TTTTTTGTG TN 472

SEQ ID NO:49
 SEQUENCE LENGTH:319
 SEQUENCE TYPE:nucleic acid
 15 TOPOLOGY:linear
 CLONE:HUMGS00060
 SEQUENCE DESCRIPTION:
 GATCTCATGG TCCGGAATGA CACCCCCTGT GGAACCACCA TTGGACCTAT CTGGCTTCT 60
 20 CGGCTGGGGC TGCGGGTGCT GGATTTAGGC AGCCCNNAAC TGGCCATGCA CTCTATCCGG 120
 GAGATGGCCT GCACCACAGG AGTCCTCAG ACCCTCACCC TCTTCAAGGG CTTCTTTGAG 180
 CTGTTCCCTT CTCTAAGCCA TAATCTCTTA GTGGATTGAG CCCTCTTGA AAGACTTCTC 240
 TGCCATCCCT TTGCACCTGA GAGGGGAAGT TCTCAGCTGA GCTGAAGCTG GATTATTAAA 300
 25 GTGGATTGTC ACTCAGAAA 319

SEQ ID NO:50
 SEQUENCE LENGTH:461
 SEQUENCE TYPE:nucleic acid
 30 TOPOLOGY:linear
 CLONE:HUMGS00061
 SEQUENCE DESCRIPTION:
 GATCTTCCTC TAATTGACAG CCTCATTACG GGTCTTACAA AATATGGAAC AGTGTGAGAA 60
 35 AAAACCAGAG AACTCGGCAG AGTCTAACAC AGAGGAAACC TAAAAGGACT GATTTAACCC 120
 AAGATGATTT CCACTTGAAA ATCTTAAAGG ATATTTTATG TGAATTTCTT TCTAATATT 180
 TTCAGGCATT AACAAAGGAG ACGGTGGCTC AGGGAGTAAA GGAAGGCCAG TTGAGCAAAC 240
 AGAAGTGTTT CTCTGCATTT CAAAACCTTC TTCCTTTCTA TAGCCCTGTG GTGGAAGATT 300
 TTATTGAAAA TCCTACGGTG AAGTTGATAA GCGCTTTGC TGGATGGGCT TGGGATAAAA 360
 40 ACCCTTTCCC AAGTTTTAAA GGGTTTCAGG TCTTTAAATC CCTGAAATTT TGGGATTCT 420
 TTCTTGTTCC AGGTTGTTTA AACCTTTTAT TTTTCCTCC N 461

SEQ ID NO:51
 45 SEQUENCE LENGTH:458
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00062
 SEQUENCE DESCRIPTION:
 50 GATCTAGCAT ATTTCACTAT TCTGTGGATG AATACATAGT TTGTGGGGAA AACAAACGTT 60
 CAGCTAGGGG CAAAAAGCAT GACTGCTTTT CCCTGTCTGG CATGGAATCA CGCAGTCACC 120

55

TTGGGCATTT AGTTTACTAG AAATNCTTTA CCTTAAGCAG CACACACATT TACTACACAC 180
 ACAGNCCTAA CAAAGCACTG TGCTTAGAGG GTAAAAAGGA ATCACAAAAC AAGAATCTTT 240
 CCAAAGTTGT CTCATTGAGC AATGTTAAGG CATCTGTATC AAATTATTTT GGATGTAAAG 300
 ATTCTGTGT CTCATAATAT GAATGTATTT TTTGATATAC AAGGAACTG GCCATAAAAA 360
 TGGTGNGGNA ANCCGCCCN TAATTTNCC CCTGGGGCCC CAATTGGTNN NNTCNANTCT 420
 NGGNTTNAGC NTTTGTCTC AAATGGGATN CANTTNNN 458

SEQ ID NO:52

SEQUENCE LENGTH:459

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00064

SEQUENCE DESCRIPTION:

GATCTATCAC CCAAACATCG ACGAAAAGGG GCAGGTCTGT CTGCCAGTAA TNAGTGCCGA 60
 AAAGTGGAAG CCAGCAACCA AAACCGACCA AGTAATCCAG TCCCTCATAG CACTGGTGAA 120
 TNACCCCCAG CCTGAGCACC CGCTTCGGGC TGACCTAGCT GAAGAATACT CTAAGGACCG 180
 TAAAAAATTC TGTAAGAATG CTGAAGAGTT TACAAAGAAA TATGGGGAAA AGCGACCTGT 240
 GGACTAAAAT CTGCCACGAT TGGTTCCAGC AAGTGTGAGC AGAGACCCCG TGCAGTGCAT 300
 TCAGACACCC CGCAAAGCAG GACTCTGTGG AAATTGGCAC GTGCCACCGN CTGGCGTTCG 360
 NTTGTGGCAG TTACTAACTT TTCTACAGTT TTCTTAATCA AAAGTGGTCT TAGGTAANCC 420
 TGTAAGGNA AGGGGTTTAN NAATTTTANG GTTGGTCTN 459

SEQ ID NO:53

SEQUENCE LENGTH:458

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00065

SEQUENCE DESCRIPTION:

GATCAGCTGG CCAACTCAGC CAATCCGCAC ATTTAGCTCT CCAACTACCA TACAACGTGC 60
 TTGGTTTAGG TCGGAGCGCA AATNTNCTTG ACCATCTCTA CGTTGGTATT CCCCGTCCAT 120
 CTGGAGAAAA ATCTATACGA AANCAAGAGT GGACTGCAAT NATTCAAAT NCCCAGCTAA 180
 TTGTCATTCC ATACCCTCAC AATGTCCCTC GAAGTTGGAG TGCCAACTG TATCTTACAC 240
 CAAGTAATAT TGTNCTGCTT ACTGCTATAG CTCTCATCGG TGTCTGTGTT TTCAATCTTT 300
 GGCAATAAAT TGGCATTTTA CCATTTGNCA GGGAAAAGGA AAGGCNGGTT GGNTTGGGGG 360
 GAAAACCGGC CAAGGGGANGG CCCCCCGGG TTTTCNATTT TTGGNGGGNT TNTTGGGNNT 420
 TTTGCCTTTT TAAANTTTTT CCNAANAAAN NGGGANTN 458

SEQ ID NO:54

SEQUENCE LENGTH:454

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00066

SEQUENCE DESCRIPTION:

GATCAGTTNC GTGTCCGCNG GAGCAGGCCT TGCTGAGTGA AGACACTGGN ACTAGCTGGG 60
 TCCTGGGGTG ACTTGGAGGC TTTGGGCTA AAAGGGCAGC CTGAACCTGG AGTCTTATCT 120

CCCCCAGGAG CCGAAAGCAC TTTTCTTGAT TTCCCCCAGG AAATCAAGCG CTGCTTCTCA 180
 GTCCTGTGG TTTTAGTATT TATATATCTG TATCTTCTTT GTAGAAATTT ATTTATTTTT 240
 GAATAAGAAT ACCTGCCTGG AAAAAATTTA AAAGGACGGG AGGGCGAANT GCAAGGGAAG 300
 GCCTCTCCTA TGCCGNCCCA GAGNAGCACT GTACCAATTT CATGTGATTC CTTAACTCTG 360
 TTAAAGGAAG CTCTGAAACT GTCATTTCTT TTGCAGATTG TTNTGAACCT GGAAACCCNG 420
 AATTTATNGN TAANNCTCAN TTNCCACCNG GAAA 454

SEQ ID NO:55

SEQUENCE LENGTH:505

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00067

SEQUENCE DESCRIPTION:

GATCGTTGGG GAACCCAGCC CCTTGGAAGT TGGAAGACCC GTGTTTCCTG GACCGCGAAT 60
 CAGTGTGTTG GGCATCAGTG TTTTCTGCAA GGGTTGTGAC CTGAACTTT TAAAAACCA 120
 CCCACCTTTG GGAAGCATT TCTGAATTTA TCCATCACCA ACCATTTCTT CTGGGATACC 180
 ATCAAGTAAC AGCTATTATT TGCCAAGTGG AGCTGTCATT TAATTGATG CACCTCTGGN 240
 TTCAGATGAA ACATTAAATT GTCTTCCTCG ATTCTCCATC GGGGTAGAG TTTTAAACT 300
 ATCANTGGCA TTTCAAGTCT TCTGANACAA CATGGCTGTA TGTGCGTGGT CCATAGCACA 360
 GTACATGCAG CATCTAATAA GNGTTTCCAT TTGTAGAATT NTTTTCNCA NACTTNTAGT 420
 TAAANNCAAA ATTTTAAAT TTGNAAANAA GNGTNGTGT GGTATTNNN GNTGTTNTT 480
 GTNTNTGGT GNTNTGTTA TTN 505

SEQ ID NO:56

SEQUENCE LENGTH:450

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00068

SEQUENCE DESCRIPTION:

GATCAGAGAC TGGAGAGGTG GAGTGAGAAG TCTCCGCTGC TCGGGCCCTC CTGGGGAGCC 60
 CCCGCTCCAG GGCTCGCTCC AGGACCTTCT TCACAAGATG ACTTGCTCGC TGTACCTGC 120
 TTCCCCAGTC TTTTCTGAAA AACTACAAAT TAGGGTGGGA AAAGCTCTGT ATTGAGAAG 180
 GTCATATTTG CTTTCTAGGA GGTGTTGTGT TTTGCCTGTT AGTTTGGAG AGCAGGAAGC 240
 TCATGGGGGC TTCTGTAGCC CCTCTCAAAA GGAGTCTTTA TTCTGAGAAT TTGAAGCTGA 300
 AACCTCTTTA AATCTTCAGA ATGATTTTAT TGAAGAGGGC CGCAAGCCCC AAATGAAAA 360
 CTGTTTTTAG AAAATATGAT GATTTTGTAT TGCTTTTGT TTTAATTCTG CAGGTGTTCA 420
 AGTCTTAAAA AATAANGATT TNTANCAGN 450

SEQ ID NO:57

SEQUENCE LENGTH:447

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00069

SEQUENCE DESCRIPTION:

GATCTTTGAT AGTNGAGAAA ATTATGCAAA GTTCCTCAGA AGTNGGTTAT NATGCTATGG 60

CTGGNGATTT TGTGAATATG GTGGAAAAAG GAATCATTGA CCCAACAAAG GTTGTGAGAN 120
 CTGCTTTATT GGATGCTGCT GGTGTGGCCT CTCTGTTAAC TACAGCAGAA GTTGTAGTCA 180
 CAGAAATTCC TAAAGANGAG AAGGACCCCTG GAATGGGTGC AATGGGTGGA ATGGGAGGTG 240
 GTATGGGAGG TGGCATGTNC TAACTCCTAG ACTAGTGCTT TACCTTTATT AATGANCTGT 300
 GACAGGAAGC CCAAGGCAGT GTTCCTCACC AATAACTTCA GAGAANGTCA GTTGGAGAAA 360
 AATGANGAAA AAGGGCTGGC TTGAAANTCA CTNTTAACCN NTTANGGTTG CTTGGGTTTC 420
 ANGTGGCCA NAGTTTTNNN TNNTGGN 447

SEQ ID NO:58
 SEQUENCE LENGTH:445
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00070

SEQUENCE DESCRIPTION:
 GATCACTGAG CAGTTTTCCC AGAGCTCCAT GGGAAAGGCAA GCTCTCCCTC CCAATGGGAG 60
 CCCCACTGTC ACTAACTGTA AACTCAGGCT CAGGCTTCAN CTGCCTACCC CCATCCTCAT 120
 ATTTCTGTCT GTCCCAGCAC CTCAGGAGCA TTCTCATTGT GGCCGGCTAA CTCCGCCTGG 180
 ATGTGAACAG GCAAGCACAG TGGGAAATNA GTCACGTACT TGTATTGCAC AGTGGACACC 240
 TCTAGAGGTC CATTGGTTTA AAGGGATAGG GAAGGAGGAG GGATGAGACC ATCTCCCCCT 300
 CCCAGGAAGT AAATCTAAGT ATCTAAGGTT TTCTTTATNG CCTTNGAGTC AAACANTAA 360
 CTGGCTAGTA CGGGAGGTGT NTGCTNGGTT TTTTCGGGT GGTTTTTTCC TAATGNAATA 420
 AACTTCATTT NTTGCNTGNT TGGNN 445

SEQ ID NO:59
 SEQUENCE LENGTH:459
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00071

SEQUENCE DESCRIPTION:
 GATCTTCGGT GGCCTCATGT AAACGTGGCA GCCAGCCTCT TCTAGAACCC TAGCCAGGG 60
 ACTGGAGCAG GAAAGGACC TTCAAAGTGA AGACTGCCTT GTCCGCAGC TCCTTCTGGC 120
 TTAGATTGAA ACATGGGCTT CCTAATGGGT TAAATCCTTT AAAACAAGGA GTTGTGGGG 180
 AAGGGTGTG TGCACCTCTA GAGAAAGGTA CACAGTTGCC CGGTTGGGAA TGTGCTTGGC 240
 GCTGACCCTG CGGGCATCTG ACTGGTCTTC CAGCTCAGGA AAAAGAATTT GAAAGAGGCT 300
 TAGCGTGAAG GGGAAATCAA GAGGAGGTTG TNATTTNGGT CGAAGGTGCC TTGGTTTAAG 360
 TCCTNGTAAT TTGTNCTTAT TAATTTTTTT TNATATAATA TNATTTTNTT GGGGGGTAAA 420
 CCATTTTTAA ATTAAACCAA CCATTTGTCT TNCTNGAAA 459

SEQ ID NO:60
 SEQUENCE LENGTH:441
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00072

SEQUENCE DESCRIPTION:
 GATCAGACAC TTCAAGGTCT AGGCTAGACA TGGCAGAGAT GAGGAGGTTT GGCACAGAAA 60

ACATAGCCAC CATT TTTTCC AAGCCTGGGC ATGGGTGGGG GGCCTTGTCT GCTGGCCACG 120
 CAAGTTCACA TGCNATCTAC ATTAATATCA AGTCTTGACT CCCTACTTCC CGTCATTCCT 180
 CACAGGACAG AAGCAGAGTG GGTGGTGGTT ATGTTTGACA GAAGGCATTA GGTGACAAC 240
 TTGTCATGAT TTTNACGGTA AGCCACCATG ATTGTTTCT CTGGCCTCTG GGTGACCTT 300
 AAAAAACCC ATTTGGAAC TGNNGACTT GAAANGGTGC TCTTGCTTA AGGCTTTNAT 360
 ATNGGCCCTT GTTTAATTGG GANGGTCNCT TNAAGGCC NTTTCCTTA NTAANGNG 420
 GGGTTNTTAN GGNTGTAGAA A 441

SEQ ID NO:61

SEQUENCE LENGTH:436

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00073

SEQUENCE DESCRIPTION:

GATCCGTCAC TCTTCCTTGT GGTAATCCCT AGACTGGGAG CTCAGGTACT CTTTATGCA 60
 TCTTTGTATG TCTTTAGCAG AGTTCCTGAC ATGTGGTAGG TGCTTAATAA ATNTTGTG 120
 TTTATCAAA TTTATGGTAG GGAGAGTAAG TCAGCATCGG TATAAATCG CTTACTCCAC 180
 GTAACCTTC TTCTGATAGG GTTTGATTT CTATTAGAAG CTCAATTTA GTTTTTTTC 240
 ATATTATAAC TAAATATGTT TCCTGAGAGA TAAGAGAAAT AATGTTCTTA CAATAGTTGT 300
 ATGTATCTAA GATAAGACAT ATAGATGCTT AAGACATTT GTTTCATTG CTATCTACTA 360
 GTGTACTTGA ACCATGGTCA TTTTtagccc TTTTCCTAGG GACCATGCTT ATTTCTCAAT 420
 AAGGAAATAC CTTCEN 436

SEQ ID NO:62

SEQUENCE LENGTH:434

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00074

SEQUENCE DESCRIPTION:

GATCTTTTTC CATCCAGCAG TGGAGTTTAG TACTTAAGAG TTTGTNCCCT TAAACCAGAC 60
 TCCCTGGATT AATGCTGTGT ACCCGTGGGC AAGGTGCCTG AATTCTCTAT ACACCTATTT 120
 CCTCATCTGT AAAATGGCAA TAATAGTAAT AGTACCTAAT GTGTGGGGTT GTTATAAGCA 180
 TTGAGTAAGA TAAATANTAT AAAGCACTTA GAACAGTGCC TGGANCATAA AAACACTTAN 240
 TAATAGCTCA TAGCTAACAT TTCCTATTTA CANTTCTTCT AGAAATAGCC AGTATTTTGT 300
 TGGAGTGCC ACNATGTTAG TTCCTTNTAC TAGTTGCTTT ACATGGATT TCTTNATATC 360
 CTGTTTTAAA GNTTNTTAC AGGTACCAGG TTTTCATGGA ATTTTCCTTT NANTAAANGG 420
 GGAGGNNAA NNTN 434

SEQ ID NO:63

SEQUENCE LENGTH:433

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00075

SEQUENCE DESCRIPTION:

GATCTGTGAA TCTTGGCTGG GACTTCCTCT GAGTGATGCC TGAGGGTCAG CTCCTCTAGA 60

CATTGACTGC AAGAGAATCT CTGCAACCTC CTATATAAAA GCATTTCTGT TAATTCATTC 120
 AGAATCCATT CTTTACAATA TGCAGTGAGA TGGGCTTAAG TTTGGGCTAG AGTTTGACTT 180
 TATGAAGGAG GTCATTGAAA AAGAGAACAG TGACGTAGGC AAATGTTCA AGCACTTTAG 240
 5 AAACAGTACT TTTCTATAA TTAGTTGATA TACTAATGAG AAAATATACT AGCCTGGCCA 300
 TGCCAATAAG GTTCCTGCTG TGTCTGGTTA GGCAGCATTN CTTTGATGC AAATTTCCCTA 360
 TTGGNCCCTN TTTTNTTCCA AAAAGGTAAA TGNCTNNAT TNCCCGGTTA AAAAAATNNTT 420
 CCCNGGNAT TTN 433

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SEQ ID NO:64
 SEQUENCE LENGTH:432
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

15

CLONE:HUMGS00076

SEQUENCE DESCRIPTION:

GATCCTGGAG GTCTTTTCTA GTCTGAGCTT CTTTAGCTAG GCTAAACAC CTTGGCTTGT 60
 TATTGCCTCT ACTTTGATTC TNATAATGCT CACTTGGTCC TACCTATNAT CCTTCTACTT 120
 20 GTCCAGTTCA AATAAGAAAT AAGGACAAGC CTAACCTCAT AGAAACCTCT CTATTTTAA 180
 TCAGTTGTTT AATAATTTAC AGGTTCTTAG GCTCCATCCT GTTTGTATGA AATTATAATC 240
 TGTGGATTGG CCTTTAAGCC TGCATTCTTA ACAAACCTCT CAGTTAATTC TTAGATNCAC 300
 TAAAACTCG AGGAACTCTA CATGTAACCTA TTTCTTCAGA GTTTGTCATA TACTGNTTGG 360
 CATCTGAATG GCTACTCAGC ATTTGGTTAA CATTNGNGTA AATTTGGAAT AAANTTCCCC 420
 25 AGTAAGCCAT TN 432

30

SEQ ID NO:65
 SEQUENCE LENGTH:459
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS00077

SEQUENCE DESCRIPTION:

GATCCATCGC AGAGTCTTAA AGAAGAAGCC ACTGAAAAAC TTGAGAATCA TGTGAAGCT 60
 35 AAACCCATAT GCAAAGACCA TGCGCCGGAA CACCATTCTT CGCCAGGCCA GGAATCACAA 120
 GCTCCGGGTG GATAAGGCAG CTGCTGCAGC ANCGGCACTA CAAGCCAAAT CAGATGAGAA 180
 GCGGGCGGTT GCAGGCAAGA AGCCTGTGGT AGGTAAGAAA GGAAAGAAGG CTGCTGTTGG 240
 TGTTAAGAAG CAGAAGAAGC CTCTGTTGGG AAAAAAGGCA GCAGCTACCA AGAAACCAGC 300
 40 CCCTGAAAAG AAGCCTGCAG AGAAGAAACC TACTACAGAG GAGAAGAAGC CTGCTGCATA 360
 AACTCTTAAA TTTGNTTATT CCATAAAGGT CAAATCATTT TGGNCAGCTT CTTTTTTGAA 420
 TAAAAGNCCT GNTTTATACC AGGGCAGTGA GGAACCAA 459

45

SEQ ID NO:66
 SEQUENCE LENGTH:626
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS00078

SEQUENCE DESCRIPTION:

GATCTACAAA GGCCATGGGA AAAATTCAGA GAGTTAGGAA GGAAAAACCA ATAGCTTTAA 60

55

AACCTGTGTG CCATTTTAAG AGTACTTAA TGTTTGGTAA CTTTATGACC TTCACTTTAC 120
 AAATTCANGC CTTAGATAAA AGAACCGAGC ANTTTTNTGC TAAAAAGTCC TTGATTTAGC 180
 ACTATTTACA TACAGGCCAT ACTTTACAAA GTATTTGCTG AATGGGGACC TTTTGAGTTG 240
 AATTTATTTT ATTATNCCCG TTTNGTTTAA TGTCTGGTGC TNNCTATCAC CTCTTCTAAT 300
 CTTTAAATGT ATTTGTTTGC AATTTTGGGG TAAGACTTTT TTATGAGTAC TTTTCTTTG 360
 AAGTTTTAGC GGTCAATTTG CCTTTTAAAT GANCATGTGA AGTTATACTG TGGGCTATGC 420
 ACCAGCTCTC ACCTACNGGG GGNCTTACCT TGGGGGTAGN GNCCATACCA GNCCACTGTA 480
 TGTTTACTTC CTCACCCATT TGGNGTTGCC CCANCTTGGT TNAACACTNG GGCANCATTN 540
 TGGTTTNAAG GGNCCTTAGG GTTNACCAGN TCNTTTTAAAC NGGNTATTN CCCGGGGTTT 600
 TTTNAAANTG GCCCAAAATN CTAAAA 626

SEQ ID NO:67

SEQUENCE LENGTH:534

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00079

SEQUENCE DESCRIPTION:

GATCAACAGT TCTAGTACTC TTCTTTGTCA GTATATCAAC CTACAGCTAT TGAATGCAAA 60
 GCCACAAGAG TGTTTAAATGG GGACAGTGGG CACTCTCCTG CTTGAAAACC CACTTGGGCA 120
 GAATGGACTC ACCCACCAAG GTCTTCTGTA TGAAGCAGCC AAGGTGTTTG GCCTTCGGAG 180
 CAGGAAGCTA AAGCTGTTTC TGAATGAGAC CCAAACGCAG GAAATTACAG AAGACATCCC 240
 CGTGAAGACT TTGAATATGA AGACTGTGTA TGTTTCTGTG TTACCAACAA CAGCAGACTT 300
 CTAGCATGTA CTTATCAATG TTGTTCCGGT AGCCCTTCCC TAATTACACC TATCCCTTAC 360
 ACATACATGC ACATAGNCAC ACACATGNAC ACACCTTGAAG GTATTTCTTT CAAGGTGTGT 420
 GTAAAAATAT GCTGCTTGGN TTTGAATTCA AATGGGGTTG NTTAGGTCAA GTACTTTGNG 480
 GCCTNANAGG NATCTTCACA CTTAACCTTA GGCACTTTGT ANGCATTGTT GGGN 534

SEQ ID NO:68

SEQUENCE LENGTH:417

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00080

SEQUENCE DESCRIPTION:

GATCTTAGTT GATATTTTGG GCTTGGGGCA GTGAGGGCTT AGGACACCCC AAGTGGTTTG 60
 GNAAAGNAGG AGGGGAGTGG TGGGTTTATA GGGGGAGGAG GAGGCAGGTG GTCTAAGTCC 120
 TGAATGGCTA CGTAGTTCNG GGCAATCCT CCAAAGGGA AAGGGAGGAT TTCCTTAGAA 180
 GGATGGCGCT CCCAGTGA CTCTTTTGAC TTCTGTTTGT NTTACGCTT TCTCAGGGAA 240
 AAACATGCAG GTCCTCTAGT GTTTCATGTA CATNCTGTNG GGGGGTGACA CCTTGGTTCT 300
 GGTAAACAA GCTGTACTTT TAATAGCTGT TNCAGGAAGG GTTAAGGCCA ACTACAAATT 360
 AATGTTGGTT GCAAAATGTAG TGTGGTTCCC TAACTTTNCG GGGTTTTCCT GAGGAAA 417

SEQ ID NO:69

SEQUENCE LENGTH:417

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00081

SEQUENCE DESCRIPTION:

5 GATCTGCCCTG CCCACCAACT GGTGATGGAA GGTACAAAGT GGCACCTCAA TGAGACGGTG 60
 CTCACCTGTGT GGTGCGCACC AACTACTGCT ACCGTGTGGG AATGTGGCAG CATCTTGGAG 120
 CTGGACGAGC ATCTCCAGAA AGATTTCATC ATCTTTGAGC TGCTCCCAAG AGCACGGGGC 180
 ATCCCTCCAA GAGCCGTGCC GCTATTCCTG TGACCCGCCG GCCTGCCCTC ACCTTTGGCT 240
 CGACATGTGC TTGCATTCTT AGCGAGCTGG CGTGGGGGCT GTCTGGTTGT GTCCCAAGAG 300
 10 GTGTTGAGGT AGGTNTTGAG AGCTGAGACT AGTCATGTCT CTCTTCCAT TACATGAGTT 360
 CATATTTTNN TTTTCTNTTT TGTGTTAGTA ATTTGGAAAT GAAATTATAA GGAATGN 417

SEQ ID NO:70

SEQUENCE LENGTH:415

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00082

SEQUENCE DESCRIPTION:

20 GATCTTTCTG GGAACACAGC CCNGCTGGCG GCTAACCTGC TGTGAGAT GCTATGTGCT 60
 CTCGCCAAAG TGACAACCGT CTGAGTCTTG TGCTCTTCAA GACAAAACAG ATTGCGTCGC 120
 TGACAAGTTC TCAAGAAGAA CTTATGAGTA AGCAGTCTGA GAACTAAAGA GTTTATGCCA 180
 AGAAAACCTT CTGCTGAAAG TGTCATTGCT GGCTGTGAAG TCGGGATAAT CAGTAGAATT 240
 25 CTCACCCAAA CAGCAACATT TCTAAGGAAC TTGGATTAAT TGGGGGAAAA AAAANGGGGT 300
 ACTTGTACTG CTTTGATTG TTTTCCTTTG GNTGAAAAGN TGGGGGGTTA AANGGGGGAT 360
 NGTGAGGGGG ANTTTNCCTN TNNAGGGNTT TTTTNTNANC CCATTNNGN NTNCN 415

SEQ ID NO:71

SEQUENCE LENGTH:415

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00083

SEQUENCE DESCRIPTION:

35 GATCAGAATC ATTAAAAAAT ATTTTGTGTT AGTAAGTTG AAGATTTCNN GCTTNAGGC 60
 CTTTCCTATT TTGTCCTATT TATTTTNCNA GGCAATCTTT TCCATGGAGG GCAGGGTATC 120
 CATTCTTTAC CATGGGTGTA CCTGCTTAGG TTAATAATCA TACCAAGGCC TCATACTTCC 180
 AGGTTTCATG TTGCGTCTTG TTGAGGGAGG GAGAGCAGGT TACTTGGCAA CCAATATTGTC 240
 40 ACCTGTNCCT GTCACACATC TTGAAAAATA AAACGATAAT AGANCTAGTG ACTAATTNC 300
 CCTTACAGTT CCTGCTTGGN CCCACCCNAC TGNGGGTNGG CTCCATTGGT NNGTTCCGGG 360
 GCCGTNNTTT AGGGGGNANT TGGGGGNTCG GTTAGGCCTN TNGGTTTGGG GAAAN 415

SEQ ID NO:72

SEQUENCE LENGTH:410

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00084

SEQUENCE DESCRIPTION:

50 GATCTCCCN CTCTAGGGGT CAGGCTCCAT TAGGATTGTC CCCTTCCAN CTCTCCTAC 60

55

EP 0 679 716 A1

5 CCAACCACTC AAATNAATCT TTCTTTACCT GAGACCAGTT GGGAGCACTG GAGTGCAGGG 120
 AGGAGAGGGG AAGGGCCAGT CTGGGCTGCC GGGTTCTAGT CTCCTTTGCA CTGAGGGCCA 180
 CACTATTACC ATGAGAAGAG GGCCTGTGGG AGCCTGCAAA CTCACTGCTC AAGAAGACAT 240
 GGAGACTCCT GCCCTGTTGT GTATAGATGC AAGATATTTA TATATATTTT TGTTGTCAA 300
 TATTAATAC AGACACTAAG TTATAGTATA TCTGGACAAG CCAACTTGTA AATACACCAC 360
 CTCACCTCTG TTACTTACCT AAACAGATAT AAATGGCTGG TTTTAGAAA 410

10 SEQ ID NO:73
 SEQUENCE LENGTH:406
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00085

15 SEQUENCE DESCRIPTION:
 GATCGTGACG CTGAATAAAT GTCTTTTTTT TAATGTGCTG TGTAAGTTA GTCTACTCTT 60
 AAGCCATCTT GGTAAATTC CCCAACAGTG TGAAGTTAGA ATTCCTTCAG GGTGATGCCA 120
 GGTTCATTTT GGAATTTATA TACAACCNGC TTGGGTGGAG AAGCCATTGT CTTCGGAAAC 180
 CTTGGTGTAG TTGAACGTAT AGTTACTGTT GTGACCTGAA GTTCACCATT AAAAGGGATT 240
 ACCCAAGCAA AATCATGGAA TGGTTATAAA AGTGATTGTT GGCACATCCT ATGCAATATA 300
 TCTAAATGA ATAATGGTAC CAGATAAANT TATAGATGGG AATGAAGCTT GTGTATCCAT 360
 TATCATNGT AATCAATAAA CGGNTTNAAT TCNCTTGGAN TGGAAA 406

25 SEQ ID NO:74
 SEQUENCE LENGTH:408
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00086

30 SEQUENCE DESCRIPTION:
 GATCACATTG TAAACTATG GATGGTCTGA TAAGGCTTNN ACTGACCCCA CTGACTTCAG 60
 AGTTATACTC TGTTGCNAC ATCATAATGC TGGTTTTCCT GACTTTTTGT NTTTTAATAT 120
 ATTTATAAAA AAAGAAAAAG TTGGTGATTG CATTGGGAAA TTCCAGGGT ATTACTGGAC 180
 CTATGTGGTG TATTGTTAAA CCAGTGTCTT TGTNATACTG TTGCTCTTGA TGTTCTGAT 240
 ACAGGTAAGG ANGCAAGTTG TCAACTCTNA TACAAAGTAT ATATACAGTT CAGTATTGTC 300
 TCTGTTTATT TTGTTTAAAT TTCATTGGNC AAANTCAANC CAGCATTCCT CATTGTGTGA 360
 AATAAATGAT TTTCTGGAA TAAAGGNAA AGGNCTTNA ATTCCAAA 408

40 SEQ ID NO:75
 SEQUENCE LENGTH:407
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00087

45 SEQUENCE DESCRIPTION:
 GATCAAACTA GCTCAGGCCA AACTTTAAGT TCATACCTGA GCTAAGAAGG ATAATTGTCT 60
 TTTGGTAACT AGGTCTACAG GTTNCATTT TTCTGTGTTA CACTCAAGGA TAAAGGCAAA 120
 ATCAATTTTG TAATTTGTTT AGAAGCCAGA GTTTATCTTT NCTATAAGTT TACAGCCTTT 180
 TNCTTATATA TACAGTTATT GCCACCTTTG TGAACATGGC AAGGGACTTT TTTACAATTT 240

55

TNATTTTATT TTCTAGGTAC CAGCCTAGGG GATTTCGGGT TAGGTACTCA TTTTGTATTC 300
 ACTGTCACTT TTTCTCATG GTCCTAATTA TAAATNGNCC CAAAATCAAG GNTTGCCTNA 360
 AAAAGGGGGN AAAATGGTTG GCCCCNNGGT TNTTNGNNNC CCCNGTN 407

5

SEQ ID NO:76
 SEQUENCE LENGTH:413
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

10

CLONE:HUMGS00088

SEQUENCE DESCRIPTION:

15

GATCTACCGA CTCACTTCTG AGAATATTTT TNACAGATTA TCTTTGGGCC TTTCCATTAG 60
 AAAGCTGTTT GTTTGTCCCC CTGTTGGTAC ATTTGGTTAC CTCATTTTGC CGTTTCAAAT 120
 TGTAAGGCT CACAGGGGTG TTTTTGGAA TCATTGCTG AGTCATTTTC TCAAATCATA 180
 TTCCATTGTA TCAGTTAACA TATAGTTTAA AATGTATGTA TTATAAATNT CTGTANCCAA 240
 ATCATTTGAA GGCTTGATAA ATTTNTAACA ANGTTTGTAC ATTTNTCATG AAAGTCACTA 300
 GTAATGCTNG GNGNGGTAGT GCAATGGANT TTTCCNTTTT TCNTCCCTGT GCCCATTITG 360
 GAGTTGAGAG GGTGTNGGT AATNAACTGT ATGGTGTACA NTGNANCCNA NNN 413

20

SEQ ID NO:77
 SEQUENCE LENGTH:417
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00089

25

SEQUENCE DESCRIPTION:

30

GATCGGCAAG CCNCNCACTG TCCCTTGCAA GGTGACAGGC CGCTGCGGCT CTGTNCTGGT 60
 ACGCCTCATC CCTGCACCCA GGGGCACTGG CATCGTCTCC GCACCTGTGC CTAAGAAGCT 120
 GCTCATGATG GCTGGTATCG ATGACTGCTA CACCTCAGCC CGGGGCTGCA CTGCCACCCT 180
 GGGCAACTTC GCCAAGGNCA CCTTTGATGC CATTCTAAG ACCTACAGCT ACCTGACCCC 240
 CGACCTCTGG AAGGAGACTG TATTCACCAA GTNTCCCTAT CAGGGAGTTC ACTGACCACC 300
 TCGTCAAAGA CCCACACCAG AGGTCTCCGT GCAGNGGACT TCAGGNTNCA GNTTGTGGTT 360
 ACAACATAGG GGNTTTTAT ACAANGGAAA NGTAAAGGTG NNNTTAAAGN GGTGAAA 417

35

SEQ ID NO:78
 SEQUENCE LENGTH:404
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00090

40

SEQUENCE DESCRIPTION:

45

GATCAGAAGA AACACTCCAA AAATTGAGAT GAAATGTTGG TGCAGCCAGT TATAAGTAAT 60
 ATAGTTAACA AGCAAAAAA GTGCTGCCAC CTTTATGAT GATTTTCTAA ATGGAGAAAC 120
 ATTTGGCTGC ATCCACATAG ACCTTTATGT TTTGTTTCA GTTGAAAAC TGCCTCCTTT 180
 GGCAACATTC GTAAATNAAG CAGAATTTT TTTCTCTTT TTTCCAAATA TGITAGTTT 240
 GTNCTTGTA GATGTATCAT GGGTATTGGT GCTGTGTAAT GAACAACGAA TTTTAATTAG 300
 CATGTGGTTC AGAATATNCA ATGTTAGGTT TTTAAAAAG TATCTTGATG GTTCTTNTTC 360
 TATTATAAT TTCNGACTTT CATAANGTGT ACCCANGANT TTCN 404

50

55

SEQ ID NO:79

SEQUENCE LENGTH:622

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00091

SEQUENCE DESCRIPTION:

GATCCCCGCA ACTCGCTTGT CCTTGGGTCA CCCTGCATTC CATAGCCATG TGCTTGTCCTC 60
 TGTGCTCCCA CGGTTCCCAAG GGGCCAGGCT GGGAGCCAC AGCCACCCCA CTATGCCGCA 120
 GCGGCCCTAC CCACCTTCAG GCAGCCTATG GGACGCAGGG CCCCATCTGT CCCTCGGTCTG 180
 CCGTGTGGCC AGAGTGGGTC CGTCGTCCCC AACACTCGTG CTCGCTCAGA CACTTTGGCA 240
 GGATGTCTGG GGCCTCACCA GCAGGAGCGC GTGCAAGCCG GGCAGGCGGT CCACCTAGAC 300
 CCACAGCCCC TCGGGAGCAC CNCACCTCTG TGTGTGATGT AGCTTTCTCT CCCTNAGCTG 360
 CAAGGGTCCC GATTTTGCCA TCGGAAAAAG ACAACCTCTA CTTTTTNCCT TTTGTATTTT 420
 TGATAAACAN TTGAAGNTTG GAGCNTGTTA AAATTTATTN TTTGGGGGGA AACCTNAAGA 480
 ACTGGGNCCT AATTTNGGNG TTCGTGGGAC CCTNTTANNT GGTTTTNAAT NAANCGGTTA 540
 NGGAATTAAA CTGTTTGGGA ANANTTGGTT TAAAGNTTAA AAATTTTGGG AAAAAAAGGG 600
 GCTTTTAAA TTTTGGGT TN 622

SEQ ID NO:80

SEQUENCE LENGTH:400

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00092

SEQUENCE DESCRIPTION:

GATCTTCCTT TTTCTNTGA ATGNGCTCTG TTGNCITTTT CTCTTTTTTC TCATGTGTTC 60
 TTCCCTCCAC CTCCACCCCT TTCTTTCTTT CTCTCTCTGA TTGAGAGGCA TTNAATTACG 120
 TTTTCAGTAG TACAGGCTTC TTGCCGATAT GAAGGGAAGT TTTCAGAAAG AGACCTACTC 180
 TGGGTCATTT AATTTTGAAT ACAGTTTCA ATCGTTCAAG TTTTGGNNNG NTTATATCTA 240
 ATGTGTGTTT CATTTTTTTG GAAAGCTATA TTTTGTATTT AGGAAATGGT ATACTATTTT 300
 GCTATTTGTA CTGAGTGAGT ACATTGGCAT AAATATAGAA ATTTATATAT ATACATATAT 360
 ATAAGTGTGC TTTTGGCCCT TTTTNTGNG GAAATTTGGN 400

SEQ ID NO:81

SEQUENCE LENGTH:396

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00093

SEQUENCE DESCRIPTION:

GATCAGACTG TGGCATTGTA AATGTCAACA TTCCAACAAG TGGGGCTGAG ATTGGAGGTG 60
 CCTTTGGAGG AGAAAAGCAC ACTGGTGGTG GCAGGGAGTC TGGCAGTGAT GCCTGGAAAC 120
 AGTACATGAG AAGGTCTACT TGTACTATCA ACTACAGTAA AGACCTTCCT CTGGCCCAAG 180
 GAATCAAGTT TCAGTAAAGG TGTTTATGAT GAACATCCCN NAATTTGAGG GTGTTCCAGC 240
 AGCTGTTTTT GGAGAAGACA AAGAAAATTA AAGTTTTCCC TGAATAAATG CATTATTATG 300
 ACTGTGACAG TGAATAATCC CCCTATGACC NNAAGNCCT GATTAAATCA AGAGATTCCT 360

TTTTTAAAAA TCAANTAAAA TTGTNACACC ATAAAA

396

SEQ ID NO:82

SEQUENCE LENGTH:400

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00094

SEQUENCE DESCRIPTION:

10 GATCGATGGT TGACAATCCA GAGTGGTGAA CAGCCCTACA AGATGGCTGG TCGATGCCAT 60
 GCTTTTGAAA AAGAATGGAT AGAATGTGCA CATGGAATNG GTTATACTCG GGCAGAGAAA 120
 GAGTGCAAGA TAGAATATGA TGATTTCTGA GAGTGGTTC TTCGGCAGAA AACGATGAGA 180
 CGTGCAGGTA CCATCAGGAA GCAGCGGGAT AAGCTGATAA AGGAAGGAAA GTACACCCCT 240
 15 CCACCTCACC ACATTGGCAA GGGGAGCCT CGGCCCTGAA CAGAGCAGCT GCTGATGTCT 300
 GGAGGCTGAT TTCTCTGTT TCTGTTCTCC ACTGGAAGG TTGTTTACGA CAAACCTCCT 360
 TGTCAAAGTN GTAAAAATA AAGGATTGCT CCATCCTAAA 400

SEQ ID NO:83

SEQUENCE LENGTH:397

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00095

SEQUENCE DESCRIPTION:

25 GATCTGGGCA CTGTACTTNA GCCTGGGCGA CAGAGAGACC CATCTCAAAN AAAAAATTGG 60
 AACCTGAGAA GGGGGTCTGT GGGTCCCCGG GGGCCACCGT CTGCACTTGG NATCTNAAGT 120
 CGGGGTGGNC TTGTGGGACT NACCCNTTAC CCTGTGGGTT CTGTACTAGC TCCGGGNAAT 180
 TGGTGACAGA NTCGAGTTAA ATTGTAGGAC ATCGCGTTGG TGTCTGAGAG GGAGTTGGAG 240
 30 AGCTGGTTGG TGTGGAGGGA AAGGNTTACA CACATGTNAT TTCAGAAAGC TTCTGTGGGT 300
 AGAGGAATCG TTTTCTCTT GAGACTGTTA TGAGTATGTA CAAATTTTAT TTCCTGTAAA 360
 AATATTNCA TTTTAAAN TGGTTATTT CTAGAAA 397

SEQ ID NO:84

SEQUENCE LENGTH:390

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00096

SEQUENCE DESCRIPTION:

40 GATCGAAGAT TTATCCCAGC AAGCACAAC AGCAGCTGCT GAGAAATTCA AAGTTCAAGG 60
 TGAAGCTGTC TCAAACATTC AAGAAAAAC ACAGACTCCA ACTGTACAAG AGGAGAGTGA 120
 AGAGGAAGAG GTCGATGAAA CAGGTGTAGA AGTTAAGGAC ATAGAATTGG TCATGTCACA 180
 45 AGCAAAATGTG TCGAGAGCAA AGGCAGTCCG AGCCCTGAAG ANCAACAGTA ATGATATTGT 240
 AAATNCGATT ATGGAATTAA CAATGTAACC ATATGGANGC AACTTTTTTT TGGTGTCTCA 300
 NAGGNGTAAC TGCAGCTTGG TTGAAANTT TGTTACCTTG TTTCTTATCA TAAATNAAN 360
 NGTTATTNGC TTCCTTTTT GGNTTGAAA 390

SEQ ID NO:85

SEQUENCE LENGTH:392

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00097

SEQUENCE DESCRIPTION:

GATCACTTTC ACTNTCAATT ATTTGCCAGG NCTCACAGAA CTCAGAAAAG CTCAGANCAC 60
 TCATGGTTAC TATTTAGTAA AGCAAAAAGA CACAAATNAA AATNAGCAAG TTTGGCCGGG 120
 ATTGCAAGCA TGAGCCACTG AGCCCGGCCC CCAACTGTTA CATCAAAATA TTATTTGAGA 180
 GTATATGTGT CCTCACGTCC CTAACAACT AGAAACTGTC AANCTTTTAA TCTTTGTCAA 240
 ACTCTCAAAA GTAGTATCTC TGCATTTGCA TGCCTTTGNG TNCTAATAAG GTTGAGTACT 300
 GCTTTAAAAG TTTGCTGGNC ATCTNTTGN TTTTTTAAAG GACCTGCGGT GGNNAGGCCC 360
 NTTCAANANA TTNTTTCNTT AATTNGGGCC TN 392

SEQ ID NO:86

SEQUENCE LENGTH:393

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00098

SEQUENCE DESCRIPTION:

GATCAGTCTG GCTGGTGGTT TAACAGGTGT CACTCTGCAA ACCTGAATGG TGTATACTAC 60
 AGCGGCCCC ACACGGCTAA AACAGACAAT GGGATTGTCT NGNACACCTG GCATGGGTGG 120
 TGGTATTCTC TGAAATCTGT GGTATGAAA ATTAGGCCAA ATGATTTTAT TCCAAATGTA 180
 ATTTAATTGC TGCTGTTGGG CTTTCGTTTC TGCAATTCAG CTTTGTTTAA AGTGATTGA 240
 AAAATACTCA TTCTGAACAT ATCCATGCGC AATCATGATA ACTGGTTGTG AGNAGTGCTT 300
 TTCATTCTTC TCACTTGCCT TTGTTACTTA ATGTGCTTTC AGGACAGCAG ATATGCAATA 360
 TTCACCAAAAT AAATGTAGGC TGGTGGTAAT AAA 393

SEQ ID NO:87

SEQUENCE LENGTH:391

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00099

SEQUENCE DESCRIPTION:

GATCCAGAAA TACTTAACAC GTGAATATTT TGCTAAAAAA GCATATATAA CTATTTNAAA 60
 TATCCATTTA TCTTTGTAT ATCTAAGACT CATCCTGATT TTAACATCA CACATGAATA 120
 AAGCCTTTGT ATCTTTCTT CTCTAATGTT GTATCATACT CTNCTAAAAC TTGAGTGGCT 180
 GTCTTAAAG ATATAAGGGG AAAGATAATA TTGTCTGTCT CTATATTGCT TAGTAAGTAT 240
 TTCCATAGTC AATGATGGTT TAATAGGTAA ACCAAACCCT ATAANCCTGA CCTCCTTTAT 300
 GGTTAATACT ATTTANGCAA GGANTGCAGT ACAGATTGG NTACAGTACG GATTGNCCA 360
 AATAANTTCA NTAAAAGCCT TAAAGCTGAA A 391

SEQ ID NO:88

SEQUENCE LENGTH:390

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00100

SEQUENCE DESCRIPTION:

5 GATCAACCCA CAGAACAAAG CGGATTTCCA AGGCATCTCC CCAGAGCGAG CCTTTGCTGA 60
 TTTTCTCTTT GCCAGCACCA TCCTGCACCT TGTGTGCATG AACTTTGTTG GCTGACTCAT 120
 TCTCATTAC TTAATTGAGG AGTAGGAGAC TAAAAGAATG TTCACTCTTT GAATTTCTCTG 180
 GATAAGAGTT CTGGAGATGG CAGCTTATTG GACACATGGA TTTTCTTCAG ATTTGCACTT 240
 ACTGCTAGCT CTGCTTTTGA TGCAGGAGAA AAGCCCAGAG TTCACTGTGT GTCAGAACAA 300
 10 CTTTCTAACA AACATTTATT AATCCAGCCT CTGCCTTTCA TTAAATGTAA CCTTTTGCCT 360
 TCCAAATTAA GGACTCCATG CCACTCCTCN 390

SEQ ID NO:89

SEQUENCE LENGTH:390

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00101

SEQUENCE DESCRIPTION:

20 GATCTTTCTN AATGTGTATT GATTGGTCTT TTCAGCTACT CTGAACAGAT TACTAAGGCC 60
 ATCTCCTCAT CTCTAAGGGA GAAAAATAGT CTGTAGATGA ATAATGTAAG GTAAAGAGTT 120
 GCATGTCAGT CTTTGTAATN ATTTACACTT TAACCTTCTC CAGAACTCAG ACATGATTTT 180
 AACATGGTGT TAGATTTGTG CATTNATTT TCCTGACCAC CTCATTCCAG CCAATGTATG 240
 25 GTTATCCACT CTGTGTGCNA AANCCAATCA TGCNTTTCAC GGCCCTTTAG TTCAGAGAAG 300
 TTCTGCACTG ATTTTATGTC TCTTGATGTC TCAATCTTAC ATGTATACCA ATCACAATGG 360
 AATAAAAAGT GTTTGAGGTT GTACTGTGGN 390

SEQ ID NO:90

SEQUENCE LENGTH:391

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00102

SEQUENCE DESCRIPTION:

35 GATCCGAGGA GGCAGAACAA GTCCACGGAG TCCCNNGCAG GCCAACGTGC AGCGGCTGAA 60
 GGAGTACCGC TCCAAACTCA TCCTCTTCCC CAGGAAGCCC TCGGCCCCCA AGAAGGGAGA 120
 CAGTTCTGCT GAAGAAGTGA AACTGGCCAC CCAGCTGACC GGACCGGTCA TGCCCGTCCG 180
 GAACGTCTAT AAGAAGGAGA AAGCTCGAGT NATCACTGAG GAAGAGAAGA ATTTCAAAGC 240
 40 CTTGCTAGT CTCCTATGG CCCGTGCCAA CGCCCGGNTC TTCGGCATA GGGCAAAAAG 300
 AGCCANGNAN GCCGCAGANC AGGATGTTNG TAAGGAAANN ATTTANAGCC CCTCCTGGGN 360
 GACCTTTGGG ATTCAGTCGN CAGTCAATAA A 391

SEQ ID NO:91

SEQUENCE LENGTH:391

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00103

SEQUENCE DESCRIPTION:

50 GATCTGTGCC AAGCTCAGGG TGTAGCGCTG CAAACGATGA AGCAAGAGAT TCTCATTAA 60

55

CTTGTGAAGC AAAAGCCACA AATAACAGAG GAACAACTTG AGGCTGTCAT TGCAGATTTC 120
 TCAGGCCTGT TGGAGAAATG CTGCCAAGGC CAGGAACAGG AAGTCTGCTT TGCTGAAGAG 180
 GGACAAAAAC TGGNGNCAAA AACTCGTGCT GCTTTGGGAG TTTAAATTAC TTCAGGGGAA 240
 GAGAAGACAA AACGAGTCTT TCATTCCGGT TGAACTTTC TCITTAATTT TAACTGATT 300
 AACACTNTTT GGTGAATTAA TGAATGNTA AAGACTTTTT ATGTGAGATT TTCCTTATCA 360
 CAGAAATNAA NTNTCCTCCA AATGTTAATA N 391

SEQ ID NO:92

SEQUENCE LENGTH:385

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00104

SEQUENCE DESCRIPTION:

GATCTTTTCC CCTGGCCAAA GGGAAAGTTGT ATTAGTCTGT GACATCTTGT GATGCTGTTT 60
 ATCTTGGTTT GACATTGGAG ATACGCTAGT AACTGTGATA CCATACTATA AAACAGAAGA 120
 ATTTTCTGCT ACTAAAACT GCCTTTTAC AAAATGACTG TAAATATTG TAAAATAAAA 180
 TAACACTAAA CTTTAAGCCC AAAAGGAGAG ATAGAGCCAT GTGTTCAAGT GTGGACCTGT 240
 CCGTGGGGCA CAGTGCCACC CCATCACAGT GTTGCTGTCA TCAGGCAAN GTGAATGTTT 300
 GTTTATGGCA AATTCGNCTT TTGCGAATGG CTTANTTCTG AACTACCTT TCTGGGAAAT 360
 GTTAATANAT TTTAATTNT TCAA 385

SEQ ID NO:93

SEQUENCE LENGTH:381

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00105

SEQUENCE DESCRIPTION:

GATCTTTGAT AGTTTGGTG AACTCTCTAA AATACATTCA CTGTGGGTCC GACGCAATTT 60
 ATAAAAATNA TGTACTCAAG AAGGGAGACC TGTTGTTTC ATTTCTCATC TGTTTGGGAG 120
 ATGATTTTAG AGCACTAGAA AGGCACTGGG GAGATTCTCA GCTTAAACA TCCAGCAGTT 180
 TGAAGTATGA TTAGGTACAT CAGGGCTGCA TTGTCAATNT TCTCTTAAAG TCTTTAACA 240
 TTTATAGCAA TTTTTTTTT CCCGGAGAGT TTAGGTTGCA AGTTTGGGT TTCTTGTGTTG 300
 TTTTGTGTTT GCTTCTGCT TTAATNCTN AATTNCAGT CATTACTGGT ATTGAAAAAT 360
 AAAATATCTT TAAANCANNG N 381

SEQ ID NO:94

SEQUENCE LENGTH:380

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00106

SEQUENCE DESCRIPTION:

GATCTAAGAG ACTCAAGAGC TGGGTTTCTT TCAGCACTCT GTACTGTCCC AAATAGCAAA 60
 CAAATNACTT TGAGCCAGA TTTCTGAATG GAAATNAGAA ATTGAATTCT CCATGGACTT 120
 TTAGGTTTAT GGGGGAGTTT TAGCTGTGTT TCTTGGTTT ATTTAGCCA AACATGTCTG 180
 CTTTGTGATT TTTTTTAAA GTATAAGTGG TCTATATATA TGTTACCTT TTAATGTAA 240

ATGTTTAAAA AGTAAGCATT TATGTGTTTC CATAACTGAC ATCTGATGCA GACCTCATT 300
 TCTCCCCCTC TTCTACCCCTC CTCTTTTCCC CCTTTTCAAT ACTCTTGTAT TGGGTTCTAA 360
 TAAAATGGGT TGCTTTTTCN 380

5 SEQ ID NO:95
 SEQUENCE LENGTH:379
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

10 CLONE:HUMGS00107

SEQUENCE DESCRIPTION:

GATCCATACT TGGATGATAT TGATGATGAG ATGGACCCAG AGATAGAAGA AGCTTATGAA 60
 AAGTTTTGTT TGGAATCAGA GCGTAANGNA NAACAGTAAA GTTAAATTTT AGCATATCAG 120
 15 TTTTATAAAG CAGTTTAGGT ATGGTGATT AGCAGAACAC AAGAGAGCAA GAAAATGTGT 180
 CACATCTATA CCAAATTGAG GATGTTGAGT TATGTTACTA ATGTATGCAA CTTTAATTTT 240
 GTTTAACTACT ATCTGCCAAA ATAACTTTA TTCCCTATAA CTAAAAATGT GTATATATAT 300
 ATAATAGTTT ATTATGTACA GTTAATTCTA CTGTTTGGC TGCAATAAAA TCGATTTTGG 360
 AAATAAATGG AATGTTGGN 379

20 SEQ ID NO:96
 SEQUENCE LENGTH:384
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

25 CLONE:HUMGS00108

SEQUENCE DESCRIPTION:

GATCTTTGCT GGCAAGCAGC TGGAAGATGG ACGTACTTTG TCTGACTACA ATATTCAAAA 60
 GGAGTCTACT CTTCATCTTG TGTGAGACT TCGTGGTGGT GCTAAGAAAA GGAAGAAGAA 120
 30 GTCTTACACC ACTCCAAGA NGAATAAGCA CAAGAGAAAG AAGGTAAAGC TGGCTGTCCT 180
 GAAATATTAT AAGGTGGATG AGAATGGCAA AATTAGTCGC CTTGTCGAG AGTGCCCTTC 240
 TGATGAATGT GGTGCTGGGG TGTATTATGGC AAGTCACTTT NGNCAGACAT TATTGTGGCA 300
 NATNTTGTCT GACTTACTGG TTNCAACAAN CCCAGAAGNC ANGTNAACTG TNTGANGTTN 360
 35 ATNAAAAGNC ATGTNCTGAA CAAA 384

40 SEQ ID NO:97
 SEQUENCE LENGTH:583
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS00109

SEQUENCE DESCRIPTION:

GATCCTCATG AATGACTATC CTAATTTTAA GTATGCAGTT CTNTTTTTCG TGGGTTTATT 60
 45 CGTGCTGGTT CATCGNGAGT NAGANGCCTG CCTTGCTGTT CCTGGGAAGA TGCCATAGTT 120
 TTCGTTACTG GATGTTTGA GTAGATACTG GTCTGTNATT GGTGGAATGG AGAACACACG 180
 TGTTGGTGCT TCTGGGTAGC ACTGGTTTGC ATTAGTTTAT GTTTCCATGC CAGAGTTTGT 240
 GTGGCGGGGC GCATGTCCAC CACAGAGTGC ACTCGAGGGG ACTTTCAGTC ACAGGATTTT 300
 50 ATAATTGTNA TTGTACACT TTCAAATTTT TGTACATCAG TGAATTTTTT TTATATTTAA 360
 AGGTTGAGCC AAAGCCCCCA GTGTTTGTG TTTTGAAGCC AAGCTTCACT TCTAAAAGTG 420

CCTACAGAGG ACTTGTA AAA TGGAAAATGC AGCTCTGCAC GGAGTTTGAA ACCGTCATAC 480
 CTCCTTCTAT TAGGGAATNG GCATATACTG AGGGTGGTCC GGAAGNNNTT AACTTCCTAA 540
 AATTTTAA TAAAAGGCCT TTGCACCATT GGACCCCNNTT AAA 583

SEQ ID NO:98
 SEQUENCE LENGTH:370
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00110

SEQUENCE DESCRIPTION:

GATCAAGAAA AGCAACTTAT GGAAACAAC ACAGAATTTA CAAAAAGGA TACTCAAACC 60
 AAAAGTATTA TTTCAGAGAC CAGTAATAAA ATTGACGCTG AAATTGCTTC CTTAAAAACA 120
 CTGATGGAAT CTAACAACT TGAGACAATT CGTTATCTTG CAGCTTCAGT GTTTACTTGC 180
 CTGGCAATAG CATTGGGATT TTATAGATTG TGGAAAGTAG ATTAATGCTC ATCCTGCTGT 240
 GGCTGTGGC TTCTTAGAAC ACCAAACCGG GAGAGATTTA CTTTGAACAT TGTCAGTTGC 300
 AGCAAAAATT TACTACACAA GATTATTGCA AGTGTATACG GACTAAAAGA GGAAGTGTTT 360
 TAGAATGAAA 370

SEQ ID NO:99
 SEQUENCE LENGTH:384
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00111

SEQUENCE DESCRIPTION:

GATCTGAAGA GCGTCCTGGG TCAACTGGGC ATCTAAGG TCTTCAGCA TGGGGCTGAC 60
 CTCTCCGGG TCACAGAGGA GGCACCCCTG AAGCTCTCCA AGGCCGTGCA TAAGGCTGTG 120
 CTGACCATCG ACGAGAAAGG GACTGAAGCT GCTGGGGCCA TGTTTTAGA GGCCATACCC 180
 ATGTCTATCC CCCCCGAGGT CAAGTTC AACCCCTTG TCTTCTTAAT GATTGNCCAN 240
 AATACCAAGT CTNCCCTCTT CATGGGAAAA GTGGTGAATT CCACCNAAAA ATAAC TGNCT 300
 GTNGGTNCTC AACCCCTTNC NNTTCATCCN TGGGCCCN TN GGCTTGGATN GANAATTAA 360
 AGAAGGGGTT GNGGCTNGGG NAAA 384

SEQ ID NO:100
 SEQUENCE LENGTH:374
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00113

SEQUENCE DESCRIPTION:

GATCTTTGAA ACCITGGTCC CGTTAACTTA CTAGTCACAT TGACCAATGT TTTATAGAAA 60
 TGCCTAGAAT TTTGAGACTA ATNGTAGTTA TCCATTAACA TTCCAAAAGT TTTGTNCTTT 120
 TNAAAATTG TNTTGGTAAT TATCACATTT NTNCTCTTA CCTTCCTTTA AATGGCCACA 180
 GTGTGTACTG CTGGANTGTN CCATCCAAAA GATGTAGCTT CAGANGCACA GTGATTGCCC 240
 CAGGGTCCAT GAGATATTGT TTGTATTATG ANGTTGGAGT GCTGTCTACT GAAATTATAC 300
 TCTTAAATAA NTATGTATGT NGTGTGTAAT ATTCCTAAT AAATNCTTN GATAAACTAA 360
 AAAACTNNNG CTNN 374

SEQ ID NO:101

SEQUENCE LENGTH:382

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00114

SEQUENCE DESCRIPTION:

GATCTGTGCA AGGTATTAAC GTGTCAGGGC TGAGTGTCT GGGATTTCTC TAGAGGCTGG 60
CAAGAACCAG TTGTTTGTG TTGCGGGTCT GTCAGGGTTG GAAAGTCCAA GCCGTAGACC 120
CAGTTTCCTT TCTTAGCTGA TGTCTTTGGC CAGAACACCG TGGGCTGTTA CTGCTTTGA 180
GTTGGAACG GTTTGCATT ACGGCTGTAA ATGTATTCAT TCTTAATTA TGTAAGGTTT 240
TTTTTTGTAC GCAATTCTCG GATTCTTTG AAGNAGATGA CAACAAATTT NGGTTTCTA 300
CTTGTTATGT GAAGACCATT AAGGCCCCAA GCAACAAGNC AATTNTGTAA GGGAAANTNA 360
AAGTTCCTTG CNGTAANCCA AA 382

SEQ ID NO:102

SEQUENCE LENGTH:368

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00115

SEQUENCE DESCRIPTION:

GATCTGTCTC TGCTGTTTAA CTTCAATTGGA TTAATCAGCT GGTTCAACT CTACTGCGAA 60
ACAAAAATAG CTCCTTAAAA GTACTGTTCT CCTTCAGTGG CATGTAGTTA TCTAATCAAG 120
ACACCTCATT CAACAAAAAC CTGCTTAGG AAAATTTAAT ATATTNAAA TNATTTTAAA 180
AGAAATACAA CATCTTATTC TTAGCTTTC TTAATCGGTG CTTTATGGAG GCCAGTGTA 240
CGNTACATGA CTGTTGAGA AAGTTGAGGA ATTCCTCTA CCACCTTGT TGCTTGAAGA 300
AAAACATGTC TTTTCAAAAT GAGAGGCTTT CATTGAAGAA AAGAAAAAA CAACAGTTAA 360
AAGCTAAA 368

SEQ ID NO:103

SEQUENCE LENGTH:367

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00116

SEQUENCE DESCRIPTION:

GATCTCGGAT GACCAAACCA GCCTTCGGAG CGTCTCTGT CCTACTTCTN ACTTTACTTG 60
TGGTGTGACC ATGTTTCAAT TAATCTCAAA GGAGAAAAA AACCTTGTA AAAAAAGCAA 120
AATGACAACA GAAAANCAAT CTTATTCCGA GCATTCCAGT AACTTTTTT TGTATGTNCT 180
TAGCTGTAAT ATAAGTAGTT GGTTTGTATG AGATGGTTAA AAAGGCCAAA GATAAAAGGT 240
TTCTTTTTT TCCCTTTTT GTCTATGAAG TTGCTGTTA TTTTTTGGG CCTGTTTGAT 300
GTATGTGTA AACANTTGTN GTCCAACATT AANCAGGANT TTTATTTTNC NGAGTNGTNC 360
TANCAAA 367

SEQ ID NO:104

SEQUENCE LENGTH:366

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00117

SEQUENCE DESCRIPTION:

GATCTTAGTA ACTATGNATG AAGATGGTGC TTGGCCTGTN CTCTTGATG AATTTGTTGA 60
 GTGGCAAAAA GTCCGTCAGA CATCATAGCA AGAACTATGT GAAGAAAATG CAAACCTTTC 120
 AATTCCCACG TGTATACAAG CTAATGTGAT GAGGGGGAAA AAAATCCAAC GGGTGCATT 180
 TCATTTCATAT GAAAGACTTC TCATAGTACT TTTTTCCTN TTTTAAAA GGAGGTTTT 240
 CTTGTTACAT GTGATGGGCA TTGAGCCACA CCNNTTCTTA GACTGAATAT NGAAGTTTT 300
 GTTTTGAGTT ATGTTTATAA CATTATTTC AGAACANTAA TGATTGAGAT TTGTGACAAA 360
 GGCAAA 366

SEQ ID NO:105

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00118

SEQUENCE DESCRIPTION:

GATCCCGAA ATTGGTGGG TTGACCTCCT GGCAAATTGC TGCGTCTTC CACTTGCTGT 60
 TCAGGACCAC TAAATGCTGA AATNTGGATG CATAACGAAA TAAAAGNAAT TCATTGTGTA 120
 AA 122

SEQ ID NO:106

SEQUENCE LENGTH:364

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00119

SEQUENCE DESCRIPTION:

GATCTTCAAT ATGAAGACAT GAGCTTTTCT CGCAGGAAAT TTTCTTTTC ACAGAACTGG 60
 TGTCAGGAAT CACTGAAGGG CTAACCGTGA TAGTCCTTGC AAGTAAAGTCA AGGTTTTATC 120
 CTGATTGGAA ATAGAAGACA TTTCCGGTTG AGAGAACAGA TTCGTTGGAA GCTTAACTTT 180
 TGTTGCCTCT TAACGCCACC AAATTTTAGG GTAATTTGAT TATGAAAGAG TGAATTTTC 240
 TGGACAGAAA AGGGAGAGCT ACCAAATTGT TTTTCTTT TTTAAAGGAA GTTTAATGTC 300
 CGTTGTATCA CAAATCAGTG TTAAACACC AGAACTTTAG CCAAAATAAA TGTCTTACAT 360
 TACN 364

SEQ ID NO:107

SEQUENCE LENGTH:358

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00120

SEQUENCE DESCRIPTION:

GATCAGCAGG GAGTTATTT GAGGACATCA GTCACCTTTG GGGTTGCCAT GTACAATNAG 60
 ATTTATAATC ATNATACTCT TCGTGGTAG TTTCAAAGA CACTACTAAT ACGCAGGAAG 120
 CGTTCAGCT ATTTAATGCT GGCAACTACT GTTTAATGGT CAGTTAAATC TGTGATAATG 180

GTTGGAAGTG GGTGGGGTTA TGA AATTGTA GATGTTTTTA GAAAAACTTG TGAATGAAAA 240
 TGAATCCAAG TGTTCATGT GAAGATGTTG AGCCATTGCT ATCATGCATT CCTGTCTCAT 300
 GGCAGAAAAAT TTTGAAGATT AAAAAATAAA ATAATCAAAA TGTTTCCTCT TTNCTAAA 358

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SEQ ID NO:108
 SEQUENCE LENGTH:430
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00121

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SEQUENCE DESCRIPTION:

GATCTGTCTC TGGGGTCCCN CATACAGAGA AATGCATCTT GCTGAACAAG TGACCAATAA 60
 TCTTAAAGAA CTTGCACAGC AAGTAACTCC AGGTGATATC GTAAGCACGT ATGGAGTTGCG 120
 AAAAGCAATG GGGATTTCCTA TTCCTCCCC CGTCATGGAA AACAACTTN TGGATTGAC 180
 AGANGNNCT GAAGAACCTA AAAAGACGGA TGTGCTGAG TGTGGACCTG GTGGAAGTTG 240
 AGGCTGCCTG GTATTGATT ATATATTATG TACATACTTT TTCATTCTTA ACTAGAAAT 300
 GCTTTTCAGA AGATATTAAT TATTTGTAAA TTGNTTTTT AATTAACTT TGAACAGCG 360
 AATTTGGNTG TTCCAGAGGT TGGGCCTTGT ATTAGGGAAA TAAAAGCTTG GACCTGGGGC 420
 CTCGTGAAAA 430

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SEQ ID NO:109
 SEQUENCE LENGTH:357
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00122

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SEQUENCE DESCRIPTION:

GATCACTNGA TATTTAGTC ATTCTGCTTC TCATCTAAAT ATTTCCATAT NCTGTATTAG 60
 GAGAAAAATNA CCCTCCAGC ACCAGCCCC CTCTCAANCC CCAACCCAA AACCAAGCAT 120
 TTTGGAATGA GTCTCCTTA GTTTCAGAGT GTGGATTGTA TAACCCATAT ACTCTTCGAT 180
 GTACTTGTTT GGTTTGGTAT TAATTNGACT GTGCATGNCA GCGGCAATCT TTTCTTTGGT 240
 CAAAGTTTTC TGTTTATTTT GCTTGCATA TTCGATGTAC TTAAGGGTG TCTTTTATGA 300
 AGGTTTGCTA TTCTTGGCAN TTAAGNTTTT TTAGGNCCTT TTAANGNGN ANNNAAA 357

35

SEQ ID NO:110
 SEQUENCE LENGTH:356
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00123

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SEQUENCE DESCRIPTION:

GATCAAGGGA CGGCTGAACA GACTTCCCGC TGCTGGTGTG GGTGACATGG TGATGGCCAC 60
 AGTCAAGAAA GGCAAAACCAG AGCTCAGAAA AAAGGTACAT CCAGCAGTGG TCATTGACA 120
 ACGAAAGTCA TACCGTAGAA AAGATGGCGT GTTCTTTAT TTTGAAGATA ATGCAGGAGT 180
 CATAGTGAAC AATAAAGGCG AGATGAAAGG TTCTGCCATT ACAGGNCCAG TAGCAAAGGA 240
 GTGTGCAGAC TTGTGGCCCC GGATTGCATC CAATGCTGGC AGATTGCATG ATTCTCCAGT 300
 ATATTTGTAA AAANTAAAAA AAAGCTAAAC CCATTAAAAA GTATTTGTTT TGCAAA 356

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SEQ ID NO:111

SEQUENCE LENGTH:375

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00124

SEQUENCE DESCRIPTION:

GATCCTACCT ATCAAGCACT AAAAAGTTGA ACCATTATAC TTTATATCTG TAATGATACT 60
 GATTATGAAA TGTCCCTCA AACTCATTGC AGCAGATAAC TTTTGTGAGT CATTGACTTC 120
 ATTTTATATT TAAAAAATTA TGGAATATCA TCTGTCATTA TATTCTANTT AANGTTGTGC 180
 ATAATGCTTT GGAANAATGG GTCTTTTATA GGAAAAAACC TGGGATAACT GATTCTATG 240
 GCTTCAAAG CTNAAATATN TAATATACTA AACCANCTCT AATATTGCTT CTTGTGTTTT 300
 ACTGTCAGNT TAANTTACAG CTTTATGCGG TGGTAACTT TTCGTNCATT TTCAAAAAAN 360
 CCNGGGGNNN NNNNN 375

SEQ ID NO:112

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00125

SEQUENCE DESCRIPTION:

GATCTCTGTT TTGTTGTTGA AAATTCATTT GTATACTTTT GTTTTATCT AGGACTTCAT 60
 GTTTTTTNA AGCACTGGCA GCCAGGAACA AAAATCAGGA GTGTGGTAGT GGATTAGTGA 120
 AAGTCTCCTC AGGAAATCTG AAGTCTGTAT ATTGATTGAN ACTATCTAAN CTCATACCTG 180
 TATGANTTAA GCTGTAAGGC CTGTAGCTCT GGTGTATAC TTTTCTTTT CAAATTATAG 240
 TTTATCTNCT GTATAACTGA TTTATAAAGG TTTTGTACA TTTNTNAATA CTCATTGTCA 300
 ATTTGAGAAA AAGGACATAT GAGTTTTTNC ATTTATTAAT GNAACTNCCT TTGAAA 356

SEQ ID NO:113

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00127

SEQUENCE DESCRIPTION:

GATCACATTA TNATAAATAA ATGAAAAAAT GATTTAATCT GTAATAAACT GGTTTATTGT 60
 GCAGTGACTG TAATATACTA GAGTTATAAT AAATTGTTTA CTCTGCCTCA CCAAACACAT 120
 GCTAGGATAT AACCCCAAAA ATAAGTATTT AACTTTGCAT TAGGTATAAA GGAGACTGGG 180
 TGCTATAATN AGATTATTTT GAGGCAGACA GAGAGCTGTT ATCCTAACTG ATTTAGTATG 240
 TTCTGTAATT GAGAAAATGT TCACCAAAATN ATACTTTTTA GTGATTTACA TGTACATTTT 300
 ATAGGGGACA TGTTCTGTGT ATAGCGAATA AATAACTTTT ATAGTATCAC N 351

SEQ ID NO:114

SEQUENCE LENGTH:352

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00128

SEQUENCE DESCRIPTION:

GATCTTGAAC CTGGTGTCC ATCCATGGNA GCNNAAGCC TTTGCATCCC CTCAAACCA 60
 CTCTGTGAAC TGCAGCCTGG AGCCAAATNT GTCTGTGGCA AGAACCTGC CAAGTACTAC 120
 ACCTTATTTG GTCGCAGCTA CTGNGGGATG NACGAAAGCC CCCTCTTCAA CTCCTCTCAC 180
 TTTTAAAGC ATTGATATTA GTATCTTCTC AGATACAGAC CGTTTATGA TTTTAAAAA 240
 AGTAAAGTT CTAATGAA GTCACACAGG ACAATTATC TTATGCCTAA GTTAACAGTG 300
 GATAAAGAC TTTCTGTAA ACAACTCCAG TAATAATAT CATGACTNA AA 352

SEQ ID NO:115

SEQUENCE LENGTH:348

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00129

SEQUENCE DESCRIPTION:

GATCAAGTCG TGCTCTGGC AGGCGCGCCC CTGGAGGATG AGGCCACTCT GGGCCAGTGC 60
 GNGGTGGAGG CCCTGACTAC CCTGGAAGTA GCAGGCCGCA TGCTTGGAGG TAAAGTCCAT 120
 GGTTCCTGG CCCGTGCTGG AAAAGTGAGA GGTCAAGNTN NTNAGGTGGC CAAACAGGAG 180
 AAGAAGAAGA AGAAGACAGG TCGGGCTAAG CGGCGGATGC AGTACAACCG GCGNTTGTG 240
 AACGTTGTGC CCACCTTGG CAAGAAGAAG GGCCCAATG CCAACTCTTA AGTCTTTGT 300
 AATTCTGGGC TTTCTTCTAA TAAAAAGCC ACTTNAGTTC AAGTCAAA 348

SEQ ID NO:116

SEQUENCE LENGTH:344

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00130

SEQUENCE DESCRIPTION:

GATCTCCAC AATTAATTTA TCTTTGACA AAGGGGATAA AGAGTTTCAG TTAGCTCCT 60
 TTTGATTGTA TATNATTTT TCCTTTTNA TTGTGAAAAG AGGTAGGTTT TATTTGTGGA 120
 GAGAGAGTTG AAGATTAGG AACCAGTGAT TTAATTATG CTACTTTTCC TTCTAAGAGA 180
 TAAATTGATA TATCATTAG TGTATGAAA AACATGAATG TNGTACAATT TTCTNCCTCA 240
 AAAAATTTT TAAATGTAAG TATCCTTATT TNNTTTTAA AAGAGCACAA TGTAGGTGTA 300
 TTTGGGTATT TCCAAGAAAA GANTAAANCC ATTAATGCAG TAAA 344

SEQ ID NO:117

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00131

SEQUENCE DESCRIPTION:

GATCTGGGCT CCAAGCCAGG AAAGGTGAAC AGAAACCACA AGTNTCCAGC CCTCGGTGCT 60
 GGAGTGGACG TTAATTGTNA GCCACCAGAC TGTCCCGGCA CCTACAGAGA ATGTTTCACA 120
 GTTCTGGCAT TAAATCCTT TGATAGTGA TTGTGCTGCT GTTAGCCTTA GTTTCAGTGC 180
 TTTACAAGTC TCGCTTATNA TCTATTGGT ATTTAGGTAT AAAAAACAGT TGATTATTCA 240
 CCACGCCAAT ATCTGGGTCT CTGTATCTCA TGTAGAACAT AAGAAAATGG GAACTAATAG 300

GGAAATTTAT TTATAGCATG AAAATAAACC TGGTGGCTGG AGTCTGCTAA A 351

SEQ ID NO:118

SEQUENCE LENGTH:343

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00132

SEQUENCE DESCRIPTION:

GATCCTAAGG CAATAAAGA ATAAGGAGAT TTGGAAAACC ATTGTCTGTA ATCTCTGAAG 60
 AAAAGTGGAC ATTAGGGGAG TCAGTTGAAA AGCAAAGCTA TCACCATTTT CTAAAGAGGA 120
 AAAAGGTGAA CCTCACAAAC TATAGACCAA AAAAATAGGA CATCGAGAGA AAGAATATGA 180
 AGCTAGCATA GGTTCAAAA GAATGAGTCA AATCAAACAA CATGCATTTT TTATTTATAA 240
 AGCATGACTT GTTCATTGTC AATTCATGTT AGCTTAATCA TTAGGCATTA ATGCCATCAC 300
 TGCAATGCAT ATGTCAGCAA TAAATAATCA AGGCCCGGCT TCN 343

SEQ ID NO:119

SEQUENCE LENGTH:345

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00133

SEQUENCE DESCRIPTION:

GATCTTCCCA CAACACCACA GGACTGCAGG GTGCACAACCT CCCCTGCCAA GGAAAACCAT 60
 GCAGTCCTCC CCTCCCTGGT CTCCTGCTTC AGCTCTGTAC AACGAGGGCA AAGATGCTAA 120
 ATCTTGCTTT GCATTCAGTA AAGTGTCAAG TGATTAAGTG TGTATTGTA CCCTAGATGA 180
 TATGAACCAG CAGTCTTGTT TTGGCATCAT CCTCATCATG TTGTATTCCA GCTTCTTAAG 240
 TGGAAGGAAA AGAGTGCTGA GAAATGGCTC TGTATAATCT ATGGCTATCC GAATTCTCTG 300
 AAAAANTANT AAAAGTCCCC TCTNTTATAT GAGCCTGTAC AGAAA 345

SEQ ID NO:120

SEQUENCE LENGTH:358

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00134

SEQUENCE DESCRIPTION:

GATCCCCCT CTCGAGGGCG ATGAGGATGC GTCTCGCATG GAAGAAGTCG ATTAGGTTAG 60
 GAGTTCATAG TTGGAAAAC TGTGCCCTTG TATAGTGTC CCATGGGCTC CCACTGCAGC 120
 CTCGAGTGCC CCTGTCCCAC CTGGCTCCCC CTGCTGGTGT CTAGTGTTTT TTNCCTCTC 180
 CTGTCCTTGT GTTGAAGGCA GTAAACTAAG GGTGTCAAGC CCCATTCCCT CTCTACTCTT 240
 GACAGCAGGA TTGGNTGTTG TGTATTGTGG TTTATTGAA TTNCCTTCAT TTTGTTCTGA 300
 AATTAAGAGT ATGCAANAAT AAAAGAATTA TGCCCNTTTT TNATACAANA NNAANAAA 358

SEQ ID NO:121

SEQUENCE LENGTH:350

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00135

SEQUENCE DESCRIPTION:

5 GATCTTCATG CCCTGGGTTG TGCCCGNACG GACCCNCATC TCTGTGACTT CCTGGGAGACT 60
 CACTTCCTAG ATGAGGAAGT GAAGCTTNTC AAGAAGATGG GTGACCACCT GACCAACCTC 120
 CACAGGCTGG GTGGCCCGGA GCTGGGCTGG GCGAGTATCT CTTGAAAGG CTCACTCTCA 180
 AGCACGACTA AGAGCCTTCT GAGCCCANCG ACTTCTGAAG GGCCCNITGC AAAGTAATAG 240
 GGCTTCTGNC TAAGGCTCTG CCTNCAGNCA ATAGGNANGC TTTTAAACN ATCCTAACAN 300
 10 GGNTTGGGAC CAAATGGNAA TAAAGNTTGG TNGATGCAGG AGATATGAAA 350

SEQ ID NO:122

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS00136

SEQUENCE DESCRIPTION:

20 GATCTGAGCT GAATTGGAAG ACTATTAATA AGTTATGTTT GGAAGTTTTA ACTTCAATGA 60
 AGTAATTATT TGCTGTGAAA GAAACAAACA TTGAATTACT AAACAAAGAT GGTGCAATAT 120
 CTTTGTTTTT TTTTATGAG GCTCTGAGA ATCAACCCAA CTGAAGCATT TCAATTCAGT 180
 TGAATGAGAA ACGTGTGTTAG TATCAAAAGA GCCCAAGAAG ACACTGGTGT GAAAGGTACA 240
 NTCTCAGAGG TTGGTCAATT ACCGTGGCAC ANTTTCTGGT CACTTTGTAC AATGTAGATT 300
 25 TGAAGTACAG TGGTGAAAAC ATTAAATGTG ACATTTGN 338

SEQ ID NO:123

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS00137

SEQUENCE DESCRIPTION:

35 GATCAAAAAA CATGAGGNAG AAGAAGCCAA AGCTGAGCGT GAGAAGAAGA NAAAAAGAAC 60
 AGAAAGAAAA GGATAAATAG AATCAGAGAT TTTATTACTC ATTTGGGGCA CCATTTTCAGT 120
 GTAAAAGCAG TCCTACTCTT CCACACTAGG AAGGCTTTAC TTTTNNAAC TGGTGCAGTG 180
 GGAAAATAGG ACATTACATA CTGAATTGGG TCCTTGTCAT TTCTGTCCAA TTGAATACTT 240
 TATTGTAACG ATGATGGTTA CCCTTCATGG ACGTCTTAAT CTTCCACACA CATCCCCCTT 300
 40 TTTTGGAAATA AAATTGGAA AATGGAAATN AAGGAAA 337

SEQ ID NO:124

SEQUENCE LENGTH:336

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS00138

SEQUENCE DESCRIPTION:

50 GATCACCATT TGAGATACGC GGCTTAACGC ACATGTGAGT GTAGCTTGCT ACATGAAAAT 60
 GCTAGGCTCT AGGGCATGTA AAACATGAAT ACAGAATACT AGATTGTTCT AAGTAATGTC 120
 ATTTGGGTTT GTGANTTTGA TTTTCCCTT CATTTCATGT CATATTGNAA ATGCAACAAA 180
 ACTGCTCTCA AGAACACCCA GAAGCTATCT GTGTTACCAG ATGTGTTGTG NACACTCTAC 240

55

TNTTTTTCAT AGGTGCTACC TGGNAATATA TGTCCATTGT AGTGGTGGNG NGGGNCNTNGA 300
CTCTNTCAGG CTCTTNTCTN GCCAGNTGNC TNCNGN 336

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SEQ ID NO:125
SEQUENCE LENGTH:338
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

10

CLONE:HUMGS00139

SEQUENCE DESCRIPTION:

GATCTGGGCT GCAGGAGCTG GGGCCACCCA CAGCCCCCCT ACCGACCTGG TGTGGAAGGC 60
ACAGAACACC TGGGGCTGCG GGAACAGCCT GCGTACGGCT CTCATCAACT CCACTGGGGA 120
AGAAAGTGGC ATGCGCAAGT TGGTGGCCTC AGTGACTGTG GTTGAGGACG ACGAGGATGA 180
GGATGGAGAT GACCTGCTCC ATCACCACCA CGTGAGTGTA AGCCGCCGTT GAGGCCGAGC 240
CTGCACTGGG GCCACCNAGC CAGGCCTGGG GGNAGCNTTT CCCNAGNNTN CNNGTGCCAA 300
AANTTTTTTN ATTAAAAGAT TGTTTTGGGA ACTTTAAA 338

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SEQ ID NO:126
SEQUENCE LENGTH:347
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

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CLONE:HUMGS00140

SEQUENCE DESCRIPTION:

GATCAAGCAG ATTCCACGAA TCCTNCGGAC CAGGTTTAAA TANGGCAGGA AAGTTCCTTT 60
CCCTGCTCAC ACACAACGAA AACATGGTGG CCAAAGTGGG TGAGGTGAAG TCCACAATCA 120
AGTTCCAAAT NAAGAAGGTG TTATGTCTGG CTGTAGCTGT TGGTCACGTG AAGATGNAG 180
ACGATGAGCT TGTGTATAAC ATTACCTGG CTGTCAACTT CTTGGTGTCA TTGCTCAAGG 240
AAANCTGGCA GANTGTCCGG GCCTTATATA TCANNNGCA CCATGGGCAA NGCCCCAGCG 300
GCTTATATTT AAGGCACATT TTNATAAAT TCTATTNACC CGGTAAA 347

35

SEQ ID NO:127
SEQUENCE LENGTH:335
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

40

CLONE:HUMGS00141

SEQUENCE DESCRIPTION:

GATCAGTTGT AATCAGAATA CAACTGNGTC TTGTAGTTGT AATATGTTCT ATCTTAACCA 60
CCACTTTCGT ACCAGGAACC TGCTCAGGTT TGTTCCTAG AAGCTCCCA CATAGATAGT 120
CTACATTCA GACTACTAAG TTATTAACAA ACCCTTTGGG CCCATGTTCA CTTAGGGTT 180
GAGCATAGTG TGAGGAGATG TAAATTAAT TATAATCCTA TATGTGTGTG TAATAAATAT 240
TAAAGTGTAT AAATTAACA GCAGATTCTA AGTATCCAAC AAGAGTCAAA TAAATGATAC 300
AAAGTCACCA AATAAATAAT ATTTAATCTC ATCTN 335

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SEQ ID NO:128
SEQUENCE LENGTH:356
SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS00142

SEQUENCE DESCRIPTION:

5 GATCTAGTTA AAGTTATTCA ACAGGAGTCT TACACATATA AAGACCCAAT TACAGAATTT 60
 GTTGAATGTT TATATGTTAA CTTTGACTTT GATGGGGCTC AGAAAAAGCT GAGGGAATGT 120
 GAATCAGTGC TTGTGAATGA CTTCTTCTTG GTGGCTTGTC TTGAGGNNNN CATTGAAAAAT 180
 GCCCGTCTCT TCATATTTGA GACTTTCTGT CGCATCCACC AGTGTATCAG CATTAAACATG 240
 10 TTGGCAGATA AATTGAACAT GACTCCAGAA GAAGCTGAAA GGTGGATTGT AAATTTGATT 300
 AGAAATGCAA GACTGGATGC CAAGATTGAT TCTAAATTNA GGTCATGTGG TTATGN 356

SEQ ID NO:129

SEQUENCE LENGTH:333

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00143

SEQUENCE DESCRIPTION:

20 GATCAAAGNA CTCTGACTGC AGAACTGCCG CTCTCAGTGG ACAGGGCATC TNTNACCCTG 60
 AGACCTGTGG CAGACACGTC TTGTTTTCAT TTNATTTTGG TTAAGAGTGC AGTATTGCAG 120
 AGTCTAGAGG AATTTTNNTT TCCTTGATTA ACATGCTTTT CCTGGTTGTN ACATCCAGGG 180
 CATGGCAGTG GCCTCAGCCT TAAACTTTTG TNCCTACTCC CACCCTCAGC GAACTGGGCA 240
 GCACGGGGAG GGTTTGGCTA CCCNTGCCCA TCCNTGAGCC AGGTACCACC ATTGTAAGGA 300
 25 AACACTTNCA GAANTTCAGC TGGTTCTCTC AAA 333

SEQ ID NO:130

SEQUENCE LENGTH:332

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00144

SEQUENCE DESCRIPTION:

35 GATCTCTGTA GATATTCTGT TTTATTTTGG TCATCTTTAG AAGTTATCAG GAATGTGTTT 60
 AAAACAAGAA GAGAACTTTT CTAAGGAATG ATACATAGAA AAGATTTTAT TTTAAATGA 120
 GTTGTAAGC TTGTTTTTCT TTGTTGCTGC AANTATCTGC CCAAGTTAAT GCAAATGGAC 180
 ACATTTTTTA TGTGAGAAAA ACACACACAC ACACACACAC ACACACACAC ACACACNCGC 240
 GNNACACAGN GANAAAAGTG CTTGNGCTTN NNCTCNCTNC CCCTTGCNGT CTGTTGTGTG 300
 40 CGCAGCCTGT TTATNTCTCT NNTATTGTGT CN 332

SEQ ID NO:131

SEQUENCE LENGTH:332

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00145

SEQUENCE DESCRIPTION:

50 GATCTGTGAC CTTACCCCA AACCTGTNCT CTCTGAAACA TGTGCTGTGT CCACTCAGGG 60
 TTAAATGGAT TAAGGGCGGT GCAAGATGTG CTTTGTTAAA CAGATGCTTG AAGGCAGCAT 120
 GTCCTTAAAG AGTCATCACC ACTCCCTAAT CTCAAGTATC CAGGGAGACA AACACTGCCG 180

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AAGGCCGCAG GGTCTCTGC CTAGGAAAAC CAGAGACCTT TGTTCATTG TTTCTTTGTT 240
 CACTTGTTTA TCTGCTGACC TTCCCTCCAC TATTGTCCTA TGACCCTGCC AAATCCCNT 300
 NTGATGAAAA ACACCCAAGN ATANTCANTA AA 332

SEQ ID NO:132
 SEQUENCE LENGTH:333
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00146

SEQUENCE DESCRIPTION:
 GATCGAGGTT GTTGTCAACG ACCGTCTGGG GAAGAAGGTC CGCNTTAAAT GCAACACGGA 60
 TGATACCATC GGGGACCTTA AGAAGCTGAT TGCAGCCCAA ACTGGTACCC GTTGAACAA 120
 GATTGTCTTG AAGAAGTGGT ACACGATTTT NAAGGACCAC GTGTCTCTGG GGGACTATGA 180
 AATCCACGAT GGGATGAACC TGGAGCTTTA TTATCAATAG ATGAGAATCC TCATCTTNCT 240
 GCCCCGCTNT CCNCTNCCA TCCTCATCCC CCACANTNGG GATAGATGCT TNGTTGTAA 300
 AAATCANCN NAATAAGAC TTAGATGTTG AAA 333

SEQ ID NO:133
 SEQUENCE LENGTH:330
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00147

SEQUENCE DESCRIPTION:
 GATCAGGTCT GTAAATGTGT ACTAAAAAAA TNAGAGTTTA TTTATAAACA AAATAGTTTA 60
 TTTAAAGAGA AGGTCTCTTC CTTATTGATA TCATGGTATG CATTAAATCC ATTTGTACT 120
 ATGTGCACA AAAGCCCTGT TCACAGGGGA ATGGTGTAAT CATTATACT GTTTGTTC 180
 CTGTATTTAG TAGACATAAC TGTGAATAG TTAAGTGAATC ATGATGTAAA GAATATGTGA 240
 CCATCTTCAG GTATGGGATT TCTGAACGTT TCAAATTTCA ATCAATGAGC ACTGTCAACA 300
 CCCACAGGNG AGAATAAAAT TACCTGTGCN 330

SEQ ID NO:134
 SEQUENCE LENGTH:326
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00148

SEQUENCE DESCRIPTION:
 GATCGAACCA CTGCACTCCA GCCTNGGTGA CAGAGAGAGA CACTGCCTTN GAAAAAAAAA 60
 GAATCTCACT CACTATCTAG AGAGGATTGT CAGANTATTC ACGATTCAGN TCTTGAAACT 120
 TTGATTATGC AAAAGAGGTA TATATAAATA TTTCATTATG ATTCAGGTTT TAGGCTTTGC 180
 AGCTTCTATA AGGTGTTCTC AGGTGGCCCT TGTACNNCTN AAAGCATCCT TTAGGAAATN 240
 CTTAAGGGN GGCTTTNTAT AAGGAATAGG NGGNTGTTGA ATTTTACAG GGGGGTTTGG 300
 GTCATTNAGN CCCCGATTNT GTANGN 326

SEQ ID NO:135
 SEQUENCE LENGTH:325

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00149

SEQUENCE DESCRIPTION:

GATCATGANC TCTGAAAAA AGAGAAACCT TATCTTINCT TTGTGGTTCC TTAAACACA 60
 CTCACACACA CTTGGTCAGA GATGCTGTGC TTCTTGAAG CAAGGNTCA AAGGCAAGGT 120
 GCACGCAGAG GGACGTTTGA GTCTGGGATG AAGCATGTNC GTATTATTA TATGATGGAA 180
 TTTCACGTTT TTATGTNAAG CNTGACAACA CCAGGCAGGT ATGAGAGGAA AGCAAGGCC 240
 GTCCATNGCT GTCCGTACNC TTACGGNTTG CTTGTNGGAG NCATTNGGT ATTGTTTGT 300
 GTAANANCCA AAANGGGCTT TGGNN 325

SEQ ID NO:136

SEQUENCE LENGTH:326

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00150

SEQUENCE DESCRIPTION:

GATCNACGCT GTGCCTTGGC AGGGCACAAT GACCTTGTGC AAATCCACCT GTCAGGACGC 60
 CTAGGGGTCT GTACCGGGCT GGCCTGTGCC TATNACCTCT NATGCACACC TCCCACCCC 120
 TGTATTCCCA CCCCTGGAAT GGTGGCCCTT GCCTTGGGGA AGGTCTCCCC ATGTGCTGTC 180
 ACCAGGAGAC AGACAGAGAA GGCAGCAGGC GGCCTTTGTT GCTCAGCAAG GGGCTCTGCC 240
 CTCCCTCCTT CCTTCTTGCT TCTNATAGCC CCGGTGTGCG GTGCATACAC CCNCACCTCC 300
 TGCAATAAAA TAGTAGCATC GGCAAA 326

SEQ ID NO:137

SEQUENCE LENGTH:324

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00151

SEQUENCE DESCRIPTION:

GATCAAGNNG CCCTGGAGGC GGTGGGCGGC ACCGTGGTTC TGGAGTAGCC TCCAGCTCGG 60
 AGGACTTGTN TNCAGGGGTC CTGGGCCCGG GNCAAGGTCC CGCCCTCCCG TGGTCACTGG 120
 CTCCGCCCCA GCACCAGGCG CCCAGTGGAG CCGTTTGGAA GAATTGCCTG CNGCAGGAGC 180
 GGGGCCGGAC AGGCGCACAG ACCTACTGTN GCGGGAGGAA GGGGCGGCTG CTGCCTGGTG 240
 ACGGCACCCG GAGGCCACAC AGGACGCGCC ACCGGTNAAT GTNNTCTNG TGGCTGCTGA 300
 GAAAAATACA CTGTGCAAGT CAAA 324

SEQ ID NO:138

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00152

SEQUENCE DESCRIPTION:

GATCTCAGCT TTTGGTTTCC CATGATACCA TCTCTAGGGG TAGCAGCTGG CTATAATAAC 60
 TAATGTCTGG ATTATCTAA CTCCTCTGTT TGTNCTTTCA GGTATTAAAC AATGTTGTGA 120

CTAATTGGCT TCCATTATTT CCCTAGAGTA GGTTCGTGTA TNACCCTGGA ATATGTTTGT 180
 AATAGAGTGG GCTATTACAA TCATCTAGGA TAAAGATAAT CGTGGCTTGG AATAAGGGTG 240
 GTAGCAATGG AAGTGATGAG AAGTCATTAG ATGCAGAATA TATTTTATAG ATGGANTGTG 300
 ATAAANTAAA AAATAAACTG GGN 323

SEQ ID NO:139
 SEQUENCE LENGTH:322
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00153
 SEQUENCE DESCRIPTION:

GATCCATTCT CGGAATTCAC AGAATTTTNA TAACATCTNA CTCTCAGGGG GCATGAAGTG 60
 CATAATCTTC CCTAGATTAC AAAAAACATA TAGATGACGG GTTGCCTAT NAAACTTCAG 120
 TACTACAAGA AACATAAAAT ATTTAAATAT ATGANATTTA AATATATTTA AAATTATTAA 180
 AGTAATATAA ACATTTTNA GTGACTGTGT TATGTTTTTC TGGTTATTTT GTTTTCTACT 240
 AGTATATTTT TCTGTAAAAA TTGTAAAACT ATATCAGCAA TTTCTAATGC CAANAANGTA 300
 AACCTNGTG TGTATAATG CN 322

SEQ ID NO:140
 SEQUENCE LENGTH:323
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00154
 SEQUENCE DESCRIPTION:

GATCAGAGGC ACAAGTNCAG AGGCTGTGGT CATGCGGAAC ACTCTGTTAT TTAAGATGGC 60
 TATCCAGATA ATCCTGAACA CTGTGTATTT ATTTAATTTA GACTACCAGC AAAGATTAAA 120
 GCATGAAATG TAAACATCT GATAAACTT ACAGCCCCCT ACACCAAGAG TGTATCTGTG 180
 AAAGAGCTCC TACACTTTGA AAAGTTAAGA NTCCCTTNTC ATGAAGTTTG CCTGTNCTAG 240
 AATTGTAAGA TTGTAAATTT CCNTCAATCT CTAGTGACAA CACTTAATTT CTTTNTCTAT 300
 ANAAAAAGCC TNGTNGGTGN AAA 323

SEQ ID NO:141
 SEQUENCE LENGTH:328
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00155
 SEQUENCE DESCRIPTION:

GATCAAGTTT AAATGACTGT GCTGCCCCCT TCACATCAAA GAACTACTGA CAACGAAGGC 60
 CGCGCCTGCC TTTCCCATCT GTCTATCTAT CTGGCTGGCA GGGGAAGGAA GAACTTGCAT 120
 GTTGGTGAAG GAAGAAGTGG GGTGGAAGAA GTGGNGTGGG ACGACAGTGA AATCTAGAGT 180
 AAANCCAAGC TGGCCCAAGG TGTCTGCAG GCTGTAATGC AGNTTAATCA GAGTGCCATT 240
 TTTTTTTTGG GGTTCAAANG NTTTTTAATT TNTTNGGAAT NGNNCCANTT TTTTNAATTT 300
 NGCAANTAAA AANGTTTAAA ANCTTAAA 328

SEQ ID NO:142

SEQUENCE LENGTH:369

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00156

SEQUENCE DESCRIPTION:

GATCTCTGGC AGTGGAGGAA GTCTCTTTAA GAAAATAGTT TAAACAATTT GTTAAAAAAT 60
 TTNCCGTCTT ATTTCAATTC TGTAACAGTT GATATCTGGC TGTCTTTTT ATAATGCAGA 120
 GTGAGAACTT TCCCTACCGT GTTTGATAAA TGTNGTCCAG GTTCTATTGC CAAGAATGTG 180
 TTGTCCAAAA TGCCTGTTTA GTTTTTAAAG ATGGAAGTCC ACCCTTTGCT TGGTTTTAAG 240
 TATGTATGGA ATGTTATGAT AGGACATAGT AGTAGCGGTG GTCAGACATG GAAATGGTGG 300
 GGAGACAAAA TTATACATGT GAAATAAACC TCAGTATNTT AATAAAGTAG CACGGNTTCT 360
 ATTTGNAAA 369

SEQ ID NO:143

SEQUENCE LENGTH:324

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00157

SEQUENCE DESCRIPTION:

GATCATGAAG GAACACATAG CACCAAGAGA GGCCATGCTA AATCTCGCCC TGTCAGANNN 60
 NTCCACACTT CTCCTTTGGG GAAGNCITCC CTGTCCCCCT AGACTAAGTT AAATATTTCT 120
 GCACAGTGTT CCCATGGCCC CTTGCATTTC CTTCTTAACT CTCTGTTACA CGTCATTGAA 180
 ACTACACTTT TTTGGTCTGT TTTTGTGCTA GACTGTAAGT TCCTTGGGGA CAGGGCCTTT 240
 GTCTGTCTCA TCTCTGTATT CCCAAATGNC TAACAGTACA GAGCCATGAC TCAATAAATA 300
 CATGTTAAAA TGGGATGAAT GAAA 324

SEQ ID NO:144

SEQUENCE LENGTH:316

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00158

SEQUENCE DESCRIPTION:

GATCATTGAA CGAGACAGAA AGCGACCATC CTGGTTCACC CAGAATTGAC ACCAAAGATG 60
 TTAAGAGGAT AACTTCACAG TAAATCAITT CTCCTGAAAT AGAGGAAGAT TCTTTACGTT 120
 GTTGTNCTTG TTTTAAATC ATCAGTATAG TTTAACACAT TCTTTCTAAG CAGTTTTGTG 180
 TGGGATAATT TGAAGAATAT ATTATGAGTA ANCTCCGAAA ATTTTGTTTA TCCAAAGGCT 240
 CANTGGATTA TGTTTCTATT ATNTACAAGG TTTTAAGTAA ACATANNNTT TCCNGNCCNG 300
 AGNTTANAGN NATTTN 316

SEQ ID NO:145

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00159

SEQUENCE DESCRIPTION:

GATCTTCATT TTATTGCATT AGTTCATGTA GATGGGCATC TCTATGAATT AGATGGGCGG 60
 AAGCATTTC AATNAACCAT GGTGAAACTA GTGATGAAAC TTTATNAGAG GATGCCATAG 120
 AAGTTTGCAA GAAGTTTATG GAGCGCGACC CTGATGAACT AAGATTAAAT GCGATTGCTC 180
 TTTCTGCAGC ATAGCTTGTC AATAATGGAA ACACCAAAAA CTGTATTATT TGCAACTAAA 240
 TTTTCTCTGC CATACACTAA CTCAAAAATT TTGATATTTT CATTAACCTG ATGATTAAAC 300
 TTTATGTGAG TTAANCTTTG AAA 323

SEQ ID NO:146

SEQUENCE LENGTH:319

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00160

SEQUENCE DESCRIPTION:

GATCTTACTG CTGTNACTT GAATCCCGTG ATTGTNATAC ATCTCTGGTA TAAGCAACAT 60
 TTGATTTTGG AAGTGTGTAG ACCATCTCTT CATATTTTCA AGATGTAATT TTACATTNCT 120
 GCATTTTAA AACAGTTTGG CCATAATCCT AGATGCACGC TTCTAATTCA TGTACCTGCA 180
 CATGTGACCT TTGTGAACAG NAATTTGCAT GNATAATTNG TGTTTACTTG TAACTNTCTG 240
 GTTATATACT GCTTATATCT GTGGATTCAA GTTACTGAAG TGGANTNCCA ATAGAAAGNA 300
 ANCCCTAGGC CATGTTAAA 319

SEQ ID NO:147

SEQUENCE LENGTH:316

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00161

SEQUENCE DESCRIPTION:

GATCTCTGAT TACCAGCCTG ACATCAACAA ATCCCTCAG TTACAACGTA TAGGTAAAC 60
 AAAGCTTTTA AAAGCTCATG TGGTATGACC TCAAGGTTGC TAACCTGGTC ACTCATGGTA 120
 ATNAGAAACT CTGATTGGCA GCTTTGTATT TCTTGACTAA AAACCTAAAT AAAC TGATTA 180
 GGTTTTAGGC GTTCTTTCAA AGAGGTTCTT GAGAAGATTG AGAACTATCC TATTTGGTGC 240
 TTAGTGAAAA GATTTTGAAT TACTGTACGT ACCAGTTGTT GCCATTTCTT TATTAAATTC 300
 AGAAGTTTTT TTGCCN 316

SEQ ID NO:148

SEQUENCE LENGTH:319

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00162

SEQUENCE DESCRIPTION:

GATCTTGGAC AGCNTGGGTA TCGAGGCGGA CGACGACCGG CTCAACAAGG TTATCAGTGA 60
 GCTGAATGGA AAAAACATTG AAGACGTCAT TGCCCAGGGT ATTGGCAAGC TTGCCAGTGT 120
 ACCTGCTGGT GGGGCTGTAG CCGTCTCTNC TGCCCCAGGC TCTGCAGCCC CTGCTGCTGG 180
 TTCTGCCCTT GCTGCAGCAG AGGAGAAGAA AGATGAGAAG AAGTAGGAGT CTNAAGAGTC 240
 AGNTGNTGNC ATGGGATTG GCCTTTTTTG GTTAAATTCC TGNTNCNCTG CAAATAAAGG 300
 CTTTTTTTAC AGANGTAAA 319

SEQ ID NO:149

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00163

SEQUENCE DESCRIPTION:

GATCAATGCC CTCATTAAAG CAGCCGGTGT AAATATTGAG CCTTTTGGC CTGGCTTGTT 60
 TGCANAGGCC CTGGNCAACG TCAACATTGG GAGCCTCATC TGCAATGTAG GGGCCGGTGG 120
 ACCTGTCCCA GCAGCTGGTG CTGCACCAGC AGGAGGTCTT GCCCCCTCCA CTGCTGCTGC 180
 TCCAGCTGAG GAGAAGAAAAG TGAAGCAAA GAAAGAAGAA TCCGAGGAGT CTGATGATGA 240
 CATGGGCTTT GGNCTGTTTG ACTAAACCT CTTTATAAC ATNGTNCANT AAAAAGGCTG 300
 GAGCTTTAAT AAA 313

SEQ ID NO:150

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00164

SEQUENCE DESCRIPTION:

GATCCAGAAT CCACGGGGTC TGGAGCATAA GGTTCATCTC AAGTNTCAAT TGANCTGCCT 60
 CCTCTTGTA GGCAGGGACA ACTGGGAGGA TGAGCCCCAA GAGCCTCAAG AACCCAAACA 120
 GGTGCCCCCTA GAAGACACAG AGACAGATGA NCTTTGGGCA TCCTTGGAGG CAGCTGCCAA 180
 GCGGANAGCT CTCGGGTTTG GAGCAGCCCC AAGGAGCTCT CCAAACGAGA CGGAGAAAGA 240
 AGAAGCGGCC TGGGTCCACC AGCCCCTGAC GCCCCTGTNN CCACTTGTA AATAAACTTG 300
 CTGAACACCC AAA 313

SEQ ID NO:151

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00165

SEQUENCE DESCRIPTION:

GATCATCAAC AAAGAAAGTC TGAGAAATTG TCCCGGAATA AAGGGGCCTA AGGAGACATA 60
 ACATCTAAAT GTAATGTAGT ATCCTGGATG GACTCCTGCA ACAGAAAAAG AACTTTAAGT 120
 AAAAAATTAAG GGAATATTAA TAAAGTATGC ATTTTGGTTA ATAATGTATC AATATTGGTT 180
 TATTAGTTGT GACAAATGTA CCAGAGGAAT GTAAAATGTC AACAATAAAG GAATTGGATG 240
 TGGGGTCCAT GAGATGCTGT ACTATTTTGT CACTTTTCTT AAATCTAAAC TCTTATAAAT 300
 TTAANCATAA AGN 313

SEQ ID NO:152

SEQUENCE LENGTH:317

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00166

SEQUENCE DESCRIPTION:

5 GATCTGGCCA TCTACGAGCC AAAGACTTTN AAATCTTTGG CTGCCTTGGC CAGTAGGAGG 60
 CGACACGAAG GATTTNCTGC TGCCTTGGGG GATGGGAAGN AACCTGAAGG CATTTTNNCC 120
 AGAGTGGTGC AGTACCACTN AGGACTGTTG CTGTATTGAT TAGGAAAAGA GACAGAGTAA 180
 TTTNCAGTTT GTTTGATTTA TACTTTTGTT TATCTACAAC CCAATAACAG ACATGAGGGA 240
 TGGCCCTGTC TCTCTGGGAC AGAGCCTCAA AGATGATGTC CATGTTTTGT GTGAATGAAA 300
 CTCAAACACT CTTCAA 317

SEQ ID NO:153

SEQUENCE LENGTH:310

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00167

SEQUENCE DESCRIPTION:

20 GATCCCCTGC CCCCTGTCCC CTGCCTCTTT TCCCAATTCC CTTCCATTATG CTGGACTTTT 60
 AAAGCTTAAA AAAAATCCGA TTGAATATAA ATGCCTAATT TCATTCTTTG TGAATGGTT 120
 GCTTCCTCCT GATTCCCTAA TTGTGCTGTG TTCGTGTCTT GCACTGGAAT TCAACATTCC 180
 CTTCTCCTTT TGTACTGTGT TGTGCTTGCT GTCTCTCCCG GACANCCTTA AAGACTGTCT 240
 TTTTAGCAAA AAATTCAGT AAAGTGTTTT CTGTAATCTT TTTTAAAAG GTGAGAACTA 300
 ATTATTGTCN 310

SEQ ID NO:154

SEQUENCE LENGTH:309

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00168

SEQUENCE DESCRIPTION:

35 GATCACCACG GTTTTCAGCC ATGCTCAGAC AGTGGTTCTT TGTGTAGGTT GTTCAACAGT 60
 GTTGTGCCAG CCTACAGGAG GAAAGGCCAG ACTCACAGAA GGGTGTTTCAT TTAGAAGAAA 120
 GCAACACTAA TGATTCAAAC AGCTTCCTGA ATTTTAATTT TGTGTTGTCT CACAGAAAGC 180
 CTTATCATAA ATTCCATAAT TCTAATTAAT TTACCAAGAT AATGTAATTA CATTTGGTTT 240
 TGTAAGGTAT ACAGCAGTAA TCTCCTATTT TGGTGTGAGT TTTTCAATAA AGTTTGGATT 300
 ATGGGCAAA 309

SEQ ID NO:155

SEQUENCE LENGTH:307

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00169

SEQUENCE DESCRIPTION:

50 GATCACATAC AGGGGAAAAG CCCTATGNAA TGTAACACAT GCAGGAAAAC CTTCTCTCAA 60
 AAGTCAAATC TCATTGTACA TCAGAGAACA CACATAGGAG AAAANCCTTA TGANTGATTT 120
 GGATATTAGA AATTNCCAGC CACAAGTCAG CCTCCATAAT GCNTCAGAGT CTTCACTG 180
 TGGAGANGGG CCTGTTGACA TCTGATTGT TCANTAACCT TCCACAACCT CGCCTTATGT 240
 TACTCCANNG TAACAGTAGG GGTAAANCC ATAGNCTACA ACACCTNTNG GNTGGCTTTT 300

NTTAGGN

307

SEQ ID NO:156

SEQUENCE LENGTH:307

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00170

SEQUENCE DESCRIPTION:

GATCCACCAA CTTTGGCCTC CCAAAGTGTT CAGATTACAG GTGTGAGCTG CTACCATGCC 60
 TAGCCCCAGC TTCTACTGCT TGANGGCTCT CTTTGGCATC TCCACACATC ATCCTTAGCA 120
 GCCCAGACTG CATTCTGTGA GCAGCCTCTT CCCTGGTCTC TTCITTCAGT CTCTCTGCCT 180
 CTAATCCAGT GGCTTTAAGA ATTTTGGC TGTGACTTCC AGTAAGAAAT ACAATTTACA 240
 TTGTGACCTA GTAAATATGT GTGTAAGATT TATTAAGTGA AATAAAAAATG TTATGATTGA 300
 ATTTTNN 307

SEQ ID NO:157

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00171

SEQUENCE DESCRIPTION:

GATCTGTCCC TGTGGTGGTG TCTAAGAATC GGACACCTTG GTTTTGTGT TAGATTGAGC 60
 TGGGCAGCTG CAATCAGCTA CTTAATATGC AAATTAGGCA CGTCCCATCT GTGGGTCCTT 120
 GTTGGTGGCT AATGAAGTGA GGGGAGGGAG GGATGTCACC CCAAAGTAG GCCCTCCCAT 180
 TGGCTTTGGC CAGGCCAGAC ACTTCACATC GTTTACATGG TTCTGTGTAA TTTTAAAGTT 240
 TATGTGTATA AAGCGACGGT TTTCTGTGAA CTGTATATTT TGTAATAAAA TATATTGCTA 300
 CTTTGN 306

SEQ ID NO:158

SEQUENCE LENGTH:310

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00172

SEQUENCE DESCRIPTION:

GATCTTCAGA TAAATTCTGC CATTTTNATT TCACTTCCTG AAAGTNAGGG TCGGCTTGTN 60
 AAAAGTTGTT AAACAACATG CTAAATGTGA AATGTCAACC CTCACTCTAA ACTTTCCCTG 120
 TTCAGAGCAT CAGATGAAGA CTTCAATGGG TTTTATAGTG GCTTTCTGAT TTNGGTAGT 180
 CCATTGAAGA AGGGAGTTTG AAAGTTGTG TATACTGTGA ACGATTGTCT GCCCATGTCC 240
 TGCCTGAAAT ACCATGATTG TNTATGAAAA GTATCTTTAA TAAAGCTGGA TACAGTTTGG 300
 CTTGGAGAAA 310

SEQ ID NO:159

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00173

SEQUENCE DESCRIPTION:

5 GATCTACTTT GGAAAAACAA AGGATATCGT CAATGGGCTG AGGTCTGTNC AGACTTTTGC 60
 AGACAAATCA AAACAAGAAG CTCTGAAGAA TGACCTGGTG GAGGCTTTGA AGAGAAAGCA 120
 GCAATGCTAA ACCTCTGTTT CATGCTAACC AGACACGCCG TGCACTCGTT AGATTCCTTT 180
 CTTAGAAAAC TCGTTTTCTG CTCCCTTCCC TCGTCCCTC CCTCCCCGAC AGGTCACATA 240
 ACAGCTGCAT CATTGACCGC ACAGCGCCAT CTCTCCCTGA GAATAAAGCC GATAGCCACC 300
 10 NTCAAA 306

SEQ ID NO:160

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00174

SEQUENCE DESCRIPTION:

20 GATCTATTGG ACTTTTTTTT GCAGGAAAGT CATTCTCTGG TCCTTCCCTA TTTTCTGTTC 60
 TGGATGTCAG TGCAGTGCAC TGCTTACTGT TTTATCCACT TGGCCACAGA CTTTTTCTAA 120
 CAGCTGCGTA TTATTTCTAT ATACTAATTG CATTGGCAGC ATTGTGTCTT TNACCTNGTA 180
 TACTAGCTTG ANATAGTGCT GTCTCTGATT TCTAGGCTAG TTACTTGAGA TATGAATTN 240
 CCATAGAATA TGCAGTGATA CAACATTACC ATTCTTCTAT GGAAAGAGAA ACTTTTGATG 300
 25 ATGAAACAAT AAAGNTTTTA AATATCAAA 329

SEQ ID NO:161

SEQUENCE LENGTH:303

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00175

SEQUENCE DESCRIPTION:

35 GATCTGAATA AAGCAAATCT GCATAAATGG TAACCAGTAG CTCTACTTTN ATTTTNNATG 60
 TTGCTTAAC TTTTATTTT AAGGAAACCT GTGTGATTTA AAAAGTTATA GCTTTTGCAA 120
 CTTTATTACT GGTATATAC ATTTGGCCAT TATNATGTGC AAGCAATTGG AAAAAAAGTC 180
 AAGTAAATGC TTGTTTTTGT AGTAGTTTGT TCTTGTTAAA AATGTTTATA TGATAATGTC 240
 TGTAAACAGC ATCACTTTGA TTACAATAGA TGTAGTGTG TAATAAACTG TTTAATGGGG 300
 AAA 303

SEQ ID NO:162

SEQUENCE LENGTH:298

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00176

SEQUENCE DESCRIPTION:

50 GATCTCTCTA GCTTTGTCAT AGTTATGTGA TTTTCCTTTG TAGCTACTTT TGCAGGATAA 60
 TAATTTTATA GAAAAGGAAC AGTTGCATTT AGCTTCTTTC CCTTAGTGAC TCTTGAAGTA 120
 CTTAACATAC ACGTTAACTG CAGAGTAAAT TGCTCTGTTC CCAGTAGTTA TAAAGTCCTT 180
 GGACTGTTTT GAAAAGTTTC CTAGGATGTC ATGTCTGTCT GTCAAAAAGAA ATAATCCCTG 240

TAATATTTAG CTGTAACTG AATATAAAGC TTAATAAAAN CAACCTTGCA TGATTAAA 298

5 SEQ ID NO:163
SEQUENCE LENGTH:309
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00177
10 SEQUENCE DESCRIPTION:
GATCTCCTTC ATCCCTCTCC AGAAGAGGAG AAGAGGAAAC ACAAGAAGAA ACGCCTGGTG 60
CAGAGCCCCA ATTCCTACTT CATGGATGTN AAATGCCAG GATGCTATAA AATCACCACG 120
GTCTTTAGCC ATGCACAAAC GGTAGTTTTG TGTGTTGGCT GCTCCACTGT CCTCTGCCAG 180
15 CCTACAGGAG GAAAAGCAAG GCTTACAGAA GGATGTTCTT TCAGGAGGGA AGCAGCACCT 240
AAAAGGCACT CTGAGGTCAA GGATGAGGTG GGGAAANCCAT CTCATTAAC CACCATTTTT 300
TGGGTATAA 309

20 SEQ ID NO:164
SEQUENCE LENGTH:295
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00178
25 SEQUENCE DESCRIPTION:
GATCTCGGTA AAAATCTACC ATTCCTTACA TATTTCTCTG ATGGAGATGA AGAGGAACTG 60
CCAGAAGATT TGTATGATGA AAACGTGTGT CAGCCCGGTG CGCCTTCTAT TACATTTGCC 120
TAACATCTTT GGACGTGGCA GAACCTTACA TATTCTGTGA GCTTCGATGA GCCAGAGTGA 180
TATCATAACC ACCAGAAATC ATACTCTCCT TTCTTAGTCA CAACAAAATC ACACATGTCA 240
30 TCTTTGTCAA GGGCATAAAT ATATCATTCA TACCCCATTA AAATTTGTT AGAAA 295

35 SEQ ID NO:165
SEQUENCE LENGTH:289
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00179
SEQUENCE DESCRIPTION:
GATCCCCACC CCATGTGTTT TAAAAAGGCA GTAGCCTTTG CAGGGACCTG TCTGTCCCAA 60
40 CTGTTTGAAC AGTGTGCTCC TCAGATTCTG TGTTCAAGAG NCCCCTGNTG CATTGAGACT 120
TGAAACCTTT GGATAGGGGA AAAAATTATA TATATATATA TNNNTTGTG CTGTTTGCAT 180
TTCTTAATTT GTGCTTGGA TGTGTTGATG TGCACAGCTA ATGATTCAAT GCGAGACAAG 240
ATTGGCGTCT GTGTTGTGGA GGTTCAAAT AAAGAGCACT CTTCATAAA 289

45 SEQ ID NO:166
SEQUENCE LENGTH:300
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
50 CLONE:HUMGS00180
SEQUENCE DESCRIPTION:

55

GATCTGTAAA ATGTGATTTT TTA CTTCAC TTATAACT TGTGATTGGG GAGGTTTGTG 60
 GAAATTCAAT TATGATGAAA AACCTATCTT TTTTGAATG TTGGCATACT TGGGGAATTT 120
 AGTGGCAAAT ACATTCCCA GCAGGCCTTT TGTGGTTGC ACTAACTGCA AGGTTGCTGG 180
 GAAGTAGAGT CCATTGGTT GATGAGCTTT GACTGCGGT TTGGAACCTT ACCTCTCCTC 240
 CTTAGCCCAA TATGCTGTCT TGGTCCTAT TCAAATAAAG TTATTCTCC TGGTCTCAA 300

SEQ ID NO:167

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00181

SEQUENCE DESCRIPTION:

GATCAAAAA CCATCTCCAC ATTTAAAAGA GATGTAAGGT GTATTCATAG GGATGGTGGC 60
 TCAACAAATC AAGCAAAGT GAATCAAGGG GAGGGGGAAG GGAATNAAAT GGAAAGGGAG 120
 GCTGATTCCC TTCCCTGAC TTACCACTAA TTTACTAGGC TACCTACTTT NATGAGTAAC 180
 CTCTCACAGC TACCCAGCAC ATGCCACAAT CCTATGCTCT TGCCTTCTTT NATCTGCACT 240
 GTGTGAAGGG ACTCTTTTAA ATAAATNAGC AAGTGTCTTA AGCTATGTCA AA 292

SEQ ID NO:168

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00182

SEQUENCE DESCRIPTION:

GATCTTGGCT GTATTAAATG GCATAGGCTG ACTTTTGAG ATGGAGGAAN TTCTTGATTA 60
 ATGTTGAAAA AAAACCCCTG ATTATACTCT GTTGACAAA CCGAGTGCAA TGAATGATGC 120
 TTTTNTGAAA ATGAAATATA ACAAGTGGGT GAATGTGGTT ATGGCCGAAA AGGATATGCA 180
 GTATGCTTAA TGGTAGCAAC TGAAGAAGA CATCCTGAGC AGTGCCAGCT TTCTTCTGTT 240
 GATGCCGTTT CCTGAACATA GGAAATAGA AACTTGCTTA TCAAACCTTA AA 292

SEQ ID NO:169

SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00183

SEQUENCE DESCRIPTION:

GATCCACATG AACGCACGCC TGAGATTTGG CCACTCACCT ATGTTTTGGG TGGATTGCCT 60
 AGGAAAGCAA GTCATATGGC CATTGATAGT TCTCATGTAA TIAGTTTTGC TCACCACTAG 120
 TACAGATGAC CCGTTTACAC GTGGCTTCCC TCGGAAGCCT CCTCAACAGT AGCTGGTGTG 180
 AAAGACTAAA TCAGTAGAGT TGGAAAAGCT TTATAACCGG TGTGTCATAT GCTTGCTATT 240
 TAAAGCTGTG TGTGGTTTT GTTTTCTGC CACATTCCT AGTTTTTTAA TAAATATTTT 300
 CCAAAANTGG AAAAAAANA NCCCNCCN CCN 333

SEQ ID NO:170

SEQUENCE LENGTH:401

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00184

SEQUENCE DESCRIPTION:

GATCTGGANG GGACACGTCA TGCCTTGGGC CTAGAATACC CTGATGNGAA AAGAGAAGAN 60
 AAAGGGAGGC CATATCTACA ACACAGCCTC TCGGCACTGC TGCTCCTTAT TTAACTTTG 120
 TTTGCAATTG TCCTGTATTT ATCACAGTTT CTGTTGAACA GCTTTTCAAG TATTTGGGGA 180
 GTTATCTTG CCATCCTCCC CTTCTGGTTC TCTGCACCCA CCTGTCCCAC TGCAGTTCCT 240
 TCCGTGCTCT GTGACTTTAA GAGAAGAAGG GGGGAGGGGT CCCGGATTTT ATGTTTGTGTT 300
 GNTNTTCTC CTTAGCAGTA GGACTTGATA TTTTCAATTT TGGAAGAACT AAAAGATGAA 360
 TAAACTGGGT TTTTTTGTGTT GTTTGNTTTT GNAAATTCAA A 401

SEQ ID NO:171

SEQUENCE LENGTH:305

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00185

SEQUENCE DESCRIPTION:

GATCGAGCTC GCCTATNAGC AAGTGGCAAA CCCCTCAAA TAAGCCCCTC CTGGGACTCC 60
 CTCAACCCCC TCCATTTTCT CCACAAAGGC CCTGGTGGTT TCCACATTGC TACCCAATGG 120
 ACACACTCCA AAATGGCCAG TGGGCAGGGA ATCCTGGAGC ACTTGTCCG GGATGGTGTG 180
 GTGGAAGAGG GGATGAGGGA AAGAAATGGG GGGCCTGGGT CAGATTTTGA TTGTGGGGTG 240
 GGATGAGTAG GACAACATAT TTCAGTAATA AAATACAGAA TAAAAATCAA GTGTTTTTAC 300
 GCAAA 305

SEQ ID NO:172

SEQUENCE LENGTH:289

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00186

SEQUENCE DESCRIPTION:

GATCTGAGGC AAGCTGGACA GGAGAGGTGG ATATTNTTG ATGGAAGAAT TCAAGTTTAT 60
 AATCAATTCC CACTTAGCAC CTACTGTGTG CTAGGAACTT GAATGTGTAT GTTTGACAAG 120
 TCCTGCTTGG CCTGATGGGT GGGAGANGGA ACCTGAGCCT GGCTGAGATG GCTAGGCGGA 180
 GGGCTTTGAA GTCCAAGCAG CTGAAGTGGC TGGGTGGGTT TCTACCTTTG AAAGTGAAG 240
 ACTNTTTTG GAGCTCTTAA TTACAATATC TGATATTTT ACAGTCTGN 289

SEQ ID NO:173

SEQUENCE LENGTH:286

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00187

SEQUENCE DESCRIPTION:

GATCCCTACC CTTNCCGTTG GTCTCTNTCG CTGACTCGAG GCACCTAACA TCCATTGACA 60
 CCCAACACAG GCCAGCGACT TCTGGGGCTC AGCCACAGAC ATGGTTTGTN ACTNTTGAGC 120

TTCTGTTCTT AGAGAATCCT AGAGGCTTGA TTGCCCCAGG CTGCTGTNTG TNCTGGAGGC 180
 AAAGAATCCC TACCTCCTAG GGGTGAAAGG AAATNAAAAT GGAAAGTTCT TGTAGCGCAA 240
 GGCCTGACAT GGGTAGCTGC TCAATAAATG CTAGTNTGTT ATTTCN 286

5

SEQ ID NO:174
 SEQUENCE LENGTH:290
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

10

CLONE:HUMGS00188

SEQUENCE DESCRIPTION:

15

GATCGGGTTC TAAAGGAAAG GGTGGAGAGA TTCAACCACT TAGCGTGAAA GTTGGAGATA 60
 AAGTCTTCTT CCCAGAATAT GGAGGCACCA AAGTAGTTCT AGATGACAAG NATTATTTCC 120
 TATTAGAGA TGGTGACATT CTTGGAAAGT ACGTAGACTG AAATAAGTCA CTATTGAAAT 180
 GGCATCAACA TGATGCTGCC CATTCCACTG AAGTTCTGAA ATCTTTCGTC ATGTAAATAA 240
 TTTCCATATT TCNCTTTNAT AATAAACTAA TGATAACTAA TGNCATCAAA 290

20

SEQ ID NO:175
 SEQUENCE LENGTH:284
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

25

CLONE:HUMGS00189

SEQUENCE DESCRIPTION:

30

GATCAAGGCG CGGACGTATC TACGACCACA TCAACGAGGG GAAGCTGTGG AAACACATCA 60
 NGCACAANTA TGACAACAAG TAGTTCCTTG GNGGCCCTAT CCAGGCCAGA AGGCCANNGC 120
 CACCCAGCAG CTGTTTGCCA GAGCTGGAGC TCAGTTGAAG ATGATGCTCA AGGTACTCTT 180
 CATGGCCACC ATTCGTGTTG GAAGAACGNT TTACTIONNA CAGCTCTTTA CCTTCTGTGT 240
 GTTTNAGNTG TTAGNAGATN TCAGGAATAA TGTGATTGCC TTGN 284

35

SEQ ID NO:176
 SEQUENCE LENGTH:282
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS00190

SEQUENCE DESCRIPTION:

40

GATCAGAACA TGAAATGCCC TCCTAAATGT CAGCTGTTGT CACACAGTAG CTCCAACACT 60
 TTGAGCATTT TTAAGGGAGT GGCCTCATT CACTAGAGAC AAATCTTTAA GAATAGTTCT 120
 AAAATTGGGC TTGTGATTTT CATTCTGAT GTCTCCAGAT TGGCACCCCT TTCTAGTTCA 180
 ATGCCTCAGC AGATTTTGCC AGGGGCATCC AAGGCAAACA ATCCCAATCT TTCTATATAA 240
 ANTGTATTCA AGCAAACATC AAATAANTTT CTGGGATATT TN 282

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SEQ ID NO:177
 SEQUENCE LENGTH:278
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

50

CLONE:HUMGS00191

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SEQUENCE DESCRIPTION:

GATCAGAGTT TGAAATGAAA TGTTCGTCAG GGTGTTGGAA AAATTTTGGT GAGTTCTGCA 60
 CATTTCCTCCCT GGTTCAGGCT GGGCATGGAC CAGCCTTCAG ATGGCAGAAG TGGAAGATGA 120
 GCCTACTTGT GAGCGATGTG ACTTTAAGGA AATGAAGACT GGGGAAGAAT AATTAGTGTT 180
 TATAAGACAT TTAAGAGGCC CTTTTTCATA TACTGACTCA CTGATGAATC AGCATTNGCA 240
 TTNTATGGAA NAATATAAAT CCAAAGAAAT AATTAAAA 278

SEQ ID NO:178

SEQUENCE LENGTH:281

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00192

SEQUENCE DESCRIPTION:

GATCAAAAATA ACCCTCGTAA AAATATATGT ANGGGGTACA CAAAGTAAGC CTCTTTATGA 60
 AACAATTGAG GATAATNATG TGAAAGGTTT TAATGATGAT GTTCTACTTC ANATAGTTCA 120
 CTTTCTACTG AATAGACCAA AAGAAGAAAA ATCACAGCTG TTGGAAAAC TAAAAAGCAT 180
 ATTTNATTGA GAACTGTGGG AATATTTAAA TTTTACTGAA GGACCAATAA TGATGAGATT 240
 TGTAAGTGT AACTATTAAA TACATTGATT TTTGAGACAA A 281

SEQ ID NO:179

SEQUENCE LENGTH:278

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00193

SEQUENCE DESCRIPTION:

GATCAGGCC AGGAAGGGCA CAGGGGCTGA GCACTACAGA AGTCACATGG GTTCTCAGGG 60
 TATGCCAGGG GCAGAAACAG TACCGGCTCT CTGTCACTCA CTTGAGAGT AGAGCAGACC 120
 CTGTTCTGCT CTGGGCTGTG AAGGGGTGGA GCAGGCAGTG GCCAGCTTTG CCCTTCCTGC 180
 TGTCTCTGTT TCTAGCTCCA TGGTTGGCCT GGTGGGGGTG GAGTTCCCTC CCAAACACCA 240
 GACCACACAG TCCTCCAAAA ATAAACATTT TATATAGN 278

SEQ ID NO:180

SEQUENCE LENGTH:278

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00194

SEQUENCE DESCRIPTION:

GATCTACATT AATATCAAGT CTTGACTCCC TACTTCCCGT CATTCTCTAC AGGACAGAAG 60
 CAGAGTGGGT GGTGGTTATG TTTGACAGAA GGCATTAGGT TGACAACTTG TCATGATTTT 120
 GACGGTAAGC CACCATGATT GTGTTCTCTG CCTCTGGTTG ACCTCNACAA AAACCATTGG 180
 AACTGTGACT TTNAAGGTG CTCTTGCTAA GCTTATATGT GCCTGTTAAT GAAAGTGCCT 240
 GAAAGACCTT CCTTAATAAA GAAGGTTCTA AGCTGAAA 278

SEQ ID NO:181

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00195

SEQUENCE DESCRIPTION:

GATCTCTCCC CCGTGAAGGA GTTGAGCACA TTAGCAACAA TGTACATTAA TTTTGGATT 60
 TCATTTTCAT GTTTTATTTT GTAAATATTA TCTGATGTTT GGAGCTTGAG TATACAGACT 120
 GTAAATATAG TTCTTGATTT TGTACTAATT CTGATTCTTT TGCTNNCNG CCTTAGATGT 180
 GCAATGCAGA CACTATCTAA CTGTGTGTGG TAACCTTGCG TCACGGAGCT GTTAGTGAAC 240
 GAGGTAAAAA TAATAAAGGT ACAGCCAGTG CATCAAA 277

SEQ ID NO:182

SEQUENCE LENGTH:282

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00196

SEQUENCE DESCRIPTION:

GATCAAAACN GATTACGGT GGGGGAGGAA TNTGAGCTGG AGACAATNAC AGGGGAGAAA 60
 GTCAAGACAG TGGTTCAGTT GGAAGGTGAC AATAAACTGG TGACAACTTT CAAAAACATC 120
 AAGTCTGTGA CCGAACTCAA CGGCGACATA ATCACCAATA CCATGACATT NGGTGACATT 180
 GTCTTCAAGA GAATCAGCAA GAGAATTTAA ACAAGTCTGC ATTTCAATATT ATTTTAGTGT 240
 GTAAAAATTA AATGTAATTA AAAGTGANCT TTNGTTTTTA AA 282

SEQ ID NO:183

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00197

SEQUENCE DESCRIPTION:

GATCCAGATG ACCGTGGTNG TTGGGGTATA TCTCCTCGAG GAGCTGGTTA CACCTTTGGG 60
 CAAGATATTT CTGAGACATT TAATCATGCC AATGGNCTCA CGTTGGTGTC TAGAGCTCAC 120
 CAGCTAGTGA TGGAGGCATA TAACTGGTGN CNNGGCCCGG AATGTAGTAA CGATTTTCAG 180
 TGCTCAAACT ATTGTTATCG TTGTGGTAAC CAAGCTGCAA TCATNGANCT TTTGCGATAC 240
 TCTAAAATAC TCTNTCTTGC AGTTTCACCN AGNNNNN 277

SEQ ID NO:184

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00198

SEQUENCE DESCRIPTION:

GATCTGAGAT TTCCGTGTTT GGCTGAACCT GGGAGACCAG CTGGGCCTCC AAGTAGGATA 60
 ACCCCTCACT GAGCACCACA TTCTCTAGCT TCTTGTGAG GCTGGAACCTG TTTCTTTAAA 120
 ATCCCTTAAT TTTCCCATCT CAAAATTATA TCTGTACCTG GGTATCCAG CTCCTTCTTG 180
 GGTGTGGGGA AATGAGTTTT CTTTGATAGT TTCTGCCTCA CTCATCCCTC CTGTACCCTG 240
 GCCAGAACAT CTCACTGATA CTCGAATTCT TTTGGCN 277

SEQ ID NO:185

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

5 TOPOLOGY:linear

CLONE:HUMGS00199

SEQUENCE DESCRIPTION:

10 GATCGGTTTT TGTTCCTGTC TTACCATATG ATTGTAAATT GTTTTATGTA TTAATCAGTT 60
AATGCTAATT AATTTTGTCT GATGTCATAT GTTAAAGAGC TATAAATTCC AACAAACCAAC 120
TGGTGTGTAA AAATAATTA AAATTCCTT TACTGAAAGG TATTTCCCAT TTTGTGGGG 180
AAAAGAGCCA AATTATTAC TTTGTGTTGG GGTTTTAAAT ATATTAAGAA ATGTCTAAGT 240
TATTGTTTGC AACATAAAT ATGATTTTAA ATTCTCN 277

15 SEQ ID NO:186

SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

20 CLONE:HUMGS00200

SEQUENCE DESCRIPTION:

25 GATCCTGACA CTGACATGAA GGCAAGCCTT GATTCGTAT GAACGTTGCT GAAGTGGTAA 60
TTGAGGAAAA CAGTCCCA GATTGTTAAG AGTTCCTGA AGATATTGAC ACAATTNNA 120
AAAATCAGTA AAGGAATGTA TATAATATTG CNCTCGTGT TTACAGTAAG ATTTGTTGCT 180
CTCAGACTGT GTAAACAAA ATTNATNGNT GTTTCTGCA TTTAAAAAA TCTTATTGTA 240
CCANCTGGTA ANCTATTAAN TGCCTATAAN NCTAAA 276

30 SEQ ID NO:187

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00201

SEQUENCE DESCRIPTION:

35 GATCAAGGAN GAAAGANTGA CTTCAAATAT GCCTTGTTAG TGTAATGTG ACTTNTNGAA 60
CTGTATGAGT ATTTAAGAT TATTNGAGTA AAGTAAGTTT TAAAAAGCAG TCCCTAATCA 120
TCAAAAGTAA AAAACTCTTG ATGTAGTCAT ATAACCACAC TAAGAACTCT TCCAGGTGAC 180
TTCAAAACAT AGGACAGTAC ATCTCTAGTA GANTNTGCCC TGAGAATGAA AAGAATGTAA 240
CAGTGTTAGT ATTTGAATA AACATGTTAT TACTN 275

40 SEQ ID NO:188

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS00202

SEQUENCE DESCRIPTION:

50 GATCACTTTT TTTAGAGTGA AGAAAGAACA ANCTTGTTTT TTGTGTTTT TAAAGGAATA 60
TAAATAATG AAGGATGTAT AATTGATGCC AAATAAGCTT GTNCTTTAGT CACACCGACG 120

55

TCTTATTTTT CCCTTAGGC CAGTTCTGTT TTTAAGGTGT ACATGGNCAA TGTTACAGTG 180
 TAAGAACTC CATATCCATA TGTNCCCATT CGCATTTTGT ATTGGTTCAT GTATACCATT 240
 TTTNCAAAAN ANANGGAANA ANNGGNAGTN CTN 273

SEQ ID NO:189
 SEQUENCE LENGTH:271
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00203
 SEQUENCE DESCRIPTION:

GATCTGAAAA GCTCACTTTA AACTCATACT ACATTCGTNA CGAGTATTN ACGTTAACAT 60
 AATTGAAAAG TACAAGGTCC AAGCTGGCTT TCAAATNATG TCTAAACAGA AATGGGACAA 120
 ATAGACTTGA AAATAGAAGG GATTTATTCC ACCCCTGCAA GGGTAAGAGT CAGGTGAGAG 180
 TCCCTTGGTG AGTCATTGT ACATCAGTGT CATTCTTCT TAACCTCTGA AGAAAGATGG 240
 GCATCAGAAA TAAAGACAAA GCACTATCAA A 271

SEQ ID NO:190
 SEQUENCE LENGTH:270
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00204

SEQUENCE DESCRIPTION:
 GATCTGCCAC GAGGGCAGCA GCCAAGAGGA CTTGCTCTCT CCATGTGAAT GTACAGGGAC 60
 CTTGGGGACA ATTCATCGGA GCTGCCTGGA GCACTGGCTG TCATCCTCAA ACACCAGCTA 120
 CTGTGAATC TGCCACTTCA GGTTCGAGT CGAGCGAAAA CCCAGGCCGT TAGTGGAGTG 180
 CCTGGGAAAC CTTGGCCCCC AGATTGGGAG GGGNCTTTT TTTGGNGANA TGGTNNNTT 240
 TGGGTTNTAA ATCNCNNGG NNCCATNTNN 270

SEQ ID NO:191
 SEQUENCE LENGTH:166
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00205

SEQUENCE DESCRIPTION:
 GATCTCTGAG CTGCCAGCA TAGTCCAAGA CCTAGCCAAT GGCAACATCA CATGGGCTGA 60
 TGTGGAGGCC AGGTATCCTC TGTTGAAGG GCAAGAGACT GGTAAAAAG AGACAATCGA 120
 GGAATGAGGA CAATTTTGAC AACTTTTGAC CACTTGCCT AATAAA 166

SEQ ID NO:192
 SEQUENCE LENGTH:276
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00206

SEQUENCE DESCRIPTION:
 GATCTACATG AGAAGTATAG TGGCTCTACC CCCTGAAAGA GGGTGGATGC AGCTGCTTGT 60

5 GTTTCTTGGG GTGACTGTCA TTGGTAATAC GGACACAGTG ACCCATCCTC CATCCTATTT 120
 ATAGTGGAAG GGCCTTCAAT TGTATCAGTA CTTTNTTTTA AGCTCTGGCA CATTGACCTC 180
 TATGTGTTAC CAGTCATTAA TGAGCTGCTG CAGAGGTGAC TATTTGTTT ACTTTCTTGG 240
 ATGTTAACAT TACTACTCTC ACTACTCAAT CTCAAA 276

10 SEQ ID NO:193
 SEQUENCE LENGTH:273
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00207
 SEQUENCE DESCRIPTION:
 15 GATCTGACAT TTGACATGAA CACAAAGTTG CTAGATGCTC TTGTTGACTT CCAGCAGATG 60
 GGATGGGGGA AACACAGCAG TTCTTGGTAA AGTCCTTTGT AATAATAGTT TGATTTTTTT 120
 ATTTTCGAGAG AATCTTTCAT TTTCCTATGT ATGCTTTTNN CCTTTTTTGC CCAGTTTCCT 180
 TATCACTTGC TGTAGATGGC TTATNTNGCA TTCATGCAGA CTATGTTGCA AGTCTGTTTC 240
 ATCTAGTAAA CTGAAAATNA TTGCTTAATC AAA 273

20 SEQ ID NO:194
 SEQUENCE LENGTH:267
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00209
 SEQUENCE DESCRIPTION:
 GATCCAGAG AGGGAAGAGA ACCAGGGGCC CTTTCTCTT TNAGAATTN CTTTAAATCA 60
 GCCCACCTTT TGACTCCCCG CCCGCCCCAA TCCATTATNT TTTCTGCCT TCCGGGTCCC 120
 30 ATCCTTAGAG CTCGAGTCGT TCCTTCCCCT CCTGGATTCC GGGTAGCAGA GGCAGCGCCG 180
 CAGGAGGCGG GTGCCCGTTT GTCCCAGGNC TGGGCGTGGT GGAGNNAGGG GTGCTGGAAC 240
 AATAAACGGC ACNNNNCAAA TGTCAAA 267

35 SEQ ID NO:195
 SEQUENCE LENGTH:384
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00210
 SEQUENCE DESCRIPTION:
 GATCCAAAAC ACTACTCAGC TCTCTTGCAC TGAGGAAATT TTTCCCCTA CATTGACTCC 60
 TGGCCTACAT CAGCCAAACT TAACCTTGGT GGGGTTTGGG TTTGATAGCC AATTAGTTCT 120
 GTGCTGGTTG CAAAGAATTG ATATTAGAT GGTTTTAAAT ACTCAGCAGA TTGTCTTCCT 180
 45 TTATATTGTG TCTTTTTTAT GTNGCATGTN GCITTTGTTA TCAGCCTGAT TTTTGTCTCA 240
 GTATATGATA GTNCTGCTGA TGTTTTGTTT ATTGGGCAGA CATATCTTCA TTAAGAGTTT 300
 TTGGAAAAC CATCAAATC GATGAATACA TTTTCTTCAT AACCATTG GAATTATTCC 360
 TAATAAAATG ATAAAATACG TAAA 384

50 SEQ ID NO:196
 SEQUENCE LENGTH:277

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00211

SEQUENCE DESCRIPTION:

GATCTAAAAA AATTCAGAAG AAATATGATG AAAGGAAAAA GAATGCCAAA ATCAGCAGTC 60
 TCCTGGAGGA GCAGTTCCAG CAGGGCAAGC TTCTTGCGTG CATCGCTTCA AGGCCGGGAC 120
 AGTGTGGCCG AGCAGATGGC TATGTGCTAG AGGGCAAAGA GTTGGAGTTC TATCTTAGGA 180
 AAATCAAGGC CCGCAAAGGC AAATAAATCC TTGTTTTGTC TTCACCCATG TAATAAAGGT 240
 GTTTATTGTT TTGTTCCAC ATTTATGTTG CCTGAAA 277

SEQ ID NO:197

SEQUENCE LENGTH:271

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00212

SEQUENCE DESCRIPTION:

GATCGGCGGC GCGCAGNAAC CGCTCCTACA GCAAGCTGCT GTGCGGCCTG CTGGCCGAGG 60
 CGCCTGCGCA TCAGCCCGGA CAGGGTCTAC ATCAACTATT ACGACATGAA CGCGGCCAAT 120
 GTGGGCTGGA ACAACTCCAC CTTCGCCTAA GAGCCGCAGG ACCCAGCTG TCTGCGCTGG 180
 CTCCACCCGG GAACCCGCCG CACGCTGTGT TCTAGGCCCG NCCACCCCAA CCTTCTGGTG 240
 GGGAGAAATA AACGGTTTAG AGACTAGGAA A 271

SEQ ID NO:198

SEQUENCE LENGTH:264

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00213

SEQUENCE DESCRIPTION:

GATCCTGTAG TGTTCTGGA GAAGCTAGAG CCTGATTGTA GGCTACTACT CATCAATTAA 60
 CTTCTACAGT GGAGACTACT TCTGGGACTG GAATATAAAA AAGAATCAA GGTCTGATT 120
 TTNAGTTGCA ATAAAGGGAA AGACCATGCT CATAGCAGTG CCAACATCTG AAGTGTGGAG 180
 CCTTACCCAT TTCATCACCT ACAACGGAAG TAGTTAACTG GAAGAGATTA CCAAGAGAAT 240
 AAAAAGAGAC TCATTCACTG GAAA 264

SEQ ID NO:199

SEQUENCE LENGTH:257

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00215

SEQUENCE DESCRIPTION:

GATCTGCCTT AAAGAAAAGA AAATTTTAGA AAGAAATATT GTTGCTCAGT GTTGTTAATA 60
 TAGCTCAAGA ATTGAGTTTA TATTTGCAGT ATGCTATAAA TGATACCCCT CTACCACACC 120
 CACACACACA GTTTTGTCT AATGAAAATG TTGCTGTGAT TATTTATAAT TGGTAGTATT 180
 TCTTCAGAA GAAGCTAAAA TAAGACTGGC ACTTACCCTG AAGTGCATTA ATAAAACCAC 240
 ACTTTAAAAAT TAANAAA 257

SEQ ID NO:200

SEQUENCE LENGTH:374

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00216

SEQUENCE DESCRIPTION:

GATCAACCTG AGCNTGGAGA ATGCCTGGGG CATTAAACGC TCGTCATTG ACATCTGCAT 60
 GAAGCTGGAG GAGGGCAAAT ACCTCATCCT CAAGGACCCC AACAAGCAGG TCATCCGTNT 120
 CTACAGCCTC CCTGATGGCA CCTTCAGCTC TGATGAAGAT GAGGAGGAAG AGGAGGAGGA 180
 AGAAGNGGAA GAAGATGNGG ANGAACTTA AACCAGTGAT GTGGAGCTGG AGTTTNCCT 240
 TCCACCGAGA CTACGNGGGC CTTTATGCT TAGTGGAATG TGTGTCTAAC TTTGCTCTCT 300
 TGACATTTTA GCAGTTGAAA TTAAATTATA TANTCTGTTT TNNGTCTTTT NAAATAAANA 360
 AAANNANATT NTGN 374

SEQ ID NO:201

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00217

SEQUENCE DESCRIPTION:

GATCTGAACT ATTTGCTTTC TCTTCAAGAT AAGTTGTATT TTACCATGGA AAAATACAGT 60
 ATCTAACATT ACCATTACAG TTAATGAAG TTTCTCATA ACATTTATCT TTAGTTTAT 120
 GAAGTCATCG TGACCAATGT TACAGTAATT TCTGTTAGCT GATTGTGGTA AACAATGTTT 180
 AATGNGAAAA GAAATTAAAA CTTTCTTCAT CTGTTGTAGA ATATTCTCT TCTTTAAAA 240
 GGCTTCTATT CATAAA 256

SEQ ID NO:202

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00218

SEQUENCE DESCRIPTION:

GATCCCCACT GGAGCAGCCT CTGCAAAAGG GAGCCCATGT AGTGGCCAGG GGCTGTCCAA 60
 ACTCCAGCTT CTTCCCTGG GAAAAAACC AAAGAACCA AAACAAACCA CCCCAAGGAT 120
 AATAATAGCT AACTGCTAG CTTCTCAAGT TCTTGTGAAA AACAATTAC ATAATGACAC 180
 AGTAGATGTG GAACACCTAG CCAGTGCCTG GGCAGGTCCC TATTATCATA AATGAACATA 240
 AAGTGCTCTA AAAACN 256

SEQ ID NO:203

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00219

SEQUENCE DESCRIPTION:

GATCCAAATC AGGAAAAGAC GGCGCCACTA CAATGGAGAA GCATATNAGG ATGATGAACA 60
 TCATCCCAGA GGTGGTGTTC AGTGTGAGAC CTCTTAATGG GCCAGTGAAT AACACTCACT 120
 GCTGGCATT T AATGTGCAGT AGTGAATGAG TGAAGGACTG TAATCATAAT ATGCTCACTA 180
 CTTGCTCTTG TTTTGT TTTT AATAAACTAT AGTAGTGTTA TAANNNGTTA AATGAAGAAT 240
 AAACGCAAAT ATAANAGCTC TGA AAA 265

SEQ ID NO:204

SEQUENCE LENGTH:253

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00220

SEQUENCE DESCRIPTION:

GATCTAAAGA GACACTTAGA GACTCTTGGG GACCTCAGAT TTCCACCNCT CCACAGCATT 60
 CTGCCTACAC AGTTCCCTC ATTTTNCCTA GTTACTCGGA AGAGCGCTGG ACTTGAAATC 120
 AAAATAATTG CGTTATGTCT TTGGTTATGT CGCTTCATCA TAGCACTTTC TAAAACTATT 180
 TGACAAACAT GTATTGCATA CCTACNGCAT TCCAGTTCTN GTACANGTAA TTAAATGCTC 240
 GACTAACGNN AAA 253

SEQ ID NO:205

SEQUENCE LENGTH:253

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00221

SEQUENCE DESCRIPTION:

GATCTGGAAT TGGACATTTCTCTGTCAGAG CACAGAGGAG GCTCATATCA CCTCTTCCCT 60
 CTCCTACTTG GCCCAGCTGC TTGGAGGACC GACCCCATGG CTGAGAATAT NACGGCAAAGA 120
 GGAACAGAGN TTGCTCCAAG TGGGAAAGGG TCCCAAGCAG TCCAGAGAAG ATGTCTGTGT 180
 GGCTTTCCCT CCCTGCCTCC CCCAGCTCCC AACTGGCCT TTGTAAATAA ATGGCGTGGT 240
 CTTTGTGTG AAA 253

SEQ ID NO:206

SEQUENCE LENGTH:253

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00222

SEQUENCE DESCRIPTION:

GATCTGCCGT CTGTCACCTC TCTCCAAGTT GAGACAGGGG CCTGGATTTC AGCCCTTCCT 60
 GCCGAGAAAT CTTNTAAATT TCAACCTACC TTTAAAAATA AAGTCTCCCT ACTTAAAAATC 120
 CAGTAGATAT CATGGCACTA ATGCTAACAC CCCTTTCCCC AAATTAATAA AACAAAAATA 180
 AAAAAAGAA AAAANTGCAG GCATGCAAGC TTGGCGTANT CATGGNNTNA GCTGTTTCCC 240
 NGTCACGGCG TGN 253

SEQ ID NO:207

SEQUENCE LENGTH:251

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00223

SEQUENCE DESCRIPTION:

GATCGAGACA CGTGATGGGA AGCTGGTGTG TGAGTCCATN ACGTCCTNCC AAGTGAACAG 60
 CTGCGGCAGC CCTCCCAGCC TACCCCTCCT GCGCTGACCC AGAGCCTGGG AAGGAGGCCG 120
 CTATGAGGGT AGCACTGGGA ACAGGAGACC CACCTNAGNC TCAGCCTNGC CTCAGTNTAC 180
 TGGGGAGTTT ACTACCTGGG GCCCANTTGA CATGCTCCAG CTACANACAN TTANTTGCTT 240
 TTTTNTTGGN N 251

SEQ ID NO:208

SEQUENCE LENGTH:243

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00224

SEQUENCE DESCRIPTION:

GATCGATTCT TGTATATTNA TTTTATCTCT TTCTGTATCT ATAGGTAAAT CTCAAGGGTA 60
 AAATGTTAGG TGTGACATT GAGAACCCTG AAACCCCATC CCTGCTCAG AGGAACAGTG 120
 TGAAAAA TCTCTTGAGA GATTTAGAAT ATCTTTTCTT TTGCTCATCT TAGACCACAG 180
 ACTGACTTTG AAATTATGTT AAGTGAAATA TCAATGAAAA TAAAGTTTAC TATAAATAAT 240
 AAA 243

SEQ ID NO:209

SEQUENCE LENGTH:249

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00225

SEQUENCE DESCRIPTION:

GATCACANTT AATGATTCAG TATAATGTTT GAGGCCAGAC AAGATATATA TTGTGCCTCT 60
 TACAGCCTTT GGNNCNNTTG TTTCCATTTT TTAATATCT TCTATATCCA TATAGTATTC 120
 AAATNATTAA TGCTCATGTA CCAAGGTTTT GCTATAAAG TTTTGNCTGT ATGAATAATG 180
 TGGCTTTAGT AAATAATCAT TTTTCAACTG TAAACTTATT CTGAAATAAA GTAAAATTCT 240
 AATTGTTTN 249

SEQ ID NO:210

SEQUENCE LENGTH:248

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00226

SEQUENCE DESCRIPTION:

GATCATAGAA ATATATGTAA AGTATTCAAT TTTCAATCAT TTTCAAATNA CTGTTATAAA 60
 TTGTTTTTGC TGAGTTGTAA TACTTTTNG ATACAATGTA TTCCTTGAC TGAAAGAATG 120
 AAAAAGGACT TTTTCAGCAT TTGAGGTAAG TNCTTTAAGC TTTCATTAAA ANCATTTTTT 180
 ACAAATATTT TGTACATGCA CTTGCAGTAT TGAGGTAAAT CATTTTAATA AATNCGGAAA 240
 TTAACAACN 248

SEQ ID NO:211

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00227

SEQUENCE DESCRIPTION:

GATCTCAGCN TTGCAACAC ANTTNCTACA TAGATAGTAC TAGGTATNNT TTAGATATGT 60
 AAAGAAAGAA ATCACACCAT TAATAATGGT AAGATTGGTT TATGTGATTT TAGTGGTATT 120
 TTTGGCACCC TTATATATGT TTTCCAAACT TTCAGCAGTG ATATTATTTC CATAACTTAA 180
 AAAGTGAGTT TGAAGAAAGAA AATCTCCAGC AAGCATCTCA TTAAATATAA GGTTTGTCTAT 240
 CTTTAAA 247

SEQ ID NO:212

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00228

SEQUENCE DESCRIPTION:

GATCAAAACA AACAATCCAG ATGTATAAGT ACTAGGCAGA AGCCAATTTT AAAATTTTCCT 60
 TGAATAATCC ATGAAAGGAA TAATTCAAAT ACAGATAAAC AGAGTTGGCA GTATATTATA 120
 GTGATAATTT TGTATTTTCA CAAAAAAAAA NGTTAAACTC TTCTTTTCTT TTTATTATAA 180
 TGNCCAGCTT TNGGTATTTT ATTGTTACCA NGTTCTATTT TTNGANTAAA ATTGTTCTCC 240
 TTCTAAANGT TTAAAA 256

SEQ ID NO:213

SEQUENCE LENGTH:244

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00230

SEQUENCE DESCRIPTION:

GATCGGCAAG CCCACACTG TCCCTTGCAA GCCAAGGCCA CCTTTNATGC CATTTCTAAG 60
 ACCTACAGCT ACCTGACCCC CGACCTCTGG AAGGAGACTG TATTCACCAA GTNTCCCTAT 120
 CAGGAGTTCA CTGACCACCT NGTCAAGACC CACACCAGAG TCTCCGTGCA GCGGACTCAG 180
 GCTCCAGCTG TGGCTACAAC ATAGGGTTTT TATACAAGAA AAATAAAGTG AATTAAGCGT 240
 GAAA 244

SEQ ID NO:214

SEQUENCE LENGTH:243

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00231

SEQUENCE DESCRIPTION:

GATCAGATTG GGTCTGCTC CTCTCAACCT TGAAGTCCCC ACGTATGAGT TCACCAGTGA 60
 CGATATGGTG ATTGTTGGTT AAGAGACTTG GACTCAAGTC ATAGGCTTCT TTCAGTCTTT 120
 ATGTCACCTC AGGAGACTTA TTTGAGAGGA AGCCTTCTGT ACTTGAAGTT GATTTGAAAT 180

EP 0 679 716 A1

ATGTAAGANT TGATGATGTA TTGGCAAACA TTAATGTGAA GTAAATNGAA TTNAATGTNG 240
AAA 243

5 SEQ ID NO:215
SEQUENCE LENGTH:243
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
10 CLONE:HUMGS00232
SEQUENCE DESCRIPTION:
GATCGCCAGT GGAAGAAGAT TAGTGCAATC ATTGAGAAGA GGAAGAAGAT GGAAGCTGAT 60
GGGGTTGAAG TCAAAAGACC AAAATACTAA TCACTAGTTA CAACCAGAGA TGCTCCACAA 120
GGATATGCTC CCCACGGTTT TCTTTCTACA ATTCCAAAG GTTGCAAGAT GTTTTTTTGT 180
15 GGATGAATAT AAAATTTTAT TGTGTAATTA CTTGGTTCCA TTAATTTGG TTAAGTTGCT 240
AAA 243

20 SEQ ID NO:216
SEQUENCE LENGTH:243
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00233
SEQUENCE DESCRIPTION:
25 GATCGTAGAT GTTAACCAAA TCTACAAAAT CCACTACTCC CCCGTTATCA ACGGGATACG 60
TTCCAAGACC CCCAGTGGAT GCCTGAAACT GGCTAATGCT GAACCCCTACA TATACTATGT 120
TTTNTCTGTA CATATATATG ATAAAGTTTA AATNATAAAT NAGGTACAGT AACAACAATA 180
ACAGTAAAAC AACAGTTATA ACAATATACT GTAATAAAAG TCATGTGAAT GTGGTGTTTC 240
30 TCN 243

35 SEQ ID NO:217
SEQUENCE LENGTH:242
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00234
SEQUENCE DESCRIPTION:
GATCTTCTCC AGATTGGCAG AAAGTTGATA TAGGTGGACT TTTTACAGG TCAGTTGAGG 60
40 CAAAAAATA TGGGTTTTT CAGGTGAACC TCCCCATTT AAATACTCAG AAGATAAGGT 120
GTGAATGTAT GTATTATTAG AGTCCTAAAG TATTTTATAA GTACTGGTTT CACCACGCTT 180
TGTGGGAGAG AAATCATTCA AATCATTTTT TTTGTCCGTA CAATAAAGTT TACTAAAAAC 240
CN 242

45 SEQ ID NO:218
SEQUENCE LENGTH:238
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00235
50 SEQUENCE DESCRIPTION:

55

GATCTTCGTG ATACTGTACA TAGCTGTTTG AAATGCCAGA ATGACTTCTG ACATNCCAAG 60
 TTTTTCACAA AATATATTN ATCTGTGATT AGCCATTGTA CTAATAATAC TGGCTAACAG 120
 ATGTTGAAAA AAATTGTCTG TTTTCTCATT AATTTGGTC TAAACATGT TTGCACTTGT 180
 NTTTGACTTG TGTTTTATTA ACATTGATTG GCATATTAAG AGTCACTCNG AGCTTAAA 238

SEQ ID NO:219

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00236

SEQUENCE DESCRIPTION:

GATCCAAANN ATGACTTCAG AAAAACTTG AAAGTAACAG CAGTGCCTAC ACTACTTAAG 60
 TATGGAACAC CTCAAAACT GGTAGAATCT GAGTGTCTTC AGGCCAACCT GGTGGAAATN 120
 TTGTTCTCTG AAGATTAAAG TNGGTAGGAT GGCAATCATG TCTTGATGTC CTGATTGTT 180
 CTAGTATCAA TAACTGTAT ACTTGCTTTG AATTCATGTT AGCAATAAAT GATGTAAAA 239

SEQ ID NO:220

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00237

SEQUENCE DESCRIPTION:

GATCAGAGGT GAAGGGACAG AGAGAGGAGA GGAGGAAGAT TGAGCTGGGG GCAACAGCCA 60
 AGCTCACCTG GGCAGGTCTC TGCCACCTCC TTGCTCTGTG AGCTGTCAGT CTAGGTATT 120
 CTCTTTTTTT GTGGCTATTT TTAATTGCTT TGGATTTGTT AAATGTTTTT TGTCTTCTGT 180
 TAAGTGTGTT TTCTCTGGAG ATAGAATGTA AACCATATTA AAAGGAAAAA GTTTCAGACA 240
 AGCAATTAAA 250

SEQ ID NO:221

SEQUENCE LENGTH:237

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00238

SEQUENCE DESCRIPTION:

GATCAGCTTT GTCCTGAAA TTGCATCCGA AGAAGAAAGA AAGGGGATGG TGGCTGCGTG 60
 GTCCCAGAGG CTGCAGACCA TCTGGAAGGA AGAGCCCATC CCCTGCACAG CCCACTGGCA 120
 CTTGCGGCAA TAACTCTGTG GCACGTGGGC ATCACGTAAG CAGCACACTA CGAGGCCAG 180
 GCGCAGGCAA AGAGAAGATG GTGCTGTCAT GAAATAAAAT TACAACATAG CTACAAA 237

SEQ ID NO:222

SEQUENCE LENGTH:243

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00239

SEQUENCE DESCRIPTION:

5 GATCAGTGTA GAACTGGTCA TAGAGGAAGA GCTAGAAATC CAGTAGCATG ATTTTAAAT 60
AACCTGTCCT TGTTTTGTAT GTTAAACAGT AAATGCCAGT AGTGACCAAG AACACAGTGA 120
TTATATACAC TATACTGGAG GGATTTTCATT TTTAATTCAT CTTTATGANG ATTTAGAACT 180
CATTCCCTTGT GTTTAAAGGG AATGTTTAAAT TGAGAAATAA ACATTTGTGT ACAAATGCT 240
AAA 243

10 SEQ ID NO:223
SEQUENCE LENGTH:232
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00240
SEQUENCE DESCRIPTION:
15 GATCTAATAA CAGGTTGACA TAAGAAATAT TTGTCTCAA AATCAATGTA TTTAATAGTT 60
GACAGTTACA AATCTCATCA TTGAAAGATT TAATTTTAGT TACCTTTTGT TGATTANNN 120
NNNATTGCAT TTGTATATTG CTAACGTATA AGACAAATTG AGTTATTGAG CTATTAANTG 180
CACATTTTAA TATAANTGCA GAAATCCCAA ATAAATGCT AACATACTGA AA 232

20 SEQ ID NO:224
SEQUENCE LENGTH:237
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
25 CLONE:HUMGS00241
SEQUENCE DESCRIPTION:
GATCACCGTG ACATCCGAGG TGCCTTTCTC CAAAAGGTAT TTGAAATATC TCACCAAAAA 60
ATATTTGAAG AAGAATAATC TACGTGACTG GTTGCGCGTA GTTGCTAACA GCAAAGAGAG 120
30 TTACGAATTA CGTTACTTCC AGATTAAACCA GGACGAAGAA GAGGAGGAAG ACGAGGATTA 180
AATTTCAATT ATCTGAAAAA TTTGTATGA GTTCTTGAAT AAAACTTGGG AACCAAA 237

35 SEQ ID NO:225
SEQUENCE LENGTH:236
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00242
SEQUENCE DESCRIPTION:
40 GATCTTCACT TAANCTAAGT CTGTGAATTA CTTTATATT ATTTTGAAAN ACTCCTTGCA 60
GTATATTGGC ATGATACAGT AAAAGCANTT TCCACAGATT GTTATCACCT TCTTTAAAAG 120
AAGTCAAAAT TAAAAAATA CAATAGCACG TTGTTGGTGT CATATTCAAT AACATTTCCA 180
ATGCTACATA TAATTTTATA GACATAATAA AGAAGGTATT GAAAAAATA AATAAA 236

45 SEQ ID NO:226
SEQUENCE LENGTH:227
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
50 CLONE:HUMGS00243
SEQUENCE DESCRIPTION:

55

GATCGCCACC TACCGCCGCC TGCTGGAAGA TGGCGAGGAC TTTAATCTTG GTGATGCCTT 60
 GGACAGCAGC AACTCCATGC AAACCATCCA AAAGACCACC ACCCGCCGGA TAGTGGATGG 120
 CAAAGTGGTG TCTGAGACCA ATGACACCAA AGTTCTGAGG CATTAAAGCCA GCAGAAGCAG 180
 GGTACCCTTT GGGGAGCAGG AGGCCAATAA AAAGTTCAGA GTTCAAA 227

SEQ ID NO:227

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00244

SEQUENCE DESCRIPTION:

GATCAGCAAG CAGGAGTATG ACGAGTCCGG CCCCTCCATC GTCCACCGCA AATNCTTCTA 60
 GCGGACTAT GACTTAGTTG CGTTACACC TTTCTTGACA AAACCTAACT TGCAGAGAAA 120
 ACAAGATGAG ATTGGCATGG CTTTATTTGT TTTTTTTGTT TTGTTTGGT TTTTTTTTTT 180
 TTTTGGGT NNCCCCNGGT TTTAA 205

SEQ ID NO:228

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00245

SEQUENCE DESCRIPTION:

GATCTGCCCA AAGAGGTGTT GGCTGAGCTT NAGGCCCTGG AGAGACGTGT GCACAAAATG 60
 TNACCTGAGG CCCTAGTCTA GCAAGAGGAC ATAGACCCT CATCTGGGAA TAGGGAAGGC 120
 ACCTTGACAG AAATATGAGC AATTGATAT TAACTAACAT CTTCAATGTG CCATAGACCT 180
 TCCCACAAAG ACTGTCCAAT AATAAGAGAT GCTTATCTAT TTTAAA 226

SEQ ID NO:229

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00246

SEQUENCE DESCRIPTION:

GATCAGCCCC AGATTGACG TGCAACTCAA AGACCTGGAA AAATGGCAGA ATAATCTGCT 60
 TCCATCCCGC CAGTTTGGTT TCATTGTACT GACAACCTCA GCTGGCATCA TGGACCATGA 120
 AGAAGCAAGA CGAAAACACA CAGGAGGGAA AATCCTGGGA TTCTTTTCT AGGGATGTAA 180
 TACATATATT TNCAAATAA ATGCCTCATG GACTCTGGTG CTTCCAAA 228

SEQ ID NO:230

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00247

SEQUENCE DESCRIPTION:

GATCTGCGAC CATTCTGTA CAACACAAGC TGGCCTTGGC AGTTTCGGTG CATAGAAAAT 60

CAGGTGCTAC AGCTCGAGAG GGCAGAGCCA CAGTCCCTGG ACGGCGTGGA CTGAGGCCGG 120
 TTCCTTCCTG GAGGCCTCCT GTCCTCGGGG ACCCCAGCAC CTCATCATCA GCATTGCTGG 180
 AGCCAAGGGT AGGAGCCCTA CACTAGGAGC CCAGGATGGG ACGGNGNATN AGCCGAGAGG 240
 NAGGGAACCT TTNAGTNAAG TTCTCAAAA AGAGGNTTAG AATAAANCCT TNGGCTTAAA 300
 AAGAGAAA 308

SEQ ID NO:231

SEQUENCE LENGTH:230

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00248

SEQUENCE DESCRIPTION:

GATCCAAAGA CAGACCACAG ACTGGGAAAA GTTGAAGAT GAACACTTGA GGACTTCAGC 60
 TTCTCACCTA CTTAGTACAG TTGGGAACCA TACACTTCTG GCATGTTTGG AAATCAAAAT 120
 GTCACATTCT CGGGGGAGGA AGCCCAGAAA ATTGGGTATG TTCTAGAGAT TTACCACCAT 180
 TGCTTATTGC TTTTNCCTTT TAATAAAGTT TAGGAAAGTA GAATTTTAAA 230

SEQ ID NO:232

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00249

SEQUENCE DESCRIPTION:

GATCTAAAGA TTTCTCTATC CAATGAATCT AACAAAGTCA ATGGAAATTG AACTCTAGAA 60
 TTGTCCTAG AAAACATAGC TTCTTACTGA ACTTGAACAT TTTTACAACA TTCACTGGTT 120
 TTTGTTTTGT TAGCTAATAA TCTATAATAG TTGAGTATCT CTGGGAATGG GGAGGGAAAT 180
 TATATGTAAT AGAGCTTAAA AATAAAGTGT CAATTTCCAA GGNCTAAA 228

SEQ ID NO:233

SEQUENCE LENGTH:221

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00250

SEQUENCE DESCRIPTION:

GATCAATAAG CATGTCAGAC TGATTAATGT CTACTGTGAA AATTTGGTAG TAAATTTNCA 60
 TTTGATATTA GATATAAATA TCTGAATATA AATAATTNA ATATACTAGT CATGATGTGT 120
 GTTGTATTN AAAAATTATC TGCAACCTTA ATTCAGCTGA AGTNCCTTAT ATTTCAAAAG 180
 AATGAATAAC ATTGATAATA AAATCGCTAC TTTAAGGGAA A 221

SEQ ID NO:234

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00251

SEQUENCE DESCRIPTION:

5 GATCTCTATG AATGTCAGAG CCCTAACTTT CAGGCTTTGC ATTTTGTATA TGGGAAGAAA 60
 TATGACAATC CTAGGTAATT AAACCATAGA CCCAAAGCCC TTACGTTTGA TGCAATTTAT 120
 TTTTAAATA GGCCTTGTTT TTCAGCTTCA TCTGCAGTTC TATGTGAAGA TTGATAAATC 180
 AGTTTTTACT TGTTTTATTA ATAAACGTA ATNNGGAAA 219

SEQ ID NO:235

SEQUENCE LENGTH:287

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00252

SEQUENCE DESCRIPTION:

15 GATCTCCGTT CCGCTCCCAG CGGCTCCAGT GTAAATCCC CTCCCCCTG GGGAAATGCA 60
 CTACCTTGTT TTGGGGGTT TAGGGGTGTT TTTGTTTTT AGTTGTTTTG TTTTTTTGTT 120
 TTTTTTTT CNCTTTGCCTT TTNCCCTTT NATTTGGNGG GAATGGGAGG AAGTGGGANC 180
 AGGGAGGTGG GAGGTGGATT TTGTTNATTT TTTAAGCTCA TTTCCAGGGG TGGGANTTTT 240
 TTTTNAANAT GNGNCATGAA NAAAGTTTGT TTTTGAAANT AACCAAA 287

SEQ ID NO:236

SEQUENCE LENGTH:222

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00253

SEQUENCE DESCRIPTION:

30 GATCAGAATT GGCAGCACAA AGAAAACGCC CTCTCCTGAC TTGTATTGTG GCAGTCTGAA 60
 CGNCCCAGAA AAATTGTGCC AAAGAGTTTA GAAAAATAAA TATACAATAA AAGTAAACAC 120
 ATACACACAA AACAGCAAAC TTCAGGTAAC TATTTTGGAT TGCAACACAGG ATAAATTAAT 180
 TGTTCAAACA ATCTGATAAA ATAACCATTG GGGNCTTGNA AA 222

SEQ ID NO:237

SEQUENCE LENGTH:221

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00254

SEQUENCE DESCRIPTION:

40 GATCATCTTT CCTNTTCCAG AGAAGTGGGC TGGATGTCTC CATCTCTGTC TCAACTTTAC 60
 GTGTACTGAG CTGCAACNTC TTACTTCCCT ACTGAAAATA AGAATCTGAA TATAAATTTG 120
 TTTTCTCAAA TATTTGCTAT GAGAGGTTGA TGGATTAATT AAATAAGTCA ATTCCTGGAA 180
 GTTGAGAGAG CAAATAANGT CCTGAGAACC TTCCAGACAA A 221

SEQ ID NO:238

SEQUENCE LENGTH:217

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00255

SEQUENCE DESCRIPTION:

5 GATCAGACGT TTTACAAATN CATGAAGCGA ATTGCTGCTT GTAAGGAGCA GATTTTAAGG 60
 TATTCCTGGA GTGGAGAGCC ACTCTTTTAA ACCTGCCCTA CATCAGANGT CACCGAGCTC 120
 CCAGCCTGCA GCCAGTNTGG AGGCCAAAGG ATATTNNATT TTCANCTTAT GCCAGCNCTG 180
 GTCAGCATGC TCAANAGTGC TANTTTAGGT CTTNCTN 217

10 SEQ ID NO:239
 SEQUENCE LENGTH:217
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00256
 SEQUENCE DESCRIPTION:
 15 GATCTCTCTG AGTCCTGGCA ACATCCAGCA AAACACTGCT TTATTCTCCA AAGAATATTG 60
 GGAGCTCTCA ATCCTCGGTG ATATGGGAAA GAGAACTGAG TATTTGCCCT ATGACTGAGC 120
 TTTCTATAGG AATTTTATTA AAGAATGTTT AATTTNGTTG TCCTNCTNAA TGTTCCTAGT 180
 CAAATAAATG AGTGAGCTGG TTTGGGCTGC TCTTGGN 217

20 SEQ ID NO:240
 SEQUENCE LENGTH:216
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 25 CLONE:HUMGS00257
 SEQUENCE DESCRIPTION:
 GATCCCATGG ACATTGGGGG AAAGGGCTCC TTGGGCTGCT GGTGAACCTC TGTGGCCACC 60
 ACCTCCTGCT CCTGACCTCC CTGGGAGGTG CTATCAGTCT GTCCTGGCCT TTCAGTTTTA 120
 TAAGTNGNTT CCAGCCCCAG TGTCTGACT TCTNCTGCAN AATAGGAGGG AGGCCTCCTT 180
 30 TTNGGANGGN NGTACTTTGG GNGATAGTGN GGCCTN 216

35 SEQ ID NO:241
 SEQUENCE LENGTH:220
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00258
 SEQUENCE DESCRIPTION:
 40 GATCTTTTAA GTTTCCTTCC CTACCCAGTC CCCATTTTCT GGTAAGGTTT CTAGGAGGTC 60
 TGTTAGGTGT ACATCCTGCA GCTTATTGGC TTAATAATGTA CTCTCCTTTT ATNTGGTCTC 120
 TTTGGGGCCG ATNGGNGAA AGCGAAATCA NTAGTGCAAC TGTTTTGATA CTGAATATTG 180
 ACAAGTGTCT NTTTNAATA AAGACCCANT CCCTTCCAAA 220

45 SEQ ID NO:242
 SEQUENCE LENGTH:223
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00259
 50 SEQUENCE DESCRIPTION:
 GATCACTAAT CAATAATCTG ATATTTAACA AAATATGGAC AGGCCACTTA TGCTCAGTTT 60

55

TACCTTAGTT ATTCCTTGGT ATCCACAGGC CCAAGTCCCT TTAAATAAAA TACCCTCATA 120
 TTTCCATATA ATCTACATAC ATTCTCCCAT ATACTTTAAA TCATCTCTAG ATTACTNATA 180
 ATGTCTAATN CAAAATAAAT GCTATGTAAA TGTAATTATT AAA 223

5

SEQ ID NO:243

SEQUENCE LENGTH:216

SEQUENCE TYPE:nucleic acid

10

TOPOLOGY:linear

CLONE:HUMGS00260

SEQUENCE DESCRIPTION:

15

GATCAACTTA ATTCCTTTTC TTTATCTTCC NTCCCTCACT TCCCTTTTCT CCCACCTCT 60
 TTTCCAAGCT GTTTCGCTTT GCAATATATT ACTGNNTAAT NAGTTGCAGG ATAATGCAGT 120
 CATAACTTGT TTTCTCCNAA GTATTTGAGT TCAAAACGCC NGTATCTAAA GAAATACGGT 180
 TGGGGTCATT AATAAAGAAA ATCTTTCTAT CTAAAA 216

SEQ ID NO:244

20

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00261

SEQUENCE DESCRIPTION:

25

GATCTCAGAA CAATCAGATG CAAAGCTGAA AGAGATTGTA ACAAATTTCT NTGGCTGGAT 60
 TTGAAGCTTA AACTCCTGTG GATTACATC ANATACCAGT TCAGTTTGT CATTGTTCTA 120
 GTAAATTAGT TCCATTGTGA AAAGGGTTAC TCTCATACTC CTTATGTACA GAAATCACAT 180
 GAAAAATAAA GGTTCATAA TGCATAGTTA AA 212

30

SEQ ID NO:245

SEQUENCE LENGTH:221

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35

CLONE:HUMGS00262

SEQUENCE DESCRIPTION:

40

GATCCATCTG CCTTTGTGGC TGCTGCCCCC GTGGCTGCTG CCACCAACAG CTGCTCCTGC 60
 TGCTGCTGCA GCCCAGCTAA GGTGGAAGCC AAGAAAGAGT CGGAGGAGTC GGACGAGGAT 120
 ATGGGATTTG GTCTCTTTGA CTAATCACCA AAAAGCAACC AACTTAGCCA GTTTTATTG 180
 CAAAACAAGG AAATAAAGGC TTACTTCTTT AAAAAGTCAA A 221

SEQ ID NO:246

45

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00263

SEQUENCE DESCRIPTION:

50

GATCCCATTG GAAGGAATGC TCTACCTCAC AGAACTCTGA ACCCTACAGA AATATGGGCC 60
 TGCTGCCATT TCCTGAAGAC CGGGGCATCG GGGTGGGGTG ATAAAGGATA CAACCTGCAC 120

55

AGGGGGAAGT TATTAAAGAG GCTGCAAAGT CCAGCCACCC TGAAGATACT CCCCAGTGCT 180
 CCCCTCCTGC TAAAGAACCA GTTACCCAG GAAA 214

5

SEQ ID NO:247
 SEQUENCE LENGTH:208
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

10

CLONE:HUMGS00264

SEQUENCE DESCRIPTION:

15

GATCCTCAAC TATTGGAAAT NATGGACTGG TGGCCCTGGT ACAGAACCAT GACTGGCTGC 60
 TGAATTCTGA AAACCAGGAC TTGGTTCAAC ATTAAATTT GATAGTTGCC CTGATTCCCA 120
 TTTTGGGTTT GTGAAAAGTG TATGTATTTA AATTGCTGT AAAACATAAT CACTAATAAT 180
 ATGCAATAAA TATTCCTTG AAGGGAAA 208

20

SEQ ID NO:248
 SEQUENCE LENGTH:208
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS00265

SEQUENCE DESCRIPTION:

25

GATCTGTGGG AGGAATGGCA AGAGAAGCAA CCGGACCCTG AGAGAAGAGT GTTAAGGAAC 60
 CTGCGCATGT GGTAGCTTG ACCTTTCTGT TGGGCATGAC ATGGGGTTTT GCATTCTTTG 120
 CCTGGGGACC NTTAAATATC CCCTTCATGT ACCTCTTCTC CATCTTCAN TTCATTACAA 180
 GGTAAGATAA ATTGTACATG AATAGTCN 208

30

SEQ ID NO:249
 SEQUENCE LENGTH:201
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

35

CLONE:HUMGS00266

SEQUENCE DESCRIPTION:

40

GATCAAAATAT CACTAAATAC TTAAATTGT TTTACTTAAG AGTCTAATCT GGGAAGTTTT 60
 CAAATCATAC TATTAATGTG TAATCTAAGC TCTCAGATG TATCCATGAA TAATCCTGGA 120
 ACAATATTGC TTGTATTCCT GTCATAGAAC AGGTTTTGTA ATCTTTAAAA GAAATGAAAA 180
 TTTATATAAT AAAGTTTCAA A 201

45

SEQ ID NO:250
 SEQUENCE LENGTH:211
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS00267

SEQUENCE DESCRIPTION:

50

GATCACCTTG GTGTTCTTG TTTGGAAGAT TATTCCTCT GAATTTCTGG GCTTGGTCTT 60
 CCAGTTGGCA TTGCCTGAA GTTGATTGA AACAAATTAN TGAATATT AAATATTTGG 120
 TTTCAAAAGG CAGATTTATC TTCTCCAAC ATTCTGTTAT TTCTGATACT TTTGAAAAAC 180

55

TAATAAAAAT TAATAAAAGA CATGAACTAA A

211

5

SEQ ID NO:251

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00268

10

SEQUENCE DESCRIPTION:

GATCCAAGAA AACGCCTCAC TGCCTTAACC TTAAGTGTTC TTCCTGGCGC TAAAAAGAGC 60
 TGTATTTTTT AAAGTGCTGG GGCAACAAA GNANCCCCAA AAGAGTTGAT GTGTGTTTTA 120
 AAAGNAAAAA CCAATGAGG AACAATTGGA GATTTTATG CAGAACTAA ATAATCCTTA 180
 ATAAATAAAT CTCTATTTTG GAATCAAA 208

15

SEQ ID NO:252

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00269

20

SEQUENCE DESCRIPTION:

GATCTTCTAA AAAAGGAACA GAAAATGGTG TGAATGGAAC ATTAAGTCA AATGTAGCAG 60
 ACTCTCCCG GAATAAAAAA GAGAAATCTT CATAATGAAT TATAAGTCA TTGATTAATG 120
 TCCCCAAGA AATCTGCTTT CTACTATATC TTTCAGCATT AGAGATTTTC CTGTTCTNGA 180
 AAATNCAGTC TGTGCTCTTT GATTN 205

25

SEQ ID NO:253

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00270

30

SEQUENCE DESCRIPTION:

GATCTAGGCA AAGAAGAATA CAAATNAAAC CCCNTTCTTT CTCGTTTCCN GTCCAACAAC 60
 TCTGTAGAGC TCTCTGCACC CGTTACCCCT TTCCACCTTT TGTATTTAAT TTTAAAGTCA 120
 NGTGTACNTG CAAGGAATGC TGGATGCAAG ATAGATACTA TATTAACTG TACTGTTATT 180
 TAAGATGTAA TAAAGCAGTT TGACATGAGA AA 212

40

SEQ ID NO:254

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00271

45

SEQUENCE DESCRIPTION:

GATCTAAGAT GATTATTTTG TAAAAGACTT TCTAGTGTAC AAGACACCAT TGTGTCCAAC 60
 TGTATATAGC TGCCAATTAG TTTTCTTTGT TTTTACTTTG TCCTTTGCTA TCTGTGTTAT 120
 GACTCAATGT GGATTTGTTT ATACACATTT TATTTGTATC ATTTTCATGTT AAACCTCAAA 180
 TAAATGCTTC CTTATGTGAA AAAAACAAA 209

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SEQ ID NO:255

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00272

SEQUENCE DESCRIPTION:

GATCTGCCAG CAGTGTCTT GCAATATGAG GAAGACAGTT ACAGCCACAT TATGGCTCTC 60
 ATTGAACAGT ACGCAGCACC CCTGCCCCCA GCCGTCTTTC TGGGGCTTGC GCGCAAAATC 120
 TACAAGCGGA GAAAGTGACC TAGAGATTGC AAGGGCGGGG AGAGGAGGCT CTCAATAAAT 180
 AATCGTGTA CTTAAA 197

SEQ ID NO:256

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00273

SEQUENCE DESCRIPTION:

GATCTATCAC CTGTAATCAT AACTGGCTTC TGCTTGTAAT CCACACAACA CCAGGACTTA 60
 AGACAAATGG GACTNATGTC ATCTTGAGCT CTTCAATTTAT NTAACTGTA ATTTATTTGG 120
 AGTGGAGGCA TTGTTTNA GAAAAACATG TCATGTAGGT TGTCTAAAAA TAAATGTCAT 180
 TTAAACTCAT TTGAAA 196

SEQ ID NO:257

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00274

SEQUENCE DESCRIPTION:

GATCTCACCA GGAGAAATGA ATATGTGAGG TGATGGATGT AACTAGCTTG ATTGTGGTAA 60
 TCAATTCGC AATGTGTACA TATATCAAAA CATCACATTG TACAAAATAC ATACAGTTTT 120
 TGTC AATTTA AAGATATCAG AATTCTAGAA TATGATAAAG TTGTGTTTTC AAGCAAGTAA 180
 AGATAGNTTA CTTAAA 196

SEQ ID NO:258

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00275

SEQUENCE DESCRIPTION:

GATCAGATTT TNCATTTT N AATGTTCCGT GTTTTCTTAA GTAGCATGTA TGACATTTAT 60
 AATNTTAAAA AATNTTTTAA AATATGTGTA TGATACATAT TTTNATTGT CTTAGGGCAG 120
 GCTTTTGAAA ATNTCAGCCT GTAGCCAAAT GCAAGATTTT CTCCATCCTT TAATAAAAAG 180
 CACACTGAGA AATCCTN 197

SEQ ID NO:259

SEQUENCE LENGTH:199

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00276

SEQUENCE DESCRIPTION:

GATCTCTGTC TTGAGTTTCT CCTTCCCCAT CAGCTGAAGC ACTCTTCAGA GACTACGTCC 60
 ACAGACACTG ATGCTGAGGC CTCCTGGAG GAAGGAGGGT TAGGGGTGCC TATCCTCAAG 120
 TATTGGAAGA GCAGAATTGA GGGAGAGACC TTTCTTCCTT GTTGAGGGTG AAAAATAAAT 180
 ANGAATTACA TGCCTAAA 199

SEQ ID NO:260

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00277

SEQUENCE DESCRIPTION:

GATCAAGAAG GCTGGAACGG AACTGGTTAA CTTCTTGAGC TATTTCTGGT AACTTGGAAC 60
 ACAGCCTGCC ACCCAGTGAA GTGTCCAGAC CATTGTCTTC CAACCCAGC TGGCCTCTAG 120
 AACACCCACT GGCCAGTCCT AGAGCTCCTG TCCCTACCCA CTCTTTGCTA CAATAAATGC 180
 TGAATGAATC CNNNAAA 197

SEQ ID NO:261

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00278

SEQUENCE DESCRIPTION:

GATCTGAGTC AGTCGGAATT TGTGAAACAG GGTAGCAAAC AAGATATTTT ACTTCCATGT 60
 ATACAATAAT TTTTAAAN NNTGCAATTT GCGTTGCAGC AATCAGTGT AAATCATTTG 120
 CATAAGATTT AACAGCATTT TTTATAATGA ATGTAAACAT TTAACTTAA TGGTACTTAA 180
 AATAATTAA AAGGN 195

SEQ ID NO:262

SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00279

SEQUENCE DESCRIPTION:

GATCTAGTGT AATGGAAGAC CTTTGAGAAC CTGGGTGTAT TAACTTTGTG TATATAGTGT 60
 AAATATCCCC ACTGTACTGT TAGAGGCCAA CAATTCTAGT ATGGCTTGT GGCAGAGT 120
 GCTACACCGT TTCAATGAAA CAATGTATGT TTGTTTAAAC TGAACAAAA TAAATACATG 180
 CTTAATCCTG AAA 193

SEQ ID NO:263

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00280

SEQUENCE DESCRIPTION:

GATCCCTGGG ACCAACCGCA TCCTCAGCTT CTTCCCGAG AAATGCTGGA GCAGGCTGTT 60
CAGACCGACG TTGCCATCA AACACATACA CCCAGAAAGA AACAAACAGAA ACCAAAACTC 120
ACAAGGCGCA TGATTACTTG TTTTATATTT CATGTTGGGT TTTCCCTCCC ACTATTAAAC 180
AGTCTGTTTC CGTAAA 196

SEQ ID NO:264

SEQUENCE LENGTH:192

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00281

SEQUENCE DESCRIPTION:

GATCTGTAA AAAAGAAATC TGTTCACCA GATGACCGTG TACAATACCG TGTGGTGAAA 60
ATGAATTCAG ACTTATTAAT TGATGAACCT GTTAAATCTN CTCAGTGTCT ATTTATCAGC 120
ACAATACACA CAGGAGANCT GTTGATGGCA TATTGAATAG ATTNCTCTGA ATAANTTGCT 180
CTGGAAACCA AA 192

SEQ ID NO:265

SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00282

SEQUENCE DESCRIPTION:

GATCCTCGTC TTACAGCGAA TGGTTTCAAG ATAAAATTGA TACCAGGAGT TTCAATTACT 60
GAAAATTACT TGGAATAGA AGGAATGGCT AATTGTNTCC CATTCTATGG AGTAGCAGAT 120
TTAAAGAAA TNCTTAATGC TATATTAANC AGAAATGCAA AGGNNGTTA TGANTGTNGA 180
CCTCGCANN 189

SEQ ID NO:266

SEQUENCE LENGTH:188

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00283

SEQUENCE DESCRIPTION:

GATCTTTTGT ACTTTAGGAC ATTAAATTGT ACAACTTTTG TATATATAAA AGCTTAGGAA 60
CTTTCTGTTT AGCAGGAAGG CAACACATTC CTACACTTTT AATGTATATG TTTGTTATAA 120
TGTCCATGTA AACATGCCCT ATGTTTGTGC CTTTAAATTA GTTTGTCTCA ATAAACAAAA 180
TG TAGAGN 188

SEQ ID NO:267

SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00284

SEQUENCE DESCRIPTION:

GATCCTGAGA ACTTGGAATT CCTTGTAAC TGGAGCTCGGA GCTGCACCGA GGGCAACCAG 60
 GACAGCTGTG TGTGCAGACC TCATGTGTTG GGTTCCTCCT CCTCCTTCCT GTTCCTCTTA 120
 TATACCAGTT TATCCCCATT CTTTTTTTTT TCTTACTCCA AAATAAATCA NGGCTGCAAT 180
 GCAGCTGGTG CTGTTTCTAGT TCTAAA 206

SEQ ID NO:268

SEQUENCE LENGTH:190

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00285

SEQUENCE DESCRIPTION:

GATCAGAAAA AGAAAGAAGC CAAAGAGAAA GGTACCTGGG TTCAACTAAA GCGCCANCCT 60
 GCTCCACCCA GAGAAGCACA CTTTGTGAGA ACCAATGGGA AGGAGCCTGA GCTGCTGGAA 120
 CCTATTCCCT ATGAATTCAT GGCATAATAG GTGTAAAAA AAAAANTAAA GGGCCCTCTG 180
 GGGCTACAAA 190

SEQ ID NO:269

SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00286

SEQUENCE DESCRIPTION:

GATCAAGATA TAAATNTC GGATTATCT TTCCCATAT CCAAGTACCA ATNCTGTTGT 60
 AAACAACGTG TATAGTGCCT AAAATTGTAT GAAAATCCTT TTAACCATTT TAACCTAGAT 120
 GTTTAACAAA TCTAATCTCT TATTCTAATA AATATACTAT GAAATAAAAA AAANNGNTTG 180
 AAAGCTAAA 189

SEQ ID NO:270

SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00287

SEQUENCE DESCRIPTION:

GATCTTGTGT ATTGAGCTTA TTGTTGAAAG GGATTTTGA AGGACAGAAC AATTACTGCA 60
 TGATGAATCT TCCTNTCTCT GCCTTCTGAG CACCGNCTTT AATTTCATA TCTTCAAGTC 120
 TTGAAGAAGT TGATGTTAAT TGAAGAATTC ACTTGTCTGG TTGAAATAAA GCCTGTTTCT 180
 GTTGTGAAA 189

SEQ ID NO:271

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00288

SEQUENCE DESCRIPTION:

GATCTGATTT GCTAGTTCTT CCTTGTGAGA GTTATAAACT GAGAGTGACG TCACTTCAGC 60
CAGAACATAT TCTCCATACT CTGCATATAA TTTGTGGCTG CAGAATATG TAATTTGTTG 120
CACACTATGT AACAAAACAA CTGAAGATAT GTTTAATAAA TATTGACTT ATTGGAAGTA 180
ATATCN 186

SEQ ID NO:272

SEQUENCE LENGTH:185

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00289

SEQUENCE DESCRIPTION:

GATCTAAAAT GTCAGCATCA TGCAAAGTGC ACGATATATA GTGAATTNG CTCTAAAAGA 60
GCATGAACAA GTCTTTCTAA TGTTTTGTAC AGTGCCTGGC ACTCTGTGGG TGCTCAATAA 120
ATGGATAGGA GTTTTCATTT GAAGGATATT TGAATTTTAA AAATAAAGTG TTTTATTCCC 180
NTAAA 185

SEQ ID NO:273

SEQUENCE LENGTH:184

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00290

SEQUENCE DESCRIPTION:

GATCTGGTCA CTGTGGTTCC TGCATGAAGA CAGTGGCTGG CGGTGCCTGG ACGTACAATA 60
CCACTTCCGC TGTACCGGTA AAGTCCGCCA TCAGAAGACT GAAGGAGTTG AAAGACCAGT 120
AGACGCTCCT CTACTCTTTG AGACATCACT GGCCTATAAT AAATGGGTAA ATTTATGTAA 180
CAAA 184

SEQ ID NO:274

SEQUENCE LENGTH:185

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00291

SEQUENCE DESCRIPTION:

GATCTGATTT GCTAGTTCTT CCTTGTAGAG TTATAAATGG AAANATTACA CTATCTGATT 60
AATAGTTTCT TNATACTCTG CATATAATTT NTGGCTGCAG AATATTGTAA TTTGTTGCAC 120
ACTATGTAAC AAAACAACTG AAGATATGTT TAATNNATAT TGTACTTATT GGAAGTAATA 180
TCAAA 185

SEQ ID NO:275

SEQUENCE LENGTH:188

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00292

SEQUENCE DESCRIPTION:

GATCAAAGAC ATCCTCATCC AGTATGACCG GACCCTGCTG GTAGCTGACC CTCGTCGCTG 60
 CGAGTCCAAA AAGTTTGGAG GCCCTGGTGC CCGCGCTCGC TACCAGAAAT CCTACCGATA 120
 AGCCCATCGT GACTCAAAAC TCACTTGTAT AATAAACAGT TTTTGAGGGA TTTTAAAGTT 180
 TCAAGAAA 188

SEQ ID NO:276

SEQUENCE LENGTH:182

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00293

SEQUENCE DESCRIPTION:

GATCGGGNTA CTACAAAGTT CTGGGAAAGG GAAAGCTCCC AAAGCAGCCT NGTCATCGTG 60
 AAGGCCAAAT NCTTCAGCAG AAGAGCTGAG GAGAAGATTA AGAGTGTGG GGGGGCCTGT 120
 NTCCTGGTGG CTTGAAGCCA CATGGAGGGN GTTTCATTAA ATGCTAACTA CTTTNCCTA 180
 AA 182

SEQ ID NO:277

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00294

SEQUENCE DESCRIPTION:

GATCCAGCCA GAGGATGCCA CGCCAGCCCA GCGCTACCAG GCTGCCCAAG GGGGGCGGGC 60
 CTGGGAAGAG CCTACACGG GGCAGCACCT AGGATGGGGC AGAGACTTGT TGCATCTTGT 120
 TCCCCAGCAA AGGTACATG TTACCTCCTT CAATTGATAA TAAACCTTTC TGAGATGCAG 180
 AGGGTCCAGG TCAAA 195

SEQ ID NO:278

SEQUENCE LENGTH:327

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00295

SEQUENCE DESCRIPTION:

GATCCCATTA ACTCGATGCT GAGTATCTAC ATGGATACAT TAAATATATT TATGCGAGTT 60
 GCAACTATGC TGGCAACTGG AGGCAACAGA AAGAAATNAA GTGACTCAGC TTCTGGCTTC 120
 TCTGCTACAT CAAATATCTT GTTTAATGGG GCAGATATGC ATTAAATAGT TTGTACAAGC 180
 AGCTTTCGTT GAAGTTTAGA AGATAAGAAA CATGTCATCA TATTTAAATG TTCCGGTAAT 240
 GTGATGCCTC AGNTCTGCCT TTTTCTCTGG AGAATAAATG CAGTAATCCT CTCCCCAAAA 300
 AAAAAAAAAA NNNTNNNTNN NNNTNNN 327

SEQ ID NO:279

SEQUENCE LENGTH:183

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00296

SEQUENCE DESCRIPTION:

5 GATCCAAATC CTCATCTTAC TTTCCTGACC TTAAGGATGT AGCTGCTGCT TGTCTGTTC 60
 AAGTTGCTGG AGCAGGGGTC ATGTGAGGCC AGGCCTGTAG CTCCTACCTG GGGCCTATTT 120
 CTACTTTTCAT TTTGTATTTC TGGTCTGTGA AAATGATTTA ATAAAGGGAA CTGACTTTGG 180
 AAA 183

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SEQ ID NO:280

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS00297

SEQUENCE DESCRIPTION:

20 GATCAAAGTG GCTGCAGCAG AGTTAGCTGT CTAGCGCCTA GCAAGGTGCC TTTGTACCTC 60
 AGGTGTTTTA GGTGTGAGAT GTTTCAGTGA ACCAAAGTTC TGATACCTTG TTTACATGTT 120
 TGTTTTTATG GCATTTCTAT CTATTGTGGC TTTACCAAAA AATAAAATGT CCCTACCAGN 180

SEQ ID NO:281

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS00298

SEQUENCE DESCRIPTION:

30 GATCACAATG TTTTGTCTCT CAGTTCTATT AATGTTCTTG GATTCTGTTC AATGTTCTGT 60
 TCACATTGCA GAAAAAGCAT TTGACAAAAT AATTCAGTA GCTGCTGAAA AAGCATTGTA 120
 TAAAAATCAG CATACCTTTA TGATACAAAA AACCTTCAAT AACTGGGTA TATATGNACN 180

SEQ ID NO:282

SEQUENCE LENGTH:178

SEQUENCE TYPE:nucleic acid

35

TOPOLOGY:linear

CLONE:HUMGS00299

SEQUENCE DESCRIPTION:

40 GATCTTGAAT TATTTATAAA CTGGAAAAGTG GTTTGATTAT TGTGAGTCAA AACTCTAAGT 60
 GGTTAAAAAT TAGTATGAAT TTTTAGCTT CTTAATGAAT ATGGATTAA AACTCTCCAG 120
 TTCTTATTTT ATGAAATGAC TTGCCTTTCT GGTAAATCAA TGCTGATTTT TTAGTAAA 178

SEQ ID NO:283

SEQUENCE LENGTH:182

SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS00300

SEQUENCE DESCRIPTION:

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GATCCCAAAT ATGAAGTCAT CGAAAAACCC CAGGCCTGAA GAAATAAAGT AAAAATNAAT 60

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CTGGTAATTT GTCACGGATT AGTTGTACAA CTAGTTAGAA GTTTCAGAAT AAACATGCAT 120
 TTCATAACTG TCAATGTTC TTTTAATTCT GAGTCCAAAT AAATTATTG GTGATGTTGA 180
 AA 182

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SEQ ID NO:284
 SEQUENCE LENGTH:179
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00301
 SEQUENCE DESCRIPTION:

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GATCTCTGAG TGAGAGGGAA ANAGGTCAGA TTTATACAAC TGAGCGCCAG AGGGGAAAAT 60
 GCACCTTGTT GGAGTGAGAA ATGTTCTGAA ACTGAATTAC TTCTTGATCA GCTGAGATAG 120
 CTTCTTCTGA ACTATTATTA AATAAGTGAA TACAAAGGCC CTATGATGGG AAATCCAGN 179

SEQ ID NO:285
 SEQUENCE LENGTH:201
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00302
 SEQUENCE DESCRIPTION:

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GATCACCTGT TTGAAACCAT CTCCCAAGCC ATGCTGAATG CTGTGGACCG GGATGCAGTN 60
 TCAGGCATGG GAGTCATTGT CCACATCATC GAGAAGGACA AAATCACCAC CAGGACACTG 120
 AAGGCCCGAA TGGACTAACC CTGTTCCCGAG AGNCCACTTT TTTTCTNTT TTTGANATAA 180
 AATAGCCTGT CTTTCAANAA A 201

SEQ ID NO:286
 SEQUENCE LENGTH:176
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00303

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SEQUENCE DESCRIPTION:
 GATCGGAGAT GCTTTGTAAT CTA CTGTGTTCA GCTGGAAACA GCTCATGTTA CGCGGAAAAA 60
 ACTACAAGTA ATGTTCAAAT CTATTTTGGG TCATTTTAT GTACCTTTGG GTTCAGGCAT 120
 TATTTGGGGG GTTTTGTTC CAAAGGAACT AAATAAAGTC ATATTGCTTA TAGAAA 176

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SEQ ID NO:287
 SEQUENCE LENGTH:176
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00304

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SEQUENCE DESCRIPTION:
 GATCTTTGCT GGGAAACAGC TGTGAAGATG GACGCACCCT GTCTGACTAC AACATCCAGA 60
 AAGAGTCCAC TCTGCACTTG GTCCTGCGCT TGAGGGGGGG TGTCTAAGTT TCCCCTTTTA 120
 AGGTTTCAAC AAATTCATT GCACTTTCCT TTCAATAAAG TTGTTGCATT CCCAAA 176

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SEQ ID NO:288

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00305

SEQUENCE DESCRIPTION:

GATCCGCAAG ACCAAGTACC GCCCCGACCT GCGCATGGCA GCCATCCGCA GGCCAGCNTC 60
ATCCTGCGCA NCAGAAGCCT GTAATNGTGA AGAGGAAGCG GACCCGACCC ACCAAGAGCT 120
CCTGAGCCCC CTGCCCCCAG AGCAATAAAG TCAGCTGGCT TTCTNACCTG AAGAAA 176

SEQ ID NO:289

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00306

SEQUENCE DESCRIPTION:

GATCTCAAAA CACAGTGAGA GGTCTGAAGG CTGGCTTCTG AAGAATCCCT GATGCTTTAT 60
TGGAACAACC ACTGAGCTAC GGAGAGCTCT GCTGTGATGG GCTAGGCACT TTATATCTGT 120
GTGAATACAG ATTTATAAAA CAGGTTAATA AACCTATCCA AGGTCACATT TCAAA 175

SEQ ID NO:290

SEQUENCE LENGTH:165

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00307

SEQUENCE DESCRIPTION:

GATCTGAATT CTTTATGTAT ATTTGTAGCT ATATTTATA CAAAGTGCTT TAAGTGTGGA 60
GAGTCAATTA AACACCTTTA CTCTTAGAAA TACGGATTGCG GCAGCCTTCA GTGAATATTG 120
GTTTCTCTTT GGTATGTCAA TAAAAGTTTA TCCGTATGTC AGAAA 165

SEQ ID NO:291

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00308

SEQUENCE DESCRIPTION:

GATCATTCTT TCTGTAGCTC AGGAGAGCAC CCCTCCACCC CATTGCTCG CAGTATCCTA 60
GAATCTTTGT GCTCTCGCTG CAGTTCCTTT TGGGTTCCAT GTTTTCCTTG TTCCCTNCCA 120
TGCCTAGCTG GNTTGCAGAG TTAAGTTTAT GATTATGAAA TAAAAAACTA ACTGACAATT 180
NTCAAA 186

SEQ ID NO:292

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS00309

SEQUENCE DESCRIPTION:

5 GATCTTGTAG AAAATTTTGA TGAGGCATCA AAGAATGAAG CTAATAAAA GTTTGGTTTT 60
 TGGAAAGCTGG CATGGACTAG ATTTAACAAA TCAGCTATGT GGTTCCAAAG TTTTACAGAC 120
 ATGGAGAACA TCACCTGTTA CTAGTTCAGT AATATAAATA TTTTGTATAT TAATN 175

SEQ ID NO:293

10 SEQUENCE LENGTH:406

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00310

15 SEQUENCE DESCRIPTION:

GATCAGATTA CCAGGAACAT CAGGAGTGGA TTCCTGCCCC AACCAAACCG CATTGCGTGTG 60
 GATTTTTTTA TTCAACTTAA TTGGCTATTC CAAAGATTTT TTTTTCCTA TTTTGGACGA 120
 TTGGNGCCCT TAAGATGCAC GATGGAATTG TGTTTNCGT TTTTNGGTAA AAGGAGCAAA 180
 GCGNGGNCCT GGAGATAAAC GCTGGAGCAA TCTCCTTGA AGGATTCAGC ACGAGTAGAT 240
 20 GGTAAACATT TAAAGGGGAA AGGGGGGTTT GTTAAAAATA GTAAATCAGT AAGTCACITC 300
 TAAATTTAAA GAAACCAAAA TTGGGAGTTG AAGAATAAGT AGGGTTTCCA ATTGGGCTAT 360
 TGCCGNITTN CTTTGNAAAA ATTAAACCAT TTTTAAAAA CCTAAA 406

25 SEQ ID NO:294

SEQUENCE LENGTH:218

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00311

30 SEQUENCE DESCRIPTION:

GATCCCATAG ACCAGAGCCC ACCTTTTNA TAACTTAGT AAAGTCTNG AGACTAGAAG 60
 CAAGATAGTT TGTGACACAT AAGCTTCCCA AAAACTNGAA TAGATTTTNA CTGAATAGTG 120
 GTCTATCTGA TGGTATATGT TTCTTAAAGG TCCAANTGTA ATAAAAAANA TTGAAAAANA 180
 35 GGTCTCAGTG TTTTNAATGC ACTNCATATT TGTNTGCN 218

SEQ ID NO:295

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS00312

SEQUENCE DESCRIPTION:

GATCCACCAA GCACGCCTAT NAATACAAAG TAACTATNA TTTTNATTGT GAAATTTTCA 60
 45 TAGATGGAAA ATTGAATATN CTGTCCATTT CATTTTACAA TNATCTTACC ACTTATTTTT 120
 GTACCATGTA TTTCAATTGC CTGTTTAGTG AAAAAATAAA ATTAAAAAAA CCTAAA 176

SEQ ID NO:296

SEQUENCE LENGTH:172

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS00313

SEQUENCE DESCRIPTION:

5 GATCCCAGCA AGATAATGTC CTGTCTTCTA AGATGTGCAT CAAGCCTGGT ACATACTGAA 60
 AACCCATATAA GGTCCCTGGAT AATTTTTGTT TGATTATTCA TTGAAGAAAC ATTTATTTTC 120
 CAATTGTGTG AAGTTTTTGA CTGTAAATAA AAGAATCTGT CAACCATCTA AA 172

SEQ ID NO:297

10 SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00314

15 SEQUENCE DESCRIPTION:

GATCGGTGAC ATCGTCAAGA TGGGCGAGTG CCGGCCTCTG AGCAAGACAG TGCCTTCAA 60
 CGTGTCTAAG GTCACCAAGG CTGCCGGCAC CAAGAAGCAG TTCCAGAAGT TCTGAGGCTG 120
 GACATCGGCC CGCTCCCCAC AATGAAATAA AGTTATTTTC TCATTCCCAG AAA 173

20 SEQ ID NO:298

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00315

25 SEQUENCE DESCRIPTION:

GATCGTTTCC AGATGAGAAT TCACAAGCGA CTCATTGACT TGCACAGTCC TTCTGAGATN 60
 TGTTAAGCAG ATTACTTCCA TCAGTATTGA GCCAGGAGTT GAGGTGGAAG TCACCATTGC 120
 AGATGCTTAA GTCAACTATT TTAATAAAAT GATGACCAGT TGTAAA 167

30 SEQ ID NO:299

SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00316

35 SEQUENCE DESCRIPTION:

GATCTGGTGG TGGAGTGGT GGATATGGTA GCAGAAGGTT CTAACACAG CAGAAAAGGG 60
 TTGAATGAGA ACCCTACTTG CCTAAATNAG GAATGTCTTT CCTACCATCT AAAATACGAA 120
 GGTTCCTGGC TGGGTAAGGT TTGAGTTGA CAGTAAACC TGATGACACC N 171

40 SEQ ID NO:300

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00317

SEQUENCE DESCRIPTION:

50 GATCCGAGTG TGATTGAAT TCTGTGATAT TTTCACACTG GTAAATGTTA CCTCTATTTT 60
 ACTTACTGCT ATAAATAGGT TTATATTATT GATTCACCTA CTGACTTTGC ATTTTCGTTT 120
 TTAAGGAT GTATAAATTT TTACCTGTTT AAATAAAAT TAATTTCAAA TGTAAA 176

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SEQ ID NO:301

SEQUENCE LENGTH:169

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00320

SEQUENCE DESCRIPTION:

GATCTTTGTT TTGTGTTTAA CCATAATGGT TGTGTACTGA ACCACTTCAT ATTTGTAATA 60
TATAATATAT ATATATNNGN TNCCCTNAAG ACTCAGCCTC CTGGTTTACC CCCCCGGCCT 120
GGGCATCTNA CCTCCCCAC CCCAGTGTGA TTAAACATCC NGGNACTGN 169

SEQ ID NO:302

SEQUENCE LENGTH:174

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00322

SEQUENCE DESCRIPTION:

GATCTAGCTC TGAATGTATG TTTCCTGACG TTTTACATTT CCACTTTCCT ATTCCATTCA 60
TTAAGCTAGC CAACAATCCA CCATCCTTGA AAGATTGTTT TCATAACTGA AAAAAACCA 120
CATAATCTAA ATAGAGCAAA GCTACAAGAA ATAAATTAT TTAACGCAA GAAA 174

SEQ ID NO:303

SEQUENCE LENGTH:177

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00323

SEQUENCE DESCRIPTION:

GATCCTAGCA TATGTTAAAA TTCAAATTAA TGTAACAAG ATTAACAACA ACAAAGAAAC 60
TGCTATTG AGTGAAAGTCA TGCTTTCTAT TATAATAACT TGGCTTCGGT TATCCATCAA 120
ATGCACACNN ATACTGTTAT CTGATTGTTT ATAATAAAGA ATACTGTACC TNNTAAA 177

SEQ ID NO:304

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00325

SEQUENCE DESCRIPTION:

GATCAGATGG TTTTAGTATT GTGGCAGAAG CGAGAAAAC TTGTTTATTG AAAAAAAG 60
AAAAAGAAAG CAAGAAAAAA AGATACTATG GGGTCAAGTG TAACTCCATG GAAATGCCAC 120
GTCGTCTCTT CAGTGAAGAA GCTGGTTTAG AGTCTCACAG AAAACTN 167

SEQ ID NO:305

SEQUENCE LENGTH:170

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00327

SEQUENCE DESCRIPTION:

5 GATCGCTCAC AATNTTCCT CCAAGAACCG CAAAGCCATC GTGGAAAGAG CTGCCCCAACT 60
 GGCCATCANA GTCACCAACC CCAATNCCAG GCTGCGCAGT GAAGAAAATA AGTAGGCAGC 120
 TCATGTGCAC ATTTTCTGTT TAAATAAATG TAAAAACTGC CATCTGGAAA 170

SEQ ID NO:306

10 SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00328

SEQUENCE DESCRIPTION:

15 GATCGGGAAT GGTCTGTGTG TTATCAGCTG CGACTGGTTC ACTGCGNCTT AGACAAGCCT 60
 CATGGGGAAT GGGGATTCTG GCCAGTGTA TTTCTGTCAA CCACGGACGT TTGCCTTCAT 120
 GTGTAGAATT TACTGTTGTT ATGCAAAATTA TATTTCAAT TATAAATGAA A 171

SEQ ID NO:307

20 SEQUENCE LENGTH:164

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00329

SEQUENCE DESCRIPTION:

25 GATCAGACAG AATAATATT NCTAGTTATT ATGTGTAAGA TGAGTTGCTA TTTTCCTAAT 60
 GCTCATTCTG ATACAACTAT TTTCGGTGTC AAATATCTAC TGTGCCCAAA TGTACTCAAT 120
 TTAAATCATT ACTCTGTAAA ATAAATAAGC AGATGATTCT TAAA 164

SEQ ID NO:308

30 SEQUENCE LENGTH:261

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00330

SEQUENCE DESCRIPTION:

35 GATCCCCGCC CTGGGGTCTG GTCCTCGCCC ATCCTGCAGG GATTGCCAC CGTCTTCCAG 60
 ACACCCACCC TGAGGGGGGC ACCAGGTTTA GTGCTGCTGC TTTCCTGNT GCACCCGCGC 120
 CCTCGGCCGG CCCCCGAGC AGCCTTTGTA CTCTGCTTGC GGAGGGCTGG GAGACCTCC 180
 40 AGGACATTCC CACNNTCNC CATGCTGCCA AGTTNNNNCT ATAGCTACAA ATAAAAAAAA 240
 ACCTTGTTTT CAAGAAATAA A 261

SEQ ID NO:309

45 SEQUENCE LENGTH:163

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00331

SEQUENCE DESCRIPTION:

50 GATCAGTCA AGATGAGTTA GTGGAGCTGG GCTTGGCCAG GGAGTCTGGG GACAAGGAAG 60

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CAGATTTTCC TGATTCTGGC TCTAGCTTCC CTGCCAAGAT TTTGGTTTTN ATTTTTTTAT 120
 TTGAACTTTA GTCGTGTAAT AAATCACC A GTGGCAAACC AAA 163

5 SEQ ID NO:310
 SEQUENCE LENGTH:165
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00332

10 SEQUENCE DESCRIPTION:
 GATCATGCTG CTGTGATACT GAGTTTTCTA AACAGCATAA GGAAGACTTG CTCCECTGTC 60
 CTATGAAAGA GTATAGTTTT GGAGGGGAGA AGTGGGACAA AAAAGATGCA GTTTTCCTTT 120
 GTATTGGGAA ATGTGAAAAT AAAATTNTCA ACTCTTTCAG TTAAG 165

15 SEQ ID NO:311
 SEQUENCE LENGTH:164
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00333

20 SEQUENCE DESCRIPTION:
 GATCTCAGTT TCCTGGCTTT TCCTCCCTCA GCCCCTTCTC ACCCCTTTGC TGTCTGTGT 60
 AGTGATTGG TGAGAAATCG TTGCTGCACC CTTCCCCCAG CACCATTAT GAGTCTCAAG 120
 TTTTATTATT GCAATAAAG TGCTTTATGC CGGCTTTTCT CAAA 164

25 SEQ ID NO:312
 SEQUENCE LENGTH:337
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00334

30 SEQUENCE DESCRIPTION:
 GATCATTGAA TGTGAGACCC TTCTAACATG ATTTGAGAAG CTGTACAAGT ATAGGCAGAG 60
 35 TTATTTTCCT GTTTACATT TTTTTTTGTT TTGGGGAAAA AATTGGTAGG TGTCTAATNA 120
 CTGTTTACTT CATTGTTATA TTGCAGTAAA AGTTTAAAN CANCCATTGC ATGTTNGCTT 180
 TTGATGTATC CCTTTGNGAA ATTAGCACTT TTGGGGCCAN TGGNGAAATG CAGCATTAC 240
 TCTCCCTGTC TTTTCCCTT CCCTCAGCAG AAACGTGTTT ATCAGCANGT CGTGAGTCAA 300
 40 ACTGCTGCCT TTTAAAAANC CCACAAANTT GNTNNGN 337

45 SEQ ID NO:313
 SEQUENCE LENGTH:176
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00335

50 SEQUENCE DESCRIPTION:
 GATCCGCCGT CACTGGGGTG GCAATGTCCT GGGTCCTAAG TCTGTGGCTC GTATGCCCAA 60
 GCTCGAAAAG GCAAAGGCTA AAGAACTTGC CACTAACTG GGTAAATGT AACTGTTGA 120
 55 GTTTTCTGTA CATAAAATA ATTGAAATAA TACAAATTT CCTTCAGCCA GTGAAA 176

SEQ ID NO:314

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00336

SEQUENCE DESCRIPTION:

GATCACCTCT GAGACCCACC TTGCTCATAA AAAAAATGCC CATGTTGGTC CTCTGCCCTG 60
 GACCTGTGAC ATTCTGGACT ATTNNTGTGT TTATTTGTGG CCGAGTGTA CAACCATATA 120
 ATAAATCACC TCTCCGCTG TTTTAGCTGA AGNATTANGN CATCTTGCT ATTAAT 176

SEQ ID NO:315

SEQUENCE LENGTH:258

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00337

SEQUENCE DESCRIPTION:

GATCATATTT AATGAATTAT AGTATAATGC TTGCAGGCC AGTACAAGCA TATATATNGT 60
 GCCTCTTACA GCCTTTGGAA TACATTGTTT CCATTTTAA AATATCTTCT ATATCCNNNT 120
 AGTATTCAAA TTATTAATGC TCATGTACCA AGGTNTTGCT ATAAAAGTTT TGTCTGTATG 180
 AATAATGTGG CTTTAGTAAA TAATCATTTN TCAACTGTAA ACTNATTCTG AAATAAAGTA 240
 AAATNCTAAT TGTTTAAA 258

SEQ ID NO:316

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00338

SEQUENCE DESCRIPTION:

GATCTTGGAC ACTTACAGAT TGAGCTGTAT GAATTCAGCG GGTCTCACTC CAGAGGGTCA 60
 GAACGTTTGC TTTAGTTTTT TCATCTGTTT TGTTCTTGA GTCAGTGCTG TTGATGATGA 120
 GTTGTCTTGA ATAAATNATG TGTTCTTTGC AAA 153

SEQ ID NO:317

SEQUENCE LENGTH:157

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00339

SEQUENCE DESCRIPTION:

GATCAAAGCT AGAAAATGNA GATTCCTTAG CCTGGATTTC CTTCTAACAT GTTATCAAA 60
 CTGGGTATCT TTCCAGGCTT CCCTGACTTG CTTTAGTTTT TAAGATTTGT GTTTTNCNT 120
 NTCCACAAGG AATAAATGAG AGGGAATCGA CTGTAAA 157

SEQ ID NO:318

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00340

SEQUENCE DESCRIPTION:

GATCTCCTTA TATAGCAGCC AAAATCAATG AAGCTAAAGA TTTACTAGAA GGTCAAGCTA 60
 AAAAATGAAG TAAATGTATG ATGAATTTTA AGTTCGTATT AGTTTATGTA TATGAGTACT 120
 AAGNNTTTTA TAATAAAATG CCTCAGAGCT ACAATTTTAA A 161

SEQ ID NO:319

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00341

SEQUENCE DESCRIPTION:

GATCTGAAAA CATGTAGAGA AGATGAGTTG AGGACAGCTT TTCTAAGGCA ATGTNATGTC 60
 TTTCTTTTCT NATTTCTNNT TCTCTGCCGT GTTAGTTTTN AAGAGTGGAG GAGCTAGGGG 120
 CTCCAGAAAG AATCTTACAC ATGTTTTGAA GACATTGATG TCATAGGGAG CGGGGAGCTG 180
 CATTCCCTTC TGGGCTGTTA CTGCTAAATC TCAGTATGAA CAGACCAGGC GGAAAGCTTG 240
 GTGGCCAAGC AGTCTGTGTG CTTCCCCGCT GATGGAGAAC GTTGCGTTGT TCACAATAGG 300
 GCCTCATGGG TGN 313

SEQ ID NO:320

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00342

SEQUENCE DESCRIPTION:

GATCTTGTTT ACAAGTAATC TGTTGACAGT GCCAATAAAT NATAAAAAAA AAATTAACAT 60
 GTCACAATGT AACGGATGAC CATATGCACA ATTCCATGAA TAAATCTGT TTCCTGTGTT 120
 AGTCAGTATT CTTAAATAAA ATTTATAATT GAAACATGAA A 161

SEQ ID NO:321

SEQUENCE LENGTH:163

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00343

SEQUENCE DESCRIPTION:

GATCTATTGA NAGCCCTCTC TCNCATTCTG TAATGAGTAC AGCAGAGACC TTCCTGCTTT 60
 TAACTGGGGA CTCCAGATT TCCCCAACT TGCTTCTGTT GAGATTTTTC CCTCACCTTG 120
 CCTCTCAGGC ACAATAAATA TAGTTATACC ACTGCCCATC AAA 163

SEQ ID NO:322

SEQUENCE LENGTH:156

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00344

SEQUENCE DESCRIPTION:

5 GATCATCCTA ACAATGTGGG GCTGTTAGGT TTTACCTTTG ANCTTTTCATA GCACTGCAGA 60
 AACCTTTAAA AAAAAAATGN TNNATGAATT TTTCCTTTCC TACAGTTGGG TAGGGTAGGG 120
 GAAGGNGGNT AAGCTTTTTT TTTNAAATG ACTGAN 156

SEQ ID NO:323

10 SEQUENCE LENGTH:255

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00346

15 SEQUENCE DESCRIPTION:

GATCATGCTG CCTGGGACC CAACTGGTAA GATTGGCCCT AAGAAGCCCC TGCCTGACCA 60
 CGTGAGCATT GTGGAACCCA AAGATGAGAT ACTGCCACC ACCCCATCT CAGAACAGAA 120
 GGGTGGGAAG CCAGAGCCGN CTGCCATGCC CCAGCCAGTC CCCACAGCAT AACAGGGTCT 180
 20 CCTTGGCAGC TGTATTCTGG AGTCTGGATG TTGCTCTCTA AAGACCTTTA ATAAAATTTT 240
 GTACAAAGGC ACAA 255

SEQ ID NO:324

SEQUENCE LENGTH:154

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00347

SEQUENCE DESCRIPTION:

30 GATCTCTAGT ATAACACTCA GGCTACTGAG GTATTTTAGA GCAACAAGCT GGGTTACTTT 60
 CAGAGCAACC AGCTTGACTG GAACTGAGAG TAAATTGGGA ATGTATGACC AATCTTAGAC 120
 CCTGAAAAAT GGCAGAAAAT ACATGGAAAT TTGN 154

SEQ ID NO:325

35 SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00348

SEQUENCE DESCRIPTION:

40 GATCTAGGGA AGACAACGTA GTCACCCTCG GTGCTTCCTC TGTCTCCTCT TTCTCCCTGG 60
 CCTGTGGTTG TCCCCAGCC TCTGCCACCC TCCACCTCCT CGGTCAGCCC CAGCCCCAGG 120
 TTGATAAATC TATTGATTGA TTGTGATAGT AAA 153

SEQ ID NO:326

45 SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00349

SEQUENCE DESCRIPTION:

50 GATCTCTAAT ATTTTAAGC CCAAGCCCCT TGGACACTGC AGCTCTTTTC AGTTTTTGCT 60

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TATACACAAT TCATTCTTTG CAGCTAATTA AGCCGAAGAA GCCTGGGAAT CAAGTTTGAA 120
 ACAAAGATTA ATAAAGTTCT TTGCCTAGTA TAAA 154

5 SEQ ID NO:327

SEQUENCE LENGTH:158

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

10 CLONE:HUMGS00350

SEQUENCE DESCRIPTION:

GATCAAATTC TAATGGAATT GAGCCGGTTT CTTATCCTAA ATGTTTCCTC CCTTTTAC 60

ATCTCTGTCC AGCACCTCTT GGTAAATAA TGTATGCTGT GAGACATGNA ATTAAACAG 120

15 GCCTATGGAA TAAATTATTT TAAAACCAGN AGGTAAA 158

SEQ ID NO:328

SEQUENCE LENGTH:155

SEQUENCE TYPE:nucleic acid

20 TOPOLOGY:linear

CLONE:HUMGS00351

SEQUENCE DESCRIPTION:

GATCTTAAAG CAGAATGCCN TTTNCTTTTT TTGCTTCAGT TGTAAGAAG AGGGAATACA 60

25 TGATAAAGTA ACTGGTTTGA TTTCTCGTTC ATTGTACACT GCCTCTGAAC ANCTAATTGT 120

TTTTAGTTGT CTAAATAAAA TGCCTCTAAA AAAAA 155

SEQ ID NO:329

SEQUENCE LENGTH:165

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00352

SEQUENCE DESCRIPTION:

35 GATCCAAGAG GAAGAATCCA GCTGCCTATG AAAATAACAA ATNAGCAACG CATCCGGATG 60

ACGGTTCCCT GTCTCTGAAA GACCTTTCTC TGGAAGAGGA GTCTGCATTG TAGTGTCTCA 120

AAGACACAAT AACTTCCTA TGGTCTGCAC TGTGTGATA TTAAA 165

SEQ ID NO:330

40 SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00353

SEQUENCE DESCRIPTION:

45 GATCTACTTT GTTTGAGCAA AACAGCATT 60

TTTATTGGTT TTATGTTTAT TTAAATTTGT AAATGTTTGA GCATTATNA TTGTATGTNA 120

NCTATATTN CCTATTTNAT GTTGATAAA 149

50 SEQ ID NO:331

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00354

SEQUENCE DESCRIPTION:

GATCAAAATG CTAACATG ATGATTAAGT GCACACCGTG TGCCATAGAA TGGCACATGT 60
 CATTGCCAC TTCTGTGTAG ACATGGTTCT GGTTTAACTA ATATTTGTCT GTGTGCTACT 120
 AACAGATTAT AATAAATTGT CATCAGTGAA A 151

SEQ ID NO:332

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00355

SEQUENCE DESCRIPTION:

GATCTTTGTT CTAGGCAGCT GGAATAGAC ATGGTACTTA CCTTAGAGTT TTCCAATTTA 60
 TCTCAATTTT ATATGGCTTG TGATTCATTT NCTTAATCCA AATATATATA ANCGTGTGTG 120
 GTCTNATTCT NCCCCCGCA ANANNAN 147

SEQ ID NO:333

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00356

SEQUENCE DESCRIPTION:

GATCCTTACG GAAAAGGAAC AGATTGTNCC TAAACCAGAN GAGGAGGTTG CCCAGANGAA 60
 AAAGATATCC CAGANGAAC TGAAGAAACA AAAACTTATG GCACGGGAGT AAATTCAGCA 120
 TTAAATATAA TGTAATTAAA AGGAAAAGAA A 151

SEQ ID NO:334

SEQUENCE LENGTH:204

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00357

SEQUENCE DESCRIPTION:

GATCTTTGCA GTAATTCTA GGAGCTGTTT ATGTTTGGAG GTAATTGGTC CTTTGTCCAT 60
 ATATATGAGA TGTAAGTNTT ATTTCCAGT TTATCTTTT GCTTATTTT TTGACTTTT 120
 TATTGTAAAA TAAACATCA AACTGCACAG AACAGTTGAA TAGCTTAATG AATAACTACA 180
 GTAAAAGCTA TGGTAACCAC TAAA 204

SEQ ID NO:335

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00358

SEQUENCE DESCRIPTION:

5 GATCCAATTA ACATGTGGGG TTCTTGTTNT GGGTCTGGGG AGCTGAAGGA TTTNATGGAG 60
 CTGGTGCTTT GGAGGAATCT TAAGGGAAAG NAGTAGAAGC TCAGGCCTTT AAAGGATTTC 120
 ANTCCTCCT CTCTGTAATT NNTNCN 146

10 SEQ ID NO:336
 SEQUENCE LENGTH:146
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00359
 SEQUENCE DESCRIPTION:
 15 GATCGCATCT NTTAAACAGG TACAAGTTGA CATGAGGTTA GTTTAATTGT ACACCATGAT 60
 ATTGGTGGTA TTTATGCTGT TAAGTCCAAA CCTTATCTG TCTGTNATTC TTAATGTTGA 120
 ATAANCTTTG ANTTTTTCC TTAAAA 146

20 SEQ ID NO:337
 SEQUENCE LENGTH:147
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00360
 SEQUENCE DESCRIPTION:
 25 GATCAGTGTT GAAGAAAGTG CAAAAGGAAC TTTTATATAT TTAACAGTGT AGGAAATTGT 60
 CTATTCCTGA TATAATTACT GTAGTACTCT TGCTTAAGGC AAGNGTTCA NATTTACNGT 120
 TGAAATAAAC CCAACTCTTC NTGNAAA 147

30 SEQ ID NO:338
 SEQUENCE LENGTH:147
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00361
 SEQUENCE DESCRIPTION:
 35 GATCTNGAAA ATNATCATTG AACATATTAA TGGTTATTTC TTTTCTTGG ATTTCCAGAA 60
 AAGCCTCTTA ATTTTATGCT TTCTCATCGA AGTAATGTAC CCTTTTTTTC TGAAACTGAA 120
 TTAAATACTC ATTTNATCNN NTGNAAA 147

40 SEQ ID NO:339
 SEQUENCE LENGTH:140
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 45 CLONE:HUMGS00362
 SEQUENCE DESCRIPTION:
 GATCAGTTTT TTCACCTGGA AGCATTTGTT TCTACTTTGA TATGACTGTT TTTCGGACAG 60
 TTTATTTGTT GAGAGTGTGA CCAAAGTTA CATGTTTGCA CCTTTCTAGT TGAAAATAAA 120
 GTGTATATTT TTCCTATAAA 140

50 SEQ ID NO:340

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SEQUENCE LENGTH:144

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00363

SEQUENCE DESCRIPTION:

GATCTGAACT TTTCATCTGC AGAGGCAAGA AAAATATTTA ACATTGTGAC TTGACTGTGG 60

AAGATGATGG TTGCATGTTT CTAGTTTGTATATGTTTCCA TCTTTGTAAT AAGATGATTT 120

AATAAATCTC TTAAATACT TAAA 144

SEQ ID NO:341

SEQUENCE LENGTH:291

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00364

SEQUENCE DESCRIPTION:

GATCAAAAGC TTATTCATCT GTTTTNCITT TTCGTTGGTG TAAAGCCAAC ACCCTGTCTA 60

AAAAACATAA ATTTCTTTAA TCATTTTGCC TCTTTTCTCT GTGCTTCAAT TAATAAAAAA 120

TGGAAGAAGT CTAATAGAGT GGTACAGCAC TGTATTATTT CAAAGATGTG TTGCTATCCT 180

GAAAATTCTG TAGGTTCTGT GGAAGTTCCA GTGTTCTCTC TTATCCACT TCGGTAGAGG 240

ATTCTAGTT TCTTGTGGGC TAATAAATA AATCATTAACT ACTCTTCTAA A 291

SEQ ID NO:342

SEQUENCE LENGTH:139

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00365

SEQUENCE DESCRIPTION:

GATCTTAAAC CTATGATTCA GTAACCTCTT ACCATATAAA AACGATAATT GCTTTATTTG 60

GAAAAGAATT TAGGAATACT AAGGACAATT ATTTTATAG ACAAAGTAAA AAGACAGATA 120

TTTAAGAGGC ATAACCAA 139

SEQ ID NO:343

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00366

SEQUENCE DESCRIPTION:

GATCCGTGGC AGGGCTGCTG AGGCCTGTGG GTGGGACACC ANNTGCGAAA CCCTCATCCA 60

GTTTTCTCTC CATCTCTTTT CTTTGTACAA TCCCATTTCC TATTACCATT CTNTGCAATA 120

AACTCAAATC ACATGTCTGC AAA 143

SEQ ID NO:344

SEQUENCE LENGTH:139

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00367

SEQUENCE DESCRIPTION:

5 GATCCAGTGA CATTGTGAGT GAAGACGCAA ACAGGTTTTG ACTCCTGCAT GGCCGATGAC 60
 CTTTCTGTGA GGCTTACCAG AAAAGTACAT NCAACAGTTC TTTGAGGTTT AACTAGAGCA 120
 GCAAATAAAG CAAAAGTTN 139

SEQ ID NO:345

SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00368

SEQUENCE DESCRIPTION:

15 GATCAAGAAT CTTTGTGAA ATTATAGAAA TTTACTATGT AAATGCTTGA TGGAATTTT 60
 TCCTGCTAGT GTAGCTTCTG AAAGGTGCTT TCTCCATTTA TTAAAACTA CCCATGCAAT 120
 TAAAAGGTAC AATGCAGAAA 140

SEQ ID NO:346

SEQUENCE LENGTH:142

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00369

SEQUENCE DESCRIPTION:

20 GATCCAGCTT GCCAGGGACT TAGGTTTATC CTGTTTTGTT TGCTACTGGT TACAAATTCT 60
 ATTTCTGTGA CAATTAGTCA GACTAAAGTT TTCCTGTGT TTGTTGGCA AAACAAATTA 120
 AACAAAAAGT AAGGTTTTTA AA 142

SEQ ID NO:347

SEQUENCE LENGTH:156

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00370

SEQUENCE DESCRIPTION:

35 GATCTCCGTN AAACACATTT TTTTCTTAG TCTATCTCTT GTACAAACGA TGTGCTTTGA 60
 AGATGTTAGT GTATAACAAT TGATGTTTGT TTTCTNTTGT ATTTTAAACA GAGAAAAAAT 120
 40 AAAAGGGGGT AATAGCTCCT TTTTCTTCT TTCAA 156

SEQ ID NO:348

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00372

SEQUENCE DESCRIPTION:

45 GATCTACAAT NGGAGTTGTG AGTNGCAATC TTACATGGCT ACGNCTTTCG TTTGATAGCC 60
 50 AGTCATGGTN ACCACATGAG AACCATATGC TGAGATGCAA TAAAGTAAGA GAATGTTTTC 120
 TGACAAAAAA ATCTN 135

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SEQ ID NO:349
SEQUENCE LENGTH:133
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00373
SEQUENCE DESCRIPTION:
GATCTTAAGC GTGTCTTGAG TTCCATGCAA ATTCAATTCT GTTGATAATG TGTCCATAAT 60
CAAATCATCA TCTTGCAATG CAAGGGCTAC CCCATAATTA TCAGACATTA AAATAGTTTA 120
TTTCTTTTTC AAA 133

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SEQ ID NO:350
SEQUENCE LENGTH:137
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00374
SEQUENCE DESCRIPTION:
GATCTCGTTC CGCCGGTTC CCTTGGCCGC CAGTTCCGTT CTCCTCACGG GCCGAACGGA 60
ACAAGGGGTC CAGCTTGCGG GGGACCTCC CCAGCCCATTT CCTGCTGTCA AAAAAACAAA 120
ACCTTGCAAA GCGCAAA 137

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SEQ ID NO:351
SEQUENCE LENGTH:132
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00375
SEQUENCE DESCRIPTION:
GATCAAGCGT GCTTTCCTTA TCCGAGGAGC AGAAAATCGT TGTGAAAGTG TTGAAGGCAC 60
AAGCACAGAG TCAGAAAGCT AAATAAAAAA ATGAAACTTT TTTGAGTAAT AAAAATGAAA 120
AGACGCTGTA AA 132

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SEQ ID NO:352
SEQUENCE LENGTH:142
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00376
SEQUENCE DESCRIPTION:
GATCAAGTTC CCGCTGCCCC ACCGGGTNCT GCGCCGTCAG CACAAGCCAC GNTTCACCAC 60
CAAGAGGCCC AACACCTTCT TCTAGGTGCA GGGCCCTCTT CCGNGTTTTC CCCCAAATAA 120
ACTCANGAAC GNCCCGGTTA AA 142

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SEQ ID NO:353
SEQUENCE LENGTH:142
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

CLONE:HUMGS00377

SEQUENCE DESCRIPTION:

5 GATCAAGGAT ATTTGAAATC ACTACTGTGT TTTNCTGCGT ATCTGGGGCG GGGGCAGGTT 60
 GGGGGGCACA AAGTTAACAT ATTCTTGGTT AACCATGGTT AAATATGCTA TTTTAATAAA 120
 AATATTGAAA CTCACCAGTA AA 142

SEQ ID NO:354

10 SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00378

SEQUENCE DESCRIPTION:

15 GATCTCTAAT GAAAAAGGGA TGTCTTTTGT TTTATAGTCA TGTGGCAAGA TGAGAGTAAA 60
 ACCGAGAGAG AAACCTCTAT AAGTNTTGAG TATATGTATA CATTGAAAT AAACCAGAAA 120
 TTTGTTACCT TAAA 134

20 SEQ ID NO:355

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00379

SEQUENCE DESCRIPTION:

25 GATCAGCTCT GAGGTGCACT TCTTCACATA CTGTACATAC CTGTGACCAC TCTTGGGAGT 60
 GCTGCAGTCT TTAATCATGC TGTTAAACT GTTGTGGCAC AAGTTCTCTT GTCCAAATAA 120
 AATTATTAA TN 132

30 SEQ ID NO:356

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00380

SEQUENCE DESCRIPTION:

35 GATCNGGGCT GGATTGACGG ATGTCACCCC CNATCCCCTC GTGACATGCA CGTCNGCAGG 60
 AATGGGGGGT CTGCNGTGGT CGCCNGTCGT GTGAACAAGA TTCCGTCAAA ATATTTTCTG 120
 40 TTAATAAAAT GCCTTCATGT AAA 143

SEQ ID NO:357

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00381

SEQUENCE DESCRIPTION:

45 GATCTAGAAG ATGATGTTCA AACTATGAAA CTGCTTGTGA ATTGTGAAAT GACTTTGTTT 60
 50 TTTGCTTGT TTTTNAATT TCCTATAATG NACATACTAA CTTTAAAAA ATAAAGGTTA 120
 TTTTAAAGC CTGAAA 136

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SEQ ID NO:358

SEQUENCE LENGTH:133

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00382

SEQUENCE DESCRIPTION:

GATCTTCTAT GTAACAGTTG AAATNTGGAA GTGACGTCAC TTACCTGTCT AACGTGGTGT 60
GGGNGAGAAT TTACAAGTCC TTTATTGNAA GAATAATTGT TGCAAAATAT ATTGCTTCTA 120
CTTTGCCTGG AAA 133

SEQ ID NO:359

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00383

SEQUENCE DESCRIPTION:

GATCAAGAAT TTGGGTGGGA GAAAAGAAAG TGGGTATCA AGGGTGATNN GAAATTTTCT 60
GCAGCATTAA AGCTGGCGCT TAATAAGAAT AAGTAATAAT AAAGAAATTT CTAACATTCC 120
ATGTCAGAAA 130

SEQ ID NO:360

SEQUENCE LENGTH:157

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00384

SEQUENCE DESCRIPTION:

GATCTGAAAC TAATAGTAGG AGTTTCCCCA GAAGTCATTT TCAGCCTTAA TTCTCATCAT 60
GTATAAAATTA CCATAAATNA TGCATGTNTG TTTACTTTAG TGACGTTCCA CAGAATAAAA 120
GGAAACAAGT TTGCCATCTT GGTGTTGCAA TATGAAA 157

SEQ ID NO:361

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00385

SEQUENCE DESCRIPTION:

GATCTGAAAA GCGTCTNCA CTGCTTTATC TCATGATGCT TGCTTGATAA ACTTGATTIN 60
AGTTTTTCAT NNCTCAAATA GGAATACTAC CTTTGAATTC AATAAAATTC ACTGCAGGAT 120
AGACCAGTTA AA 132

SEQ ID NO:362

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00386

SEQUENCE DESCRIPTION:

5 GATCTGCCAG GNTGGGTGGT TCTACTGCTT TCTCAATTTC TAAGAACCTT TTTTTTTTCT 60
 NAAAGAGTTC TGCTGAATTA TTTGACAATA TTTGNAAGTA CCATGTTTCC TNGNGGGGTA 120
 TGCTCTGTNC TGGTTTCTGT TTTNAAATCA AATGCCTGTT TGGGAGGAGA TGAACGNATT 180
 NAGTCTATTA GATTGNN 197

10 SEQ ID NO:363

SEQUENCE LENGTH:128

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00387

15 SEQUENCE DESCRIPTION:

GATCACAGTG TCAGAGACGC GTCCTCTTTC TTGGGGAAGT TGAGGAGTGC CCTTCAGAGC 60
 CAGTAGCAGG CAGGGGTGGG TAGGCACCCT CCTTCCTGTT TTTATCTAAT AAAATGCTAA 120
 CCTGCAAA 128

20 SEQ ID NO:364

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS00388

SEQUENCE DESCRIPTION:

30 GATCCCAGGA GACACCAGGG CCAGAGTGAC CACAGCAGGG CAGGCATCAT CGTGTGTGTG 60
 TGTGTGTGGA TGTGTGTGTG TGGGTTTTNT AAAGAATTCT TGACCAATAA AAGCAAAAAC 120
 TGTCAAA 127

SEQ ID NO:365

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear

CLONE:HUMGS00389

SEQUENCE DESCRIPTION:

40 GATCTACAAA TGGGAAGCTT GTGAGTGGCC CATCTTTGTT GGCCTACGAA CTTTGGTTTG 60
 ATGCCAGTCA GGTGCCACAT GAGAACCTTT GCTGAGATGC AAATAAAGTA AGAGAATGTT 120
 TTCCTGAAA 129

SEQ ID NO:366

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS00390

SEQUENCE DESCRIPTION:

50 GATCAGCTAT TAAATTTATA TAAACATAG GCATGTTTGT ACTAATGAAA CGTACTGTCA 60
 ACCTCTATCA CATTGTAAAA TTAACACTTT TGGTGGTAAC TCAATAAAAT TGAGAAAAAT 120

GGAAA

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5 SEQ ID NO:367
 SEQUENCE LENGTH:246
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00391

10 SEQUENCE DESCRIPTION:
 GATCTTTTAA ATTATAATTT TGTGTATTT GTTCCTAGG AGCAAGTGT CCTGCTGCCA 60
 GTTCTTTCT CTTAGGCGT GGTGAGAAA AAGCAGAAAC TTACATAAA GCTGTATTC 120
 TTAATCATCT TTAATTGAA ACTTAAGNAA ATGAATTAT TCTGTNATAT TTATGTAAC 180
 15 NATTTCCCTGG NAGTNATATC TACTAGTNTT GNTTGATAAT AATAAAATTN GGCTATACCT 240
 TGNAAA 246

20 SEQ ID NO:368
 SEQUENCE LENGTH:132
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00392

25 SEQUENCE DESCRIPTION:
 GATCTAAAAT TTATTGTGGT GATGTTTGCA TAACAGTGCA AATATACTGA AAACCACTGA 60
 ATTTTACACT TTAAATCAGT GGCTTCTGTG GTATGTTATC AATATTTCTC AATAAAACTT 120
 CAAAAAATA AA 132

30 SEQ ID NO:369
 SEQUENCE LENGTH:131
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00393

35 SEQUENCE DESCRIPTION:
 GATCTGGTAT TAGGAAATTA CTTTCACAGT AAATATCAAA GAAAAAAGAT TAAGGGTCTC 60
 TTTGCCATGC TTTTCATCAT ATGCACCAAA TGTAAATTTT GTACAATAAA ATTTTATTC 120
 CTAAGTAGAA A 131

40 SEQ ID NO:370
 SEQUENCE LENGTH:123
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00394

45 SEQUENCE DESCRIPTION:
 GATCTGAAAA AGAACACTGT GCGAGATTGT ATTCCTGCTT ATCCTTTCCA AGTTAGTAGG 60
 CAGATTGGAA CTATAGAATT TATCCGTGAT AATAATAAAG TCCGCATAAC TTTTGTCTCG 120
 AAA 123

50 SEQ ID NO:371

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SEQUENCE LENGTH:123
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00395
 SEQUENCE DESCRIPTION:
 GATCTAAAGA GAAACTGTAG ATTGTTTTCC TGACAGCAA AGACTAATGT GACAAAATGA 60
 AGTCATTGTA AAGAAGCGAT GCAACTTGTC AAATATTAA TAAAGAATTA TGGAAAGCTGG 120
 AAA 123

SEQ ID NO:372
 SEQUENCE LENGTH:124
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00396
 SEQUENCE DESCRIPTION:
 GATCACAAC GNAAGATAAC AAGAGATTTA AGTTTAAAGG GCATTAAATC AGGAGGAAAG 60
 GTTTGGAAAA CTAACCTCAGG TGTATTNTT GTTTAAGCAG AAATAAAGTT TAATTTTNC 120
 TTGN 124

SEQ ID NO:373
 SEQUENCE LENGTH:122
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00397
 SEQUENCE DESCRIPTION:
 GATCTGTGTT AGAATGAGTG CTTTCCCTTC CTAATGATGT GATTGTGGAT TAGGAATTCG 60
 TGACCGAGTG ATTTTGGCC AGTGTTGGG TTTAAATTC TATTAATTT TGTAGTTTGG 120
 GN 122

SEQ ID NO:374
 SEQUENCE LENGTH:121
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00398
 SEQUENCE DESCRIPTION:
 GATCGCCGCC CTGCTGGCCA CCTGCGNTGG NGCTGGCNCT CGTGGTCGTC GCGCTGAGAA 60
 AGTTTCTCC CTCCTGAAGC GAATAAAGGG GCCGCNGCCG GCCGCGGCGC GACTCGGCAA 120
 A 121

SEQ ID NO:375
 SEQUENCE LENGTH:120
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00399
 SEQUENCE DESCRIPTION:

GATCAGGCCC GGTGCCTGCA GACCTGGTGC TCCCTCGGGC AGGGCTGGGT GCCGCACCGC 60
CTGCTGGCTT TTCTGGCAGC TCCTCTGTAT CAGAACCAAT AAAGTGCACT TGTTCCTCGGN 120

5 SEQ ID NO:376
SEQUENCE LENGTH:119
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00400

10 SEQUENCE DESCRIPTION:
GATCAGGCAG TCCTTNAGGA TAGACAGATA TACACACCAC ACACACACAC CACATACACC 60
ACACACACAC GTCCCCATCC ACTNACCCAC ACACTACACA GNCTGNTNCC TTATAGCTN 119

15 SEQ ID NO:377
SEQUENCE LENGTH:225
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00401
20 SEQUENCE DESCRIPTION:
GATCTNATTT GTAACCCACT GAGAGGACAG AGAGAAATAA GTGCCCTCTC CCACCCTCTN 60
CCTACTGGTC TCTCTATGCC TCTCTACAGT CTCGTCTCTT NTACCCTGGC CCCTCTCCCT 120
TGGGCTGTGA TGAAAAATTG CTGACTGTAG CTTTGGGAG TTTAGCTCTG AGAACCGTAG 180
25 ATGGATTNCA GTTCTGGGAA AATAAAACCC GTTGATTACT NNAAA 225

SEQ ID NO:378
SEQUENCE LENGTH:125
SEQUENCE TYPE:nucleic acid
30 TOPOLOGY:linear
CLONE:HUMGS00402
SEQUENCE DESCRIPTION:
GATCTTAATA TATTGAAAA AAACCTTCATT CTCGTGAGTC ATTTAAATGT GTACAATGTA 60
35 CACACTGGTA CTTAGAGTTT CNGTTTGATT CTTTTTAAAT AAACACTCTT TTGATTTAAA 120
GCAAA 125

SEQ ID NO:379
SEQUENCE LENGTH:147
40 SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00403
SEQUENCE DESCRIPTION:
45 GATCTCAGTT CTGCGTTTAT TGTAAGTTGA TAAAAACATC TGGAAGAAAA TAACTAAAC 60
TGTTTGATC TTTGTATGTA TTTATTACTT GATGTAATAA AGCTTATTTT CATTAAACAAT 120
TTGTATTAAA ATNTGGGTTT CTTGAAA 147

50 SEQ ID NO:380
SEQUENCE LENGTH:116

55

SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00404
 SEQUENCE DESCRIPTION:
 GATCACCTTT TCAGAAATTT AGATGTGAAC ACCAAAAGAA GCATTTTCTC AACAAAAATT 60
 AATAGCTGGT TCTATTTTTT TTAACCTAG AAAAAATAAA GTTGATTTTT TTCAA 116

SEQ ID NO:381
 SEQUENCE LENGTH:119
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00405
 SEQUENCE DESCRIPTION:
 GATCAATAGG GAGAGAAAAT CCACATTCTT GGGCTGAACG CGGGCCTCTG AACTGCTTA 60
 CACTGCCTC TGACCTGTA GTACAGCAAT AACCGTCTAA TAAAGAGCCT ACCCCCAA 119

SEQ ID NO:382
 SEQUENCE LENGTH:115
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00406
 SEQUENCE DESCRIPTION:
 GATCTTTATT ATGGAAANCA TTTCAAGTTT ACTCCTTCTG TTTTAAGTTT TGTAGCAGTG 60
 TACCCACGCT GGTATTACN NCCNAAATAA TCTGTNAGTG AAAGTTGCCA TTATN 115

SEQ ID NO:383
 SEQUENCE LENGTH:115
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00407
 SEQUENCE DESCRIPTION:
 GATCGANCTG CGCAANTGNG NAAGCTGCAG AGGACATCGC GTACCANCTC TCACGCTCTC 60
 GGAACATCAC CTACCTGCCA GCGGGGCAGT CCGTGCTCCT CCAGCTGCCC CAGTN 115

SEQ ID NO:384
 SEQUENCE LENGTH:113
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00408
 SEQUENCE DESCRIPTION:
 GATCTCTCAA AAAACAAAGA ATTACATGAG TTAGTACATG AAAAAATTAT GGGAAACTAC 60
 ATGAAATATA CTGTTACGTT CAATAAACAT TAGCTTCTGT ATATAATANT AAA 113

SEQ ID NO:385
 SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00409

SEQUENCE DESCRIPTION:

GATCTCTTCC CCCAACTTCC TAACACTTAT TAATTATGA AACTGTTTT CTCAGCGCAG 60
TTTTGTTTTG TGTGTCCATT GGATTACAAA CTTTATTAAA AAATATAAAA CACAAA 116

SEQ ID NO:386

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00410

SEQUENCE DESCRIPTION:

GATCTCTCTC TTCTCGCGCG CGCACTCTCT CTTCAACACT CCCCTGCGTA CCCCggTTCT 60
AGCAAAACACC AATTGATTGA CTGAGAATCT GATAAAGCAA CAAAAGATT GTCCCAA 118

SEQ ID NO:387

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00411

SEQUENCE DESCRIPTION:

GATCTATAAA AAGTCAGCAA CTGATGTGTT TGAAAAGCAT CCTTGCTTNT ATATCCTAAT 60
GTTTGGATGT GTCTTTNCTA AAGTCTCACA AAAATTAGTG GTAGCTCACA TGACCAAAAG 120
TGAACATAT CTNCAAGACA CTGTCTNNGG GGGGCCAGGT CTTTTGTTT TAGGNCCAGT 180
ACTNNATAA TTTNTAGAC GGATATGGTT GTCCTATGGA TGGCAATGGG TGNTTNTCC 240
ATTGNN 247

SEQ ID NO:388

SEQUENCE LENGTH:112

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00412

SEQUENCE DESCRIPTION:

GATCCTAGGA AGAGAGAACA GAGTGGCTCA CAAGCCCCAA CACAGTNAGC AGCAGATGAC 60
AGGCACNCTN AGACCACACT NTAGGCCACC CATGGGNCCA AAAGGGAACA GN 112

SEQ ID NO:389

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00413

SEQUENCE DESCRIPTION:

GATCACCACN TAAGTCAGAA AAATGTATT TTAATGTTT CTTGAAGTGC CTTTGAACA 60
TTTTTAAACA GCGGATTAA ATAATGCATA AANTAAATTG CCATGNTCAA A 111

EP 0 679 716 A1

SEQ ID NO:390
SEQUENCE LENGTH:109
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00414
SEQUENCE DESCRIPTION:
GATCACCTTA GTTTGATTCT ATTTTITAGC TTGCAAAAAG TGACTTATAT TCCAAAGAAA 60
TTAAATGTT GAAATCCAAA TCCTAGAAAT AAAATGAGTT AACTTCAAA 109

SEQ ID NO:391
SEQUENCE LENGTH:111
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00415
SEQUENCE DESCRIPTION:
GATCGTNACG CTCGCATCTA TAGATAACGG CTCTCCAGAC CTGAGCTTTC CGCGTCANAA 60
TGTAAGAAATN GTTTTCTCTG CAGAGAATAA AAGGACCACG TGNAATACTT N 111

SEQ ID NO:392
SEQUENCE LENGTH:109
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00416
SEQUENCE DESCRIPTION:
GATCTTATTG AAGGACATCT TACAGCTTCC CAATGAGAGG CCAGGAAGTG TGAACATACT 60
GATAGAAAAA GACTATATTT TATCCCTCAT AAAATGTTTT AAATGTAAA 109

SEQ ID NO:393
SEQUENCE LENGTH:116
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00417
SEQUENCE DESCRIPTION:
GATCACTGAG TGTACAGAAG AGAGAAATTC AAACAAAATA TTGCTGTTCT TCAGTTTTGT 60
TTGTGGAATT TAAATNACT CAAATTTAAA ATAAATNACT GGACTGTGGA AATAAA 116

SEQ ID NO:394
SEQUENCE LENGTH:115
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00418
SEQUENCE DESCRIPTION:
GATCTCAAGA GTTCACCTGG CTNACAGAAA GAAGATGCCA GATGACACTT AAGACCTACT 60
TGTGATATTT AAATGATGCA ATAAAGACC TATTGATTG GACCTTCTTC TTAATA 115

5 SEQ ID NO:395
 SEQUENCE LENGTH:114
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00419
 SEQUENCE DESCRIPTION:
 10 GATCATTCTG AACTGTACAT ATTTATGTNG CGAGAGGCAA AGGGCAAGTT TTGGATTTTC 60
 CTCTCTCCAA GTTTGTTTT AAACGACAAA TAAAAAAGA ACATTTTAAA TAAA 114

15 SEQ ID NO:396
 SEQUENCE LENGTH:106
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00420
 SEQUENCE DESCRIPTION:
 20 GATCTGAATC TNTGACTTAT TGATTATGGA ACCTGTCAAG TAGTTTTNAA CTCTCCCAGT 60
 GAGGATAATT AAACATGCTC AGCCTGAGCC ACCTCTAAGT NTCAAA 106

25 SEQ ID NO:397
 SEQUENCE LENGTH:107
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00421
 SEQUENCE DESCRIPTION:
 30 GATCGTTCTT CATGGGGGTA AGAAAAGCTG GTCTGGAGTT GCTGAATGTT GCATTAATTG 60
 TGCTGTTTGC TTGTAGTTGA ATAAAAATAG AAACCTGAAT GAAGAAA 107

35 SEQ ID NO:398
 SEQUENCE LENGTH:112
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00422
 SEQUENCE DESCRIPTION:
 40 GATCCCCCTCA AAAGGCAGGA NTGCTGCCCT CTNCCATGGT GCCCGTNCCT CTTTGCTGTN 60
 TATGTNAACC ACCCATGTAA GGAATAAAC CTGGCACTAG GTCTTAAATA AA 112

45 SEQ ID NO:399
 SEQUENCE LENGTH:105
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00423
 SEQUENCE DESCRIPTION:
 50 GATCANCTCT AAGGTGCAAC TNCCTCCACA TACTGTACAT ACCTGTNACC ACTCTTGGAA 60
 GTCCTGCAGT CTTTAATCAT NCTGTTTAAAN CTGTTGTGGC ACAAN 105

55

5 SEQ ID NO:400
 SEQUENCE LENGTH:104
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00424
 SEQUENCE DESCRIPTION:
 10 GATCTGGAAC TTGAAGATGC CATTACATACA GCCACTTAAC CTAAAGGGAA AGCTTTGAAG 60
 GGCAAATGAC AGAGGGTAAC ATAGGAGGTN GGATNCTNAA TNNN 104

15 SEQ ID NO:401
 SEQUENCE LENGTH:104
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00425
 SEQUENCE DESCRIPTION:
 20 GATCTTTGAT ATATCATAGT CATTAAAAGA CNTTTTCGTA TTTGTATTGA TAATGTATTA 60
 AAAGTNGTTT GTNCTTAATA AAAGACTTCT TTAANCACT NAAA 104

25 SEQ ID NO:402
 SEQUENCE LENGTH:109
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00426
 SEQUENCE DESCRIPTION:
 30 GATCCCCGGC CTCAGTCCCT ACTCTGCTTT GGGATAGTGT GAGCTTCATT TTGTACACGT 60
 GTGACTTCGT CCAGTTACAA ACCCAATAAA CTCTGTAGAG TGGAACAAA 109

35 SEQ ID NO:403
 SEQUENCE LENGTH:110
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00427
 SEQUENCE DESCRIPTION:
 40 GATCACCTGC AGCTGGCCAC ACCACAGGCC CCCGNTGCCT GCAGCACTAC TCNGTNCCTN 60
 AAACACCTGG CCTGCTAGGA GGCTCCAATA AAGCTAACCC GGACCAGAAA 110

45 SEQ ID NO:404
 SEQUENCE LENGTH:157
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00428
 SEQUENCE DESCRIPTION:
 50 GATCCTCAGA ACTTCTCTGG GACAATTCA GTTCTAATAA TGTCTTAAA TTTTATTTC 60
 AGCTCCTGTT CCTTGAAAAA TNTCCATTGT ATGTGCATTT TTAAATGAT GTCTGTACAT 120

55

AAAGGCAGTT CTGAAATAAA GAAAATTTTA AAATAAA

157

SEQ ID NO:405

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00429

SEQUENCE DESCRIPTION:

GATCAGCAAC ATTTGCTGAG CCTGTTTTN AAGCTAATGT GTATTCTNAC TAATNTNCCT 60
 ATCAAGAAATG GATTGTGAAT ATATNCTGTC TATTCTAAT GTN 103

SEQ ID NO:406

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00430

SEQUENCE DESCRIPTION:

GATCTGTAAG CACAGTCTTA TTTNCTTTTG TTGTCCAGAA TACTTATAAT TCTTGAGCCT 60
 CCCAGAAATT GGAAGCTAAA TAAAGCAACT CAAGTTTCCT TTAA 105

SEQ ID NO:407

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00431

SEQUENCE DESCRIPTION:

GATCAGCATC ATTGGAACAT GGGGACGAGT GACGGCAGGA GGACCACGAG GAAATACCCCT 60
 CAAACTAAC TTGTTTACAA CAAAATAAAG TATTCACCTAC CAAA 104

SEQ ID NO:408

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00433

SEQUENCE DESCRIPTION:

GATCTATCAC TCTGTCNCTT GTAGCTCCCA GCCGAGGACG TCGGATGTAA TCGTCCTTNC 60
 TGCTTTGCCA CCCCATTTCC GTCAATAAAG TGGTTTGAAC CAAA 105

SEQ ID NO:409

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00434

SEQUENCE DESCRIPTION:

GATCAAACCT TTCTGGCCTG TTATGATTCT NAACATTTGA CTTGAACCAC AAGTGAATCT 60

TTCTCCTGGT GACTCAAATA AAAGTATAAT TTNACCTGC GGAAA 105

SEQ ID NO:410

SEQUENCE LENGTH:101

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00435

SEQUENCE DESCRIPTION:

GATCAACACA AAGCACAATG NATTACNCGN AATTCAGTAT TTTCAAATTT ACATATTTAA 60
AGTCATGCAA GCTGTAACCT CCCNGTCAAA ATTACTNGCT N 101

SEQ ID NO:411

SEQUENCE LENGTH:100

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00436

SEQUENCE DESCRIPTION:

GATCATAAAG NNCTATCAAG GAGTTCTATC AAGGCATCCA TGTCAGTGGT GCTATGCTGG 60
TTACAACTTG AGATTTTGA AATAAAAAAT TTGTCATAAA 100

SEQ ID NO:412

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00437

SEQUENCE DESCRIPTION:

GATCAACAGG CTTATTAGAA GAATGAACTA AGGTGTCTAC CATGATTATN TTTCTAAGCT 60
GGTTGGTTAA TAAACAGTAC CTGCTCTCAA ATTGAAAAAG AAA 103

SEQ ID NO:413

SEQUENCE LENGTH:99

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00438

SEQUENCE DESCRIPTION:

GATCTTGTCG TGTGTCAAAG TAACAGACTA GAACCTTCTT TCAAGTACCT GAATTGAAAT 60
NAAACTCATT TTGAATAATA AAAACTCTAG AAACTCAAA 99

SEQ ID NO:414

SEQUENCE LENGTH:99

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00439

SEQUENCE DESCRIPTION:

GATCTGTAAT AGCATATTGT AGATGCACTT TGCAGCAGTT GGAAGAGAAA GTGTTGTGTG 60

ATTTGATTGA AATAAACTA AATGTGTTGT CCTCCTAAA 99

5 SEQ ID NO:415
SEQUENCE LENGTH:96
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00440
10 SEQUENCE DESCRIPTION:
GATCCCTGTG CCAGGAGCCA ACCTGGTCTT CCCGAGGGTC AGTGCCCCAG TGAAGACAGA 60
AGCGAGAGAA TAAAGTTCCC TGTAAGTCCT CTGTCN 96

15 SEQ ID NO:416
SEQUENCE LENGTH:97
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00441
20 SEQUENCE DESCRIPTION:
GATCCTCCCA TCCGTGTTGT GAGCACAGGC ATTTGTGTNT GGNCTGTCCT CCCTGTTGAT 60
TGGTCTGGCA TTTCCGGTAT TAAAATGATA ANATAAA 97

25 SEQ ID NO:417
SEQUENCE LENGTH:93
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00442
30 SEQUENCE DESCRIPTION:
GATCTGCAT ATCTCAAGGA CCCTAAAGTT TGTAACATCA GATATCGGGA ATAAATTCTA 60
TCACGTTACC ACTAATAAAC TTATTTTACA GTN 93

35 SEQ ID NO:418
SEQUENCE LENGTH:97
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00443
40 SEQUENCE DESCRIPTION:
GATCTGTATT TTGCAAATAT TTTCTTCAAT ATGTGGCTTG TCTTTTGGTT CTCTTAACAA 60
GGTCTCTTCC AGAGTATAAN CTGTAAATAT TAAGAAA 97

45 SEQ ID NO:419
SEQUENCE LENGTH:98
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00444
50 SEQUENCE DESCRIPTION:
GATCTGGACA GAATCGCCGG ACAGGTGGCA GCTGCAACAA GAAGCATTAG AACAAACCAT 60

55

GCTGGGTAA TAAATTGCCT CATTCGTAAT CCTGGAAA

98

5

SEQ ID NO:420

SEQUENCE LENGTH:100

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00445

10

SEQUENCE DESCRIPTION:

GATCTATTCT GAGTATTTT TAGAGAGTTA ATATTTATAT TTTTAGTAAT TTTCTGGTAG 60

AAGGAAATTG CACAATAAAA TNATTGGTT TGGTTTGAAA 100

15

SEQ ID NO:421

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00446

20

SEQUENCE DESCRIPTION:

GATCGTTGGC ACCATAGCCT TATGGCCAAC AGGTGGTNTG TGGTGAAAGG GGCCTGGAGT 60

TTCAATATCA ATAAACCACC TGATATCAAT AAA 93

25

SEQ ID NO:422

SEQUENCE LENGTH:94

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00447

30

SEQUENCE DESCRIPTION:

GATCTGTGTT TNCCCTGACG AATGGAATTT ATCCTCACAA ATTGGTGTTT TAAATGTNTT 60

AAGAACCTAA TTAAATAGCT GACTACAAAA CAAA 94

35

SEQ ID NO:423

SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00448

40

SEQUENCE DESCRIPTION:

GATCCCAAAC CTTACGGCCA AGTTTCTTCT AGTATGATGG AAAGTTTCTT TTTTCTTTGC 60

TCTGAATAAA ACTGAACTGT GGGTCTCTA TAAGTGGCAT TTGGGGCTTT CCCTCTTTT 120

TGTAAGCAA TGCTGCCTA GTTATTGTC CAGTAACTT TAGTGACCTT TTAAGATTG 180

GCATTGTAAA TAAACAAC TGC AAA 206

45

SEQ ID NO:424

SEQUENCE LENGTH:481

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00450

50

55

SEQUENCE DESCRIPTION:

5 GATCTCACCA CTGCACTCCA GCCTGGGCAA CAGAGCGAGA CTCTGTCTCA ACAACAACAA 60
 CAAAAAGTCC TGAACATGAT TGTGGAAGTG TGTGCTCTT TCAAGTTCTA TCACTTTTTG 120
 TTTGCAAAGT TCAAAGCTGT ATTGTTTGGT ACATATACAT GTAGGTTTGC CAAGTCTTTG 180
 TGGTGAATTG ACTCTTCTGT CATTATGTGA TGTCATTTTT TGCCTTTTA ATAGTCTTGT 240
 CAATACTTTA CCTGATGTTT TCATAGTGAC TCCTGCATAT TTTGATTAAT GTTTGCATGG 300
 TTAATATTTT TTTCAITTTAT TTTAAAGCTT ACCTGTATCA TTAATTATGA AGTCAGTTTC 360
 10 TTTGAACAGC ATATACTCAG GCCATGCTTT TTTTNATTCA TTCCTGCATA TGGCTCTCCT 420
 TAAATTGGGA ATGGTGGAAG ATGGNTTAC CATTANAAT AAATTAATG GTATTTTAA 480
 A 481

SEQ ID NO:425

15 SEQUENCE LENGTH:87

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00451

SEQUENCE DESCRIPTION:

20 GATCTGGTCC ATGAGGCTGC CCAGAGAAAG CACTGCTTCT NTATGTCTCT TGTGGTATTG 60
 GAACAATAAA CCCGTACAAC CTGCAAA 87

SEQ ID NO:426

25 SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00453

SEQUENCE DESCRIPTION:

30 GATCATACTT GAAAGTGAAC TTAAACATTG AAAATCGTA CAGTCATTTC AAGAATAAGA 60
 AAATAAAATT TTCTCTTTGT CTGAACCTGC AAA 93

SEQ ID NO:427

35 SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00454

SEQUENCE DESCRIPTION:

40 GATCCCATGT GCTCTCACAC CATGTTTTT TACAGAACTG ATGGTTGAAT CTTTGTCTC 60
 TTGAAATAAA CAGAAGAAAA TGAAA 85

SEQ ID NO:428

45 SEQUENCE LENGTH:87

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00455

SEQUENCE DESCRIPTION:

50 GATCTATTAA AGAAGTAATT GGCCTTTCTG AGCTGATTTT TCCATCTTTT GTAATTATCT 60

55

TTATTAAAAA ATTGTACTTG GATTAAA

87

SEQ ID NO:429

SEQUENCE LENGTH:91

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00456

SEQUENCE DESCRIPTION:

GATCTCATTG CATGGGAAAA AAAAAATCC TGTCTTNTTC ANAAATTGAC AATGTAAATA 60

AATTNAAATA TGGTTCCTG TTAATCTTAA A 91

SEQ ID NO:430

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00457

SEQUENCE DESCRIPTION:

GATCTGAGAA ACAGGTGTGA CAAGAGCATG AACCANAGGT GCACCTGGGG CAGTCCCTA 60

ATAAACTGG TTTGTACAGT CAAA 84

SEQ ID NO:431

SEQUENCE LENGTH:83

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00458

SEQUENCE DESCRIPTION:

GATCATGAGA GTGCCTGTCC CTTGTGAGCA CTATGAAAGT GTTAGCTGTT CTTTACCAGA 60

ATAAATGCAT TTCTATATCT TCN 83

SEQ ID NO:432

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00459

SEQUENCE DESCRIPTION:

GATCACCGAC TGAAAAATATT GTTTTACAAT AGTTCTGTGG GGCTGTTTTT TTGTATNAA 60

ACAAATAATT TAGATGGTGG TAAA 84

SEQ ID NO:433

SEQUENCE LENGTH:80

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00460

SEQUENCE DESCRIPTION:

GATCTTGATG GATTTCATA CGATTGTAAA TGNAGCTATA TTAAAGTCTA TTAAAGGAAG 60

CCCTTCTTGT TTGAGGGAGN 80

5 SEQ ID NO:434
SEQUENCE LENGTH:86
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00461

10 SEQUENCE DESCRIPTION:
GATCTATGCT TGTGTTGTTT TGTAATCCAT ATCATAGTTG CTTTCTTTAA TTGTTCCCTC 60
TGAATAAACA GTTTATTTAA GATAAA 86

15 SEQ ID NO:435
SEQUENCE LENGTH:83
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00462

20 SEQUENCE DESCRIPTION:
GATCCAGTCA CTGACTCTGT CTGGTGTTGA CAGAGGATTT ATTTAAGCTA TTATTTTAAT 60
AAAGNACTTT GTACATTTT AAA 83

25 SEQ ID NO:436
SEQUENCE LENGTH:85
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00463

30 SEQUENCE DESCRIPTION:
GATCTACATA CAAACAAATG CAACCAACTA TCCAAGTCGT TATACCAACG TAAAACCCCC 60
AATAAACCGT TGAACATGTG ACAA 85

35 SEQ ID NO:437
SEQUENCE LENGTH:86
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00464

40 SEQUENCE DESCRIPTION:
GATCTGCTTT TACTTTGTAA TTTGTAGTTC TCAAAAGACT TTTTTTTAAA AAAATAAAGN 60
CCATACTTAC ACTTAGGCTT TATAAA 86

45 SEQ ID NO:438
SEQUENCE LENGTH:83
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00465

50 SEQUENCE DESCRIPTION:
GATCATTCTG AGTGTGCGAG TGTGTGTGCA CATGTTACAA AGGCANCTGC CATGTTAATA 60

55

AAATATTCAA TTTGAAATCC AAA 83

5 SEQ ID NO:439
 SEQUENCE LENGTH:78
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00466

10 SEQUENCE DESCRIPTION:
 GATCCAACT GTCTTTTTT TGTATCTGTT ATTTAAAGCC CAGTGGATAT TTCAATNAAA 60
 AAAAAAATCT AAAGATGN 78

15 SEQ ID NO:440
 SEQUENCE LENGTH:80
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00467

20 SEQUENCE DESCRIPTION:
 GATCTGACCA CCTCTGCCCT GTCCACCAGG ATAAGTGACA CCTAGGACCC AGGAAATAAA 60
 TGCCGATGAT TTGTGTGAAA 80

25 SEQ ID NO:441
 SEQUENCE LENGTH:73
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00468

30 SEQUENCE DESCRIPTION:
 GATCTTACAG GGAGAGAGAT TGGGTGCAAT TTGCCTCTTT CTTTGAATAA AAAGCTCTTT 60
 GCTCACCTC AAA 73

35 SEQ ID NO:442
 SEQUENCE LENGTH:197
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00469

40 SEQUENCE DESCRIPTION:
 GATCAAAAGT CTACATACT AATACTCACA GCTGAGCTAT GTAGTATGCT ATGATTAAAT 60
 TTAATTATGT AACTTTTATT GTCITTGGCA TTAACAGTGT TTCAAAAAAT TTCCTGTGTA 120
 TACCCATCAG TGATTCATTC CCAAATCTNC TAGAAGCATA AGTGTCTCAA TATATTAAAA 180
 CATATTGAAT AATCAAA 197

45

50 SEQ ID NO:443
 SEQUENCE LENGTH:75
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00470

55

SEQUENCE DESCRIPTION:

GATCCAGGCG CCACGCTGGC GGTTCGTGAG TGTCGAGGCA CCACTAAATA TAGCTGTCTG 60
CCGTCCACTC ATAAA 75

5

SEQ ID NO:444

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

10

CLONE:HUMGS00471

SEQUENCE DESCRIPTION:

GATCANATTG TAAGCTTTTC TGTTNATTT CTTTAAAGAA CCTTTGAATA AAAAACATCT 60
GAAATTTTAA NAAA 74

15

SEQ ID NO:445

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

20

CLONE:HUMGS00473

SEQUENCE DESCRIPTION:

GATCTCTTTG TAGCCATCCT GTTAAATTTG TAAACAATCT AATTAAATGG CATCAGCACT 60
TTAACCAATG AAA 73

25

SEQ ID NO:446

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30

CLONE:HUMGS00474

SEQUENCE DESCRIPTION:

GATCATGTCT GAATTATGTA TGAAAATTAT TCTATGTTTT TATAATAAAA ATAATATATC 60
AGACATCGAA A 71

35

SEQ ID NO:447

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40

CLONE:HUMGS00475

SEQUENCE DESCRIPTION:

GATCTCTACC CACCCCATGC CTCTCCCNAG TCTTGGATAC TAATAAAATG ATAAGCATTC 60
TGGTTCTCN 69

45

SEQ ID NO:448

SEQUENCE LENGTH:68

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50

CLONE:HUMGS00477

55

EP 0 679 716 A1

SEQUENCE DESCRIPTION:

GATCGTAATG TAAAATTCTT TTACCATGTA CAAGAATTAT TAAAATACAG GTACTTGACC 60
ACATTCTN 68

5

SEQ ID NO:449

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

10

CLONE:HUMGS00478

SEQUENCE DESCRIPTION:

GATCGGGCCC CGGGGGCCTG AGCCTGGGAC CCCACCCNGT GTTAATGAAA AATGAGTTTT 60
GGCAGCGCCA AA 72

15

SEQ ID NO:450

SEQUENCE LENGTH:64

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

20

CLONE:HUMGS00479

SEQUENCE DESCRIPTION:

GATCCTTTTG TAATGACTTA CACTGGAAAT GCGAACATTT GCAGTAAAAA AATATATATA 60
TAAA 64

25

SEQ ID NO:451

SEQUENCE LENGTH:66

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30

CLONE:HUMGS00480

SEQUENCE DESCRIPTION:

GATCATGCAT TTAGATTTAT ATTTTNNCCA NAAAATACAA GGTATAATA AACTAAGAN 60
CTACCN 66

35

SEQ ID NO:452

SEQUENCE LENGTH:70

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40

CLONE:HUMGS00481

SEQUENCE DESCRIPTION:

GATCTCTATT GTAATCTCTA TTGGAGATTA CAATGATTAA ATCAATAAAT AACTGAAACT 60
TGAANATAAA 70

45

SEQ ID NO:453

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50

CLONE:HUMGS00482

55

SEQUENCE DESCRIPTION:

GATCACTAAT TTTGCATCAG TAAATGAAT TTTTAAAAA CCAATAAATC ATCAATTATT 60
 AGAAA 65

SEQ ID NO:454

SEQUENCE LENGTH:63

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00483

SEQUENCE DESCRIPTION:

GATCACAGTT GCGTCATTGT GTATTAAATA CTTGGAATAA ATCAAGCAGG TCTCAACGCC 60
 AAA 63

SEQ ID NO:455

SEQUENCE LENGTH:68

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00484

SEQUENCE DESCRIPTION:

GATCATTAAAT TGTAAGCGC TTTGTAAAAAT TCACATTAC AAAATAATAA AGTCAGTTCA 60
 AACCTAAA 68

SEQ ID NO:456

SEQUENCE LENGTH:63

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00485

SEQUENCE DESCRIPTION:

GATCTGTGTC TGAGTCATCT TTGTATCTTG CCTAGCACCT ATCAATAAAT ACTTCTTGAA 60
 TGN 63

SEQ ID NO:457

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00486

SEQUENCE DESCRIPTION:

GATCATGGGA ATATGCAGAA TTTCCAATGT ATTTTAAAT ACAAATAAAA TTGTAATTTA 60
 GN 62

SEQ ID NO:458

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00487

SEQUENCE DESCRIPTION:

GATCTAACAC TAACTGTATT GTTTTGTTC CATCAAATAA ACATCTTCTG TGGACCAGGA 60
AA 62

SEQ ID NO:459

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00488

SEQUENCE DESCRIPTION:

GATCTCGGCT CACTGCAATC TCTGCCTCCC GGGTTTCAAG CTTGTCCAGG NNNATCTCAA 60
A 61

SEQ ID NO:460

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00489

SEQUENCE DESCRIPTION:

GATCAACCTG AGTTTTAAAA TACCTTTAAT AAATATNAGT NGAAAAAATG TCTACTTNAA 60
A 61

SEQ ID NO:461

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00491

SEQUENCE DESCRIPTION:

GATCAAACAC CCCACCCTCA CAAAAATGGC CACGTTGCAA TAAAAATTGT GGCATATTAC 60
N 61

SEQ ID NO:462

SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00493

SEQUENCE DESCRIPTION:

GATCTTTATT TTCCCTTTGT ATTCATTTTA AGCATCTAAA TAAATTGCTG TATTGTGCTT 60
AATGTAAATA TTTGCTTTAT TACAAA 86

SEQ ID NO:463

SEQUENCE LENGTH:66

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00494

SEQUENCE DESCRIPTION:

GATCTCTACT ACTGTTGATT TTGCCCTCGG AGCAAAGTGA ATAAAGCAAC AAGATGAAAA 60
CTGAAA 66

5

SEQ ID NO:464

SEQUENCE LENGTH:70

SEQUENCE TYPE:nucleic acid

10

TOPOLOGY:linear

CLONE:HUMGS00495

SEQUENCE DESCRIPTION:

GATCAAACTA GAACTCATAT GCCATACTAG ATATGGTTGT CAATAAACTT ATGACGTGAA 60
AAAAAAGAAA 70

15

SEQ ID NO:465

SEQUENCE LENGTH:57

SEQUENCE TYPE:nucleic acid

20

TOPOLOGY:linear

CLONE:HUMGS00496

SEQUENCE DESCRIPTION:

GATCCAAAA GTGCGCGATG CGAGTAGTCA AGTCGTACTC CGCCATCTTG CCAAAGN 57

25

SEQ ID NO:466

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30

CLONE:HUMGS00497

SEQUENCE DESCRIPTION:

GATCTAAAGC TCTTTCGATT TTATACTGAT TAAATCAGTA CTGCAGTATT TGATTAACTA 60
AGAAA 65

35

SEQ ID NO:467

SEQUENCE LENGTH:55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40

CLONE:HUMGS00498

SEQUENCE DESCRIPTION:

GATCTAAGGC AAGAGTTTCA GATTTACTGT TGGAAATAGA CCCAACTCTT CATGN 55

45

SEQ ID NO:468

SEQUENCE LENGTH:56

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00500

50

SEQUENCE DESCRIPTION:

GATCATAAAT ATTAATGGNG AAAAACTGT AGTAATAAAT TTCNATATGC CAGAAA 56

55

SEQ ID NO:469
SEQUENCE LENGTH:52
SEQUENCE TYPE:nucleic acid
5 TOPOLOGY:linear
CLONE:HUMGS00503
SEQUENCE DESCRIPTION:
GATCTGTTCA GTGTCACCTCT GTACCCTCAA CATATATCCC TTGTGCGATA AA 52

10 SEQ ID NO:470
SEQUENCE LENGTH:54
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
15 CLONE:HUMGS00504
SEQUENCE DESCRIPTION:
GATCCCCGGT NGGTTTTGTG CTCAAAATAA AAAGCCTCAG TGACCCATGA GAAA 54

20 SEQ ID NO:471
SEQUENCE LENGTH:57
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00505
25 SEQUENCE DESCRIPTION:
GATCATCCGG TTATAGAGCA TAATTGCCA ATAAAGCTTT TGAAGCGGG AAAGAAA 57

30 SEQ ID NO:472
SEQUENCE LENGTH:60
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00506
SEQUENCE DESCRIPTION:
35 GATCCAGTGT TGGNATTCTT TGGTGTAAT AAACGTTTGG TTTATTAT NCAGGTAAA 60

40 SEQ ID NO:473
SEQUENCE LENGTH:51
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00507
SEQUENCE DESCRIPTION:
45 GATCTCATTT ATTGCCACAG ATGCACAAAA TAAATAACCC AAAATCACAA A 51

50 SEQ ID NO:474
SEQUENCE LENGTH:80
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
55

CLONE:HUMGS00510

SEQUENCE DESCRIPTION:

5 GATCATATAT TTTGACAAAA TATATTTATA ACTACGTATT AAAAGAAAAA AATAAAATGA 60
 GTCATTATTT TAAAGGTAAA 80

SEQ ID NO:475

SEQUENCE LENGTH:77

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00511

SEQUENCE DESCRIPTION:

15 GATCCAAAAC TTTAATGTTG CACNTGTATT CCAAATAAAG GGTAAAAACA GAACCAAAGT 60
 TATAACTCCA ACACAAA 77

SEQ ID NO:476

SEQUENCE LENGTH:669

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00532

SEQUENCE DESCRIPTION:

25 GATCAAAAAG AAGGCTTAGA ATTCTGCAGT TAAGCTGAGG TTTAAACTAA AAANTGTTTC 60
 CTTGGGTCAG TGGTTTTNAG GTCCAGTAGC TAGGCTTTTT TCTTTTGTCC TTCCTGTTGG 120
 AATGAAAACA TTTGATTTT CCTTCATCTG TGAAGGTGC CATAGACACA GGTTTATAGT 180
 TTTAACTTAC AGTATTGTTT GAAATTTACC TGTTTTTNTT GTCAAACTG AGCACTCCTC 240
 CTGCTGAAGT TTCTTATTTA ATTCCAGAGT ACTGTCCTCT ACTCTAAGGC ATTACTTTTA 300
 30 AGTGTATTAT GAAGGCAGTT TTCAAAGGAT ATGACCAGTT GGGGGTAATT CAAATTAAAA 360
 AGGAAAAGAT TTGTTTGGGA AGTAACTGGG TGTCTCTAAG AGGGAATTTT TAGGATGTCC 420
 AGTTTGGGAG GCTCTTTCCC CCTCAAAAT GAGANGCTCC TTGGTTAATT CAGAGCTCCC 480
 ANGACTAGGC CCTGGGCTAA CCAANCATTN GGGNGGCCAA AGGTTAGGGA ACCATTNGNT 540
 35 ACCAAGCTTT TGNANCAGGG GGNTTTNTNC CATTGGGTA ATAGGGCCCT TTTCANGCCT 600
 TTANGGGTAN GCTTTTTTAN CCCNGAAACC NTTNNTNNNT TTGNAATTAA ACCGGAACCT 660
 TTTGNCAAA 669

SEQ ID NO:477

SEQUENCE LENGTH:651

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00533

SEQUENCE DESCRIPTION:

45 GATCAACCTG GAGCTCTACG CCTCCTACGT TTACCTGTCC ATGTCTTACT ACTTTNACCG 60
 CGATGATGTG GCTTTNAAGA ACTTTGCCAA ATACTTTCTT CACCAATCTC ATGAGGAGAG 120
 GGAACATGCT GAGAACTGA TGAAGCTGCA GAACCAACGA GGTGGCCGAA TCTTCCTTCA 180
 GGATATCAAG AAACCAGACT GTGATGACTG GGAGAGCGGG CTGAATGCAA TGGAGTGTGC 240
 50 ATTACATTTG GAAAAAATG TGAATCAGTC ACTACTGGAA CTGCACAAAC TGGCCACTGA 300
 CAAAAATGAC CNCCATTTGT GTGACTTCAT TGAGACACAT TACCTGAATG AGCAGGTGAA 360

55

AGCCATCAAA GAATTGGGTG ACCACGTGAC CAACTTGC GC AAGATGGGAG CGCCCGANTC 420
 TGGCTTNGGC GGAATATCTC TTGACAAGC ACACNTGGG AGACAGTGNT AATGGAAGCT 480
 5 TAAGCCTTGG GGNTAATTN CCCCATANGC NGTTGGGTG ACTTCNCTGG TCANCAGGGC 540
 AGTTCANTGA ATGTTNGGG TTNCCTTTAC CTTTNCNTTA GGTNGTCCNA AACAAATCCNT 600
 NAAAGTCTTT GNTTTGNACC NTTCCGNAA TAANGGATTN GGGCCCGAA A 651

SEQ ID NO:478
 10 SEQUENCE LENGTH:617
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00534

SEQUENCE DESCRIPTION:

15 GATCAAGAAA GTGGGGGGAA AAAAAACAAA CGTTAAAACC TCAATCCTCA GTAGGAAGGT 60
 AGATTACATT AGGTGAAATT ATAGGTAATC TATGTATGTN CTAATGGGGT TGGAAAGAAC 120
 CTTACAGAGC ATATTACCTG ATAACTGGA GTGGGTTTGG GAGAACAAAC TAATAGGATT 180
 20 ATNGTNTCTC CTAGTTGGTA CCTGGGAGCA ATTGACATGC CCCCTTCAGA ACCTTAACTG 240
 TTAGTAGCAG TGGCTGTAAC AACACAAACC AGTGACCAGA GATAACAGCT TTTNGGCCAA 300
 GCTGGCCTGA CGGTATGGCT GCAGGANGTG ACTGAGCAGT AGCGGTACTC AGCCAGACCA 360
 AGACGGAGAG GGGAGAGTCC ACAGCTTTCT GGAGCTAAGG CATTCTGGTG GTAGAAAAGT 420
 GTGCCNAAG CCTTCATNGG CGGGTTATAN GGTCTNAAGA TAAGTCTCCT CTGTNTGGG 480
 25 ATNCCATACT NTGCTAAATA ACCNNGGTAT TANCCGGGTT TTCNTGTAA CNGCCTCTNG 540
 GGAGGAANTG ACTNNGAAG NTGGCACAGG TNTTAAGCN TNAATGGAAA GGGNNAATC 600
 CTNCTCAAAAN TAGAACN 617

SEQ ID NO:479
 30 SEQUENCE LENGTH:569
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00535

SEQUENCE DESCRIPTION:

35 GATCTGTGAG CTGCTTAAAT AATTGAACT TCTCTGTCAT TGATGTTGCA TTTCCAAGGA 60
 GATAATCTCC TTCTTGGTGC CTAATTTTCT AGATGATAAT AGGCTAGTTT TGATTTCTTG 120
 CTCATTTTCA GAATAACTTT CCAGGAAGAG ATGGCATTTA GAACTTCAGC TTTGGTGCTC 180
 40 AGGTATAAAG CCAATTAAGG TACAATTGTA CCATAAAGGG AACAATCTGT TTCTGATTGC 240
 ACAGTTTCTA ATTTTAAAA CTGNNGTGGT TTGCATTTC TAAAAGGCAA AGTTTACAGA 300
 NCCATAAACA TTCTCAATTT TCTTTATGCT AGACATATAA ATTTATTTT CCAAAGTGA 360
 ATAGGATTG GGGTAAAAAG NTTGTCTCAG GTNCTCTNC CCANTTTGCC AATGGGGNAA 420
 45 AAAAAAGGCT TAATTTTTC CATNNTACT TNAATTTTC TAAAACCNT GGTAAACCCC 480
 CATTGGNACC CCNATTTTC CANCTTTAAG GGTCTNGCAT NGGCNGGCTT TTTNAATTNN 540
 CCCTGGGGGG GTTTTNCCTG GGAGGGCCN 569

SEQ ID NO:480
 50 SEQUENCE LENGTH:556
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS00536

SEQUENCE DESCRIPTION:

5 GATCCTGAGC NTGGTGCTGT GCTGTGGCAT CCGGAACAGC TCCGTGTACT GAGGCCCCGC 60
 AGCTCTGGCC ACAGGGACCT CTGCAGTGCC CCCTAAGTGA CCCGGACACT TCCGAGGGGG 120
 CCATCACC GC CTGNTATAT AACGTTTCCG GTATTACTCT GCTACACGTA GCCTTTTAC 180
 TTTTGGGGTT TTGTTTTGT TCTGAACTTT CCTGTTACCT TTTCAGGGCT GACGTCACAT 240
 GTAGGTGGCG TGTATGAGTG GAGACGGGCC TGGGTCTTGG GGA CTNGAGG GCAAGGGGTC 300
 10 CTCTGCCCT GGGGTCCCAG GGTGCTCTGC CTGCTCAGCC AGGCCTNTCC TGGGAGCCAA 360
 TNGNCCAAGA GACTCAGCTT GGNCAAAANTT GGGGGGGNTN TGTNCAACCA NGCCCGCNNN 420
 TCCTNTTNGG GTTGAAGAAGT TTAACCTTGT TTCCCTTTCT NGCCCCGGTT TTGGAGAACC 480
 CGANTTTTTT GGGGNAATTT TTTGCTTTNA ATNAACTTNT NCCTTTTTTA AAAANGTGGG 540
 15 TTAAAACTN TNAATN 556

SEQ ID NO:481

SEQUENCE LENGTH:551

SEQUENCE TYPE:nucleic acid

20 TOPOLOGY:linear

CLONE:HUMGS00537

SEQUENCE DESCRIPTION:

25 GATCTACTGT CTTTGTTC AA AGGTCAAATA AAAACCTAGT CTCCTTTTAT TCTACTTTCT 60
 ATTCTTAGCT AGAATGAAAC TCAGCATATA TACACTTCTG GACATAATAA TATTGAATAG 120
 TAATTACCTT TACTAGATGA AAGAAATTTT CATTACAAAC TTAAATCATG TAAAACTCAA 180
 CAACTCAGAT TCCTGGACCT GGTGCTCTGG NTGGGTCCAA GGTGATTTTA CAGAAGNAAA 240
 AANCAACTNA AGCATTCTGG TGGCAACATA GAGATTGTAG GCTGCTTCTA AGGAAGTNAT 300
 TAACAATTNG GAAATTCNA AGTAGGATGA GAGTTAGTAA CTGGATACGA GTGAAGTTTA 360
 30 TATCCAAGTT CAGNCTCAA GGCATNATTA TGATTNGCTT CTTCCCATGT CTNCCATGGN 420
 CCTGCTTCTC AAAGTTTTTC TNATCNATCA CACTGCTGCC TAACTGCTCT GAGNATGCAT 480
 GNGGTNTTCA ATTCAGCGTN NTNTNAATCN GGNNTANCTN TGGATTGGGA TGGGGATACG 540
 GACNTTAAGG N 551

35 SEQ ID NO:482

SEQUENCE LENGTH:520

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS00538

SEQUENCE DESCRIPTION:

45 GATCTTAATT TTGAAATTGA CATGAAAGTG TCATATCAGT AATCTGTGAA CCACCAGTCC 60
 TTGGTACCTA TCAGAGGGTC AAAAATCAGC ATTAATATA ACCAAAAAAC TTTATAGTGA 120
 CTGATTCAA TTTGAATACT GGTTTTAGCT AATGTAGTAG TAATGAACTG GTTTGGGGGT 180
 AAGATTTTCC TGGTATCTTA TTGCTGTAGA AATTTTCCTT TAACAGTTAC AGTGTTTTCT 240
 TCCAAATCCT TCACTTCTCT GTCCTGGCTT GTAAAGAAAA CATCTGAGGA CTGAGGGGTC 300
 ATATTTGAAT TGCTCTNTAT AATACCATAG ACTACTCATT GCTTAGACTN TACTAAGCTA 360
 GAAATCACA GAGCATAAGC NACTCTNAAA ATTNATATNA TGNGAATGTA AAAGGTACCT 420
 50 GNCTGCAAAT ATCTNGANCN TCACTTTGGC TCAAGTNTCN NGTTAACCTG TNNNNTAATA 480
 CNGNNATGTG AATTNGGCCA CCAGGTCCAT GNTTGGCAAA 520

55

SEQ ID NO:483

SEQUENCE LENGTH:517

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00539

SEQUENCE DESCRIPTION:

GATCATGCTT TTNGTGCCTG TCACCAGGTC TCCCAAGTGC ACTCATCCAG GTCAGTGCTC 60
 AGATGTGTTT AAGGAGACCC TATATTCAGG GAAGTTGCGT GAACACTGCA GTGGGGAGAA 120
 TTGAGAATAG TCAGGCCTAT CAGTCTCACA GAATCACCCC TCTACCTTTG ATATTCCACT 180
 TAGCTGTAGA GTCCATCTGT TTGTCCATCT GCTGAAATGA GAAAAGAAAA ATTTATGCAC 240
 TGATTAAAA CAAACCAAAA AAAAAGAAAA AAACAAAAAA AAAATCCNT CCTTTCTNGC 300
 TGACCAAAAN TGTGCAGTTA ATNCTGGGNG CTTGAAANTG CAGTGGTGAA TNTGGACCA 360
 GCCTGTCTGT ATATCTGGTA GCTCTTTTCT GGCTTNGTTT TTNCTTACCA GTATTCNGGC 420
 CTAACGTTTT GCTTCGGGNN TGGTAATATN NCCTNGNAAG NACANCNGTG GGTGTGGAA 480
 ATGGGTNGG CAAAANGGAA NTTCCNGGGG TNTTGGN 517

SEQ ID NO:484

SEQUENCE LENGTH:515

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00540

SEQUENCE DESCRIPTION:

GATCTTCTGG CTCTACCACC ACAAGATATT ATCCTTGCACT CTNATGTGTT CTTTGAACCA 60
 GAAGATTTTA AAGACATTTT GGCTACAATA TATTTNTTAA TGCACAAGAA TCCCAAGGTC 120
 CAATTGTGGT CTACTTATCA AGTTAGGAGT GCTGACTGGT CACTTGAAGC TTTACTCTAC 180
 AAATGGGATA TGAATGTGT CCACANNNT CTTGAGTCTT TTGATGCAGA CAAAGAAGAT 240
 ATAGCAGAAT CTACCNTTCC AGGAAGACAT ACAGTTGAAA TGCTGGTCAT TTCCTTTGCA 300
 AAGNACAGTC TCTGAATNAT ACCNACAACC NGTNTGGGA CAGTATCAAT ACTGATGAGC 360
 AACCNGGCAC ACAAATATG AGCAGACCAC TTCAGCTTGA GGAATGCAGT GGGTCTGAGG 420
 ATGGTCAAGT CTGTTTGCCT TAGATTTTGN TGTCACTTGG CCACACTTGA AANCTNNTTT 480
 GGAACAAAAN TTAAATTCTG GGTTCCTAAG GTAAA 515

SEQ ID NO:485

SEQUENCE LENGTH:510

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00541

SEQUENCE DESCRIPTION:

GATCTGCAGC TCTCAGAGGA CGACTGAGGC AGCCCATCTG GGGGGCCTGT AGGGGCTGCC 60
 GGGCTGGTGG CCAGTNTTTC CACCTCCCTG GCAGTCAGGC CTAGAGGCTG GCGTCTGTGC 120
 AGTTGGGGGA GGCAGTAGAC ACGGGACAGG CTTTATNATT TATTTTNNAG CATGAAAGAC 180
 CAAACGTATC GAGAGCTGGG CTGGGCTGGG CTGGTGTGGC TGCTGAAGCC CCACAGCTGT 240
 GGGCTGCTGA AGTCAGCTCC GCGGGGGAGC TGCCCTGACG TCAGCAGACC GAGACCAGTC 300
 CCAGTTCAG GGGGAGGCCT GCAGGCNCTG GCCCTTCCAC CACCTNTGCC CTNCGTCTGC 360

AGANCTTGGT NCATCTGCAC CAGGCTCTGC TTNACTCINN NANAGTNTTT GGAAATTTGT 420
 TCTNNTCCTN TGAAAGTCAC ATTTGNTTNT AAAAATTTTG TGGNTTGAAT CGGAAACGGG 480
 AAGNAATAAA GCGGTGGGNG GNAGGGCAAA 510

SEQ ID NO:486

SEQUENCE LENGTH:507

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00542

SEQUENCE DESCRIPTION:

GATCCTTACA TCTGCCCATT CTGTGGTTAG TCAATGGCTT GCAATAAATG TGCAAACTGC 60
 ATCTATAGGA AACATTTTGG TGATTACGGA ATACTTTAGT TGATTGCTGA AAATATTGAA 120
 AGGTCTTCAT TTTACAGTGA TGAGTACATA TGCATGTTTC GGGGACTTGG CCCTTCTGAT 180
 GAGGGGCCCT CGGTACTCTG GATAACGAAG CTTGTGCAGA GTGGTAACCA TGCTTACACA 240
 CTAAACTATA ATATAAAGGA AATGAAGCCA TGTTAATCTG AGAGCAGTGT CGCCATAGTT 300
 GTGTTGTTTA CAATACTCTA TAAATGGGGT TCCTGTTGCC CTGTAATTAA CCTGCTGCCC 360
 GTAGAGGCCT TTCCAGTTCC TTTCTGTGCC TTNCCCCTTT CTTAACACAA GCTCAAATTT 420
 TCCTAACTNG GTTTTNNATT TGGAGGNCCT TTAANGGN CCATTTTCAA TACCATNAAA 480
 ANTAACCAGG GCTTTATAAT ANTTAAA 507

SEQ ID NO:487

SEQUENCE LENGTH:155

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00543

SEQUENCE DESCRIPTION:

GATCCACTAC CGGAAGAAGA AACAGCTCAT NAGGCTACGG AAACAGGCCG AGAAGAACGT 60
 NGAGAAGAAA ATTGACAAAT ACACAGAGGT CCTCAAGACC CACGGACTCC TGGTCTTAGC 120
 CCAATAAAGA CTGTTAATTC CTCAAAAAAA NGAAA 155

SEQ ID NO:488

SEQUENCE LENGTH:499

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00544

SEQUENCE DESCRIPTION:

GATCTTAAAA ACTAACTTCT AAGATGATTT CATCTTCTCA TAGTATAGAG TTTACTTTGT 60
 ACACGTTTGA AACCAACTAC TGTAGAAGAT GAGGAATCTA TTGTAATTTT TTGCTTTATT 120
 TTCATCTGCC AGTGGACTTA TTTGAAATTT TCACITTAGT CAAATNATTT TTNGTATTAG 180
 TTTTGTATGC AGACATAAAA ATAGCAATCA TTTTAAATNG TCAAAATTTT CAGATTACTG 240
 GTAAAAATTA TTTGAAAACA AACTTATGGG TAATAAAGGC TAGTCAGAAC CNTATACCAT 300
 AAAGTGTAGT TACCATACAG ATTAATATGT AGCAAAANTG TATGCTTGAT ATTNCTCACC 360
 NGTGNTAATG TTNCTGCNGT ATTCCAGCNG ACCAAACCAA TATTAAGNAT GCATCTGTAT 420
 AAAATGGGNG CCTATNGGNT AATGGGAATN ATNNGGGTAA TNGGCCTNTA CCNGGNTGGT 480
 NATAATGGNG CCCTNTGGN 499

EP 0 679 716 A1

SEQ ID NO:489

SEQUENCE LENGTH:516

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00545

SEQUENCE DESCRIPTION:

GATCTACCCC GGACACGGGA GCGCTACGC CAGGNCAGAC GGAAGGTTT TCCAGTTTCT 60
 TAATGCGAAA TGCGAGTCGG CTTTCCTTTC CAAGAGGAAT CCTCGGCAGA TAACTGGAC 120
 TGTCTCTAC AGAAGGAAGC AAAAAAGGG ACAGTCGGAA GAAATTCAA AGAAAAGAAC 180
 CCGCCGAGCA GTCAAATTCC AGAGGGCCAT TACTGGTGCA TCTTTGCTG ATATAATGGC 240
 CAAGAGGAAT CAGAAACCTG AAGTTAGAAA GGCTCAACGA GAACAAGCTA TCAGGGCTGC 300
 TAAGGNAGCA AAANAGGGCT AAGCAAGCAT CTAAGAGNC TTGCAATGG CTGCTTGCTA 360
 AGGCACCTTC AAAGGGCAGC ACCTTAGGCN AAAAGGATTT GTNTAAGCCN TGTGAAAAAG 420
 TTTCCAGCTT CCCCGTNTTT TGGTTGGGAA NNGGNTAAAC CTGGCAGGG TTTGNTTTT 480
 TTTAATTAAN AGGTTTGGGG TTTAANCTN TTAAAA 516

SEQ ID NO:490

SEQUENCE LENGTH:497

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00546

SEQUENCE DESCRIPTION:

GATCAAGCTG ACAGACCCNN CTCTGCTCTG ACCTGGAGGT CTCCACTCTG GTCAGCAAGT 60
 ATCCAGACAT CAGGGATGAC CACATCGGTG CGCTNCTGGC TGTGCGTGGG GACGCCAGCC 120
 GTGACATGAA GCAGACCATC ATGGAGACCC TGGAGCAGGG CCCAGCACAG GCCAGCCCCA 180
 GCTACGTGCC CCTCTTCAAG GACATTGTGG TGGCAGCTG AACGTGGCCA AGCTGCTCAA 240
 GTAGCCTCCG CGGCTGCCT GCTGCCCCC CACAGCTNGG TCCTGCTTTA GAACGCGGGC 300
 AGTNATTGTC TCTTGGCACA CGTGTCTTT TAGTGACGGC TGTNTTTAGG TGCANTGTNA 360
 TGACNGGGTG TGCCTCGAGT GANGTCNGAG GGCACGTGCG GAGGCNGTAN TTTGCTGTAA 420
 AGGCTGTGGG TTCAGNGTTT NCNGACAGCG TTNNTTGGGT GTTGTNTTC AGNGGTGAAG 480
 TGTNNGGAA AGNGNCN 497

SEQ ID NO:491

SEQUENCE LENGTH:494

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00547

SEQUENCE DESCRIPTION:

GATCCAAGAA ACAATTTCTG ATAATTGTGT GGTGATTTN TCAAAAACAT CCTGTTCTTA 60
 CTGTACAATG GCAAAAAAGC TTTTCCATGA CATGAATGTT AACTATAAAG TGGTGGAAGT 120
 GGACCTGCTT GAATATGGAA ACCAGTTCCA AGATGCTCTT TACAAAATGA CTGGTGAAAG 180
 ANCTGTTCCA AGANTATTTG TCAATGGTAC TTTTATTGGA GGTGCAACTG AACTCATAG 240
 GCTTCACAAA GAAGGAAAAT TGCTCCACT AGTTCATCAG TGTATTATA NNNNAAGTAA 300
 GAGGAAAGAA TTTAGTGAT GTTTATACTA ATAAGTTTGC TAGTACAGTG TCAGTTATTT 360

AAAGTGGTAA TGCCCGNTAA TGTCTTTTAA ATGTTTTGAG GGATGTTTAA AAATACATGC 420
 NATTTGCTTC ACGGAGGAGG GNTGTAAAAA TTANTGGGCC AATAAATTGC GGGTGGGAAN 480
 CCNTNTTCTT NAAA 494

SEQ ID NO:492

SEQUENCE LENGTH:489

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00548

SEQUENCE DESCRIPTION:

GATCTTGACG AGGCTGCGGT GTCTGCTGCT ATTCTCCGAG CTTGCAATG CCGCCTAAGG 60
 ACGACAAGAA GAAGAAGGAC GCTGGAAAGT CGGCCAAGAA AGACAAAGAC CCAGTGAACA 120
 AATCCGGGGG CAAGGCCAAA AAGAAGAAGT GGTCCAAAGG CAAAGTTCGG GACAAGCTCA 180
 ATAACTTAGT CTTGTTTGAC AANGNTACCT ATGATAAACT CTTTAAGGAA GTTNCCAAC 240
 ATANACTTAT AACCNAGCT GTGGTCTCTG AGAGACTGAA GATTGAGGC TCCCTGGCCA 300
 GGGCAGCCNT TCAGGAGCTC CTTANGTAAA GGNCTTATCA AACTGGTTTC AAAGCACTGA 360
 GCTCANGTAA TTTACACCAG AANTACCANG GGTNGAGATG CTCCAGCTTG CTTGTGAAGA 420
 TGCATGATTA GGTCCACCAG CTGTACATT GGAAGAANTA NANCTTNTGT TAAATCAATG 480
 GNGTNAAAA 489

SEQ ID NO:493

SEQUENCE LENGTH:487

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00549

SEQUENCE DESCRIPTION:

GATCCTCTGN CACGGGATAA ATTTNCAGGN GAAGAGTGAG GTTGTGATGG CCTCAGCTAT 60
 GCTTCCNGGC TCTCCCTCAA GAGTGCAACC TTGGCTAGAG AACTCACAGC TCTGGGAAAA 120
 AGAGGAGCAG ACAGGGTTCC CTGGGCCAG TCTCAGCCCA GCCACTGATG CTGGATGACC 180
 TTGGCCTGAC CCTGGTCTGG TCTCANAATC ACTTTTCCCA TCTGTAAAAT TGAGATGAAT 240
 TTTNGTGTTG AAAGTNCTTC CNNGAGCAGA TGTCTAGAA GGTTTTAGGA ATAGTGACAG 300
 AGTCAGGNCA CCCNAAGGGC CATGGGGAGC CAGCTGACCT GCTTNGCCGA AGGATTCTG 360
 ACAGACTATC TTTGGGGATG TTTTCAAAGA AGGGATATAG GTTATTGACN TNNGGGCATT 420
 TAAAGNAAAT TNTNTCTCGG GGATTAANTT TTTAGGANAA TNAAGCTTT NGTGTCTANN 480
 GGCAAGN 487

SEQ ID NO:494

SEQUENCE LENGTH:481

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00551

SEQUENCE DESCRIPTION:

GATCCCCAGC TGCCACTGAA TCTGGCTGCC CTTCAGGCC ACCTGGCCCA GGAGAACCGT 60
 GTGGTGGCCT TCTCAGCCT GGCTCTACTG CTTGCCCCAC TGGTGAGAC GCTTATTCTA 120
 CTGGACCGGC TGCTGTACCT TCAGGAACAG GGTTCATG CTGAGCTCCT GCCCATCTTC 180

AGTCCTGAAC TCTCTCCCAG AAACCTGGTT CTGGTGGCCA CCAAGATGCC CCTGGGTCAG 240
 GCTCTTTNTG TTCTGGAGAC TGAAGACAGC TGATGCAGCC TGAGGAGACA TCTCAGACCC 300
 CATCATCTGA AAGTGNCCAG AGAGCACAGT GGCAGAGTAC ATCTNATCCA GAGAAACAGC 360
 ATCTGCATC CTCCAGAGTC CTGGTTCCTT CAAGTTTCAT CNCTTTTNTC TCCTTTCCAT 420
 GGGNTTATGT AAATACAATT GTAAAGTTT AATTAAATTA AAAAATTGGG TTATCTGGAA 480
 A 481

SEQ ID NO:495

SEQUENCE LENGTH:472

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00552

SEQUENCE DESCRIPTION:

GATCTAAGCT CCAGGCACGC CTGAAGATGT GTTGCTACTC TNACATCCCG AGTTTCTGTC 60
 CACACATTGC ATGCACAGCG CCCACACAT TGGATACTGT TGTTCACGAT AATTTCTCCC 120
 GTTTTCCAGA GCATTAAACA TAGCTTGGAG GCGTAAATG GCTCTGTATT TTAATAACAC 180
 AGAAACATTT GAGCATTGTA TTTCTCGCAT CCCTTCTCGT GAGCNCTTAG ACCTTTTNTC 240
 ATTTTAGTCG GATTTTGTG TGAATTTTG CTTTNGTATG AACACTCAGC AGAAAAGTAC 300
 TTACTTCTNG CCAGTTATCT ATTAACCAAA ACCNTTGATT TGTAATTTA AAGNTTAAAC 360
 GNCAAAAGTC TNTNCATAAC TGCCTTGGCC AGTNNGGGGT NGTNCGGGTN CTGGTTAATN 420
 GCCTGTGGCN TTTTNGGTGG TTTGTGNTG GTNTTACNT GNGCANTTAA GN 472

SEQ ID NO:496

SEQUENCE LENGTH:461

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00553

SEQUENCE DESCRIPTION:

GATCAACCAA TTTTNTAAA AGTTCAGTCG AAAGCTTTTA AGTATAGCTT CCTCCCTTGA 60
 AAAAAATGT AAACATGAC TGCTGAGTGA TAAACACTG TGGTGTGAAA GTNTCATCTT 120
 CACTGCCAAT CAGGCAAAGA CCGGAAAGAT TTGCATTTTA TTATGTCTGT CTTATCATGC 180
 AATGGAAATN ATGCTTTTNG TAAGTATGCA TCTTACCAAT GATGTAACGG TTTAATACCN 240
 TTGAATGTTT TAATAACCAA GTNGCTGCTG AACTTATACT AAATCAGGGG CCAAAAAACT 300
 NGCTCTNATC NNCTCAAATN GTATNCNATA TCCATTAATG TATCAGITAT NCCAAAGCCT 360
 TCAGGTGGAG GGGTTTACCA CCNCTCTAGG TCGTTCAACC AGGTTTTGTG AGGAATGCAT 420
 TCAAAGTGGC TNTATAAAG ANGATTTTCT TTAGCATGAA A 461

SEQ ID NO:497

SEQUENCE LENGTH:459

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00554

SEQUENCE DESCRIPTION:

GATCCCAAAA TTCCACTTTT CAACACAGAT GTGGACAACC TAGAAGGGAA GACACCACCA 60
 GTTTTNTCTT CTAAAGGCAA ATACAGGGCT CTGAAAATGG ATTTTCTCTT ACCCCCTTCT 120

5 ACTTACGNCA CCATGGCCAT TCGAGAAGTG CTAAAAATGG ATACCAGTAT CAAGAACCAG 180
 ACGCAGCTGA ATACAACCTG GCTTCGCTGA GCAGTACCTT GTCCACAGAT TAGAAAACGT 240
 ACACAAGTGT TTGCTTCCTG GCTCCCTGTG CATTTTGTN TTAGTTCAGA CTCATATATG 300
 GATTTCAAAT CTTTGTAAATA AAAATTATTT GTATTTTAA GTNTTTATTA GCTTAAAGAA 360
 ATAATTNGCA ATATTNGTAC ATGTACACAA AATNCNGGAG GTTCTTANTT TTAGCTCAGG 420
 NTATAAATNA GTCAAATNCN NNGGTNNNGG NTNNGNTGN 459

10 SEQ ID NO:498
 SEQUENCE LENGTH:481
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00555

15 SEQUENCE DESCRIPTION:
 GATCCAGCAG AGAAGGATGA AAAGGGCATG CCTGTGACAG CTCGTGTGGT GTTTGTTTTT 60
 GGTCTGATA AGAAGCTGAA GCTGTCTATC CTCTACCCAG CTACCACTGG CAGGAACTTT 120
 GATGAGATTC TCAGGGTAGT CATCTCTCTC CAGCTGACAG CAGAAAAAAG GTTGCCACC 180
 20 CCAGTTGATT GGAAGGATGG GGATAGTGTG ATGGTCCTTC CAACCATCCC TGAAGAAGAA 240
 GCCAAAAAAC TTTCCCGAA AGGAGTCTTC ACCAAAGAGC TCCCATCTGG CAAGAAATAC 300
 CTCGCTACA CACCCAGCC TTAAGTCTCT TGGAGAAGCT GGTGCTGTNA GCCAGAGGAT 360
 GTCAGCTGCC AATTGTGTTT TCCTGCAGCA ATTCCATAAA CACATCCTGG GTGTCATCAC 420
 AGCCAAGTTT TTTANGGTTN CTATACCAAT GGGTTATTT AAATGAAAAT GGGCACTTAA 480
 25 A 481

SEQ ID NO:499
 SEQUENCE LENGTH:453
 30 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00556

SEQUENCE DESCRIPTION:
 35 GATCCAGATG CAGAGGCCAG GATGTGGGCC CAGCCCTGTG CCAGGAGGCT GGCTGGAATA 60
 AAGGTACAGA TAGAGGCCTC ACCCCCTCTG GGACCACTGG CACTCAGGCT GTTTGCAGCC 120
 TCAGAGCCCA CCTGCCCCCA GGGCCACAGC TGCATCTCCT GCCCTGCTGT CATTACAGGG 180
 ATGGGCAGGC TGGCATGGGG GCACCCGCTG CCCCTGCCTG GNTGTTGCTG TGTATTCCTG 240
 CCGGCCAGGG GCACTGCCAG GACCACGCCT CCNTTTTAT ATCCNGATTC TTAAGTTCTG 300
 40 CTATTGTGGT ATTCTGGTGG AGAAAAAAGA CCGNGTGGCT GTTTTGAAC TGCTGGAAC 360
 CTAAGACCCT GAATTCCTTT CCCCCAAGG GAAATCTAT ATGGAAACAT TTATTAAAT 420
 ACAGGATGAA GTAATTAAAA GNTTAAATC AAA 453

45 SEQ ID NO:500
 SEQUENCE LENGTH:446
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00557

50 SEQUENCE DESCRIPTION:
 GATCAAAGTT GGCAAGGTGC GGAATCGAGA CATGGGCGGC TACAGACCAC AACCGACTTC 60

55

ATCAAGTCTG TCATCGGTCA CCTGCAGACT AAAGGGAGCT AGAGCCCTTT ATTTCTTCCA 120
 ACCTTGCAAG GACCACACTN CCCATACCNT TCAGTGCACT GTACCAGGGA AGAGCCTTGT 180
 GCCTCTAAGC AGTGGACCAT GGTACCTTG CTGGGTAGAG CCTAGGTTGT CCTTGGGCCG 240
 GCTTCCTTAG GGGACAGACT NTGGGTGGT GATGGGGATT GTAGGATGGA GCCAGGCACA 300
 TGGATGATGA TGATTCTCC NCACAGGTTG GAACCTCTGA CATGGGTGGC TATGCTACTN 360
 GCNATGCTTA NTGAGGNTGT CATTGCTGCT TTNCCNAACC ATAGGCCTGT CATACNNTGT 420
 AAGGNGTCAA TAAGGACATG ACCAAA 446

SEQ ID NO:501

SEQUENCE LENGTH:434

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00558

SEQUENCE DESCRIPTION:

GATCCAATTC AGGTTAGGCT TGTGTTGTTT TTTTTTCAG AAAATGTATT CCATAAAGTT 60
 TGTACTTAGA CCAGACGGGT GTACTAAGAA TCATTCATGA GTAAATGTGT GTTGAATATC 120
 TACCCTTGAC CTTTTTTGA GAAATAGAGT AAACACAGTC CCTGTAGTCT GACAGCTAAT 180
 GGGGAGAGAG GGTAGACTTT TCATCGAATT AAATTTCTAC ATGCACCTTT CCCCCAGAAA 240
 TCTTACTCAT GGCTGGTCTC AAGTAAGTCT TTATTGAAAA ATATNGACAT ATCTNCTTCC 300
 TCTTCCTTCT CTTCACTGTC TTCCTTTTAG TAGTTAGGCA GAGTAAATAG GTAAGAAAAA 360
 TTATCTGCAT TTATGTGTAG TTTGTAATCT ACTAAAGGGG TTCTAGAATA AATGTNGNCA 420
 TNTNGTAACN GAAA 434

SEQ ID NO:502

SEQUENCE LENGTH:430

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00560

SEQUENCE DESCRIPTION:

GATCAAAACAG GTTCAAAGTA AAACGTAAAT TTTTACATTT NTTTTAAAGA ACTCTTAAAG 60
 TGTAACAGTT ACGCCATACT TCATAAGTGG TAAAGAAAGG TATAAAATTT GGAAACATTT 120
 TGTGGGCAT AGTAGTGATT GGGTGAAAAG GATAAATTAT ATCAAAATGA GAATGTNCTG 180
 TAATTGGAAG TAGGGAGCTA AAGGATGTTT CTTTCAGTTT AGTAGAACTG GAACGTTTTA 240
 CTATTAAACA TGGCTTTTAT AAATNCATGG TCCAATAATT TTATTCAGT TTAGTATTTA 300
 ATTCACTGTC AGCTTATTAA TGTGTTCTGT ACCCATTAAT GAATTTTAAA TTACAAAAAA 360
 TTGTCTAGCA GCTTCCAGTT TAANAAATGG AACCTAGGCC ATTAATAATTA AATTGGTAA 420
 ATTTTTTAAA 430

SEQ ID NO:503

SEQUENCE LENGTH:428

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00561

SEQUENCE DESCRIPTION:

GATCCTAAAT GTGTTGCTGA AATCAGGCAG CCCGAGCCTC TGGTCTCTCC AGAGAGCCCG 60

TNTTCACATT TGTNTATTCC TCAGCACTCA CCCGAAACTG AACAGATGGG GAGTGGTCTT 120
 GATTGTCAAG ATAAAACTGG TGAAGAAAGC TAAATGCTGA GAAACTGAGC ATCTATTGTG 180
 GTGTTTAAGC TTAGCTGGGT CCTTTCTAGT TTGTTTTTAC AGCTTACTAG GTGAAGTAGT 240
 TTGCACTATT TTNGCAATAA ATTCATGGAA AACCTAACAG TTACTIONTNT NGTTTCTNAC 300
 TGTGTGTATA TAANCTAATA CTAAANGTNT GGCATAGTGT TTNTGCACCT NCNTACATAA 360
 CCNCTAACAT GCACAGAATG CTGGTAAATN TGATAAANTA TGANGTGANT GATGATNNGA 420
 TANAGTGN 428

SEQ ID NO:504

SEQUENCE LENGTH:422

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00562

SEQUENCE DESCRIPTION:

GATCCTCACC CTCCTGAGGC CCACTGGGGA AGAATGAACA TGGCTTCATC CAGGTAACT 60
 NATGCTGCCA TTGCCCCAGC CTCTTCCATC CCAGCCCTGT CAGTNAGCCC AGGTCTGGTG 120
 CAACTNCTGC AGGATGCCTG TAGTAGGGAA CTCTGGAAGT GTATTGGGCT GAGGTGGGAT 180
 TTTCCCTCCC CACAGTGCCAC TGAGCAATGG AGGGTGTGTA GGGAGCCATG CTGCTGAATT 240
 CTGGTTGGCA TTTCCCCATT ATGTAAAATG GGGTGTGGG TAGGGCAGAC TCTGCTGGG 300
 TTTGGTTGTA AGATAAACCT GGAGGAGAAG CACAGTTGTC CCATTGAATT ATTTGAGCAA 360
 AAACACTGT AAATAACTTT TTTGGGCTNT TGTCAAATAA AATTTTTTTT TGTNTTTTA 420
 AA 422

SEQ ID NO:505

SEQUENCE LENGTH:417

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00564

SEQUENCE DESCRIPTION:

GATCTGATTC AGAAGGGCGT CATCCAACAC AAAGAGAAAT GCAACCAATG AAGAATCAAG 60
 CCACTGAGGC AGGGCAGAGG GACCTTTGAT AGGCTACGAT ACTATTTTCC TGTGCATCAC 120
 ACTTAACTCA TCTAACTNNT TCCCCGGACA CCCTCCACCT CTAGTTGTTA CTAAGTAGCT 180
 GCAGTAGGCA TTGCTGGGGA AGAAACAAAC ACACACCAA CAGTACTGCT ACTTAGTTTC 240
 TAAGGCTGCA CAGGGAAGGG AAAGACTGGG CTTTGACAA TCTAGAGGTA ATTTATATCC 300
 GCCCCAGGT GGAGCAACAT GCGATTNTGG AGGCACGGGG GTAAGTAAA GTGAGTACAT 360
 ATAGTNTTTC TGGTTTCTGG GGATAACCCA TCAATAAAG CTGCTTCTC TNGTAAA 417

SEQ ID NO:506

SEQUENCE LENGTH:421

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00565

SEQUENCE DESCRIPTION:

GATCTTCTTT ATAATTCTAC TTTGAGTGCT GTCTCCATGT TTGATGTATC TNAGCAGGTT 60
 GCTCCACAGG TAGCTCTAGG AGGGCTGGCA ACTTAGAGGT GGGGAGCAGA GAATTCTCTT 120

ATCCAACATC AACATCTTGG TCAGATTGGA ACTCTTCAAT CTCTTGCACT CAAAGCTTGT 180
 TAAGATAGTT AAGCGTGCAT AAGTTAACTT CCAATTTACA TACTCTGCTT AGAATTTGGG 240
 GGAAAATTTA GAAATATAAT TGACAGGATT ATTGGAAATT TGTATAATG AATGAAACAT 300
 TTTGTCATAT AAGATTCTNT ATTTACTTCT TATACATTG ATAAAGTAAG GCATGGTTGT 360
 GGGTAAANCT GGGTTTATTT TTNGTTCCAC AAGTTAAATA AAATCCATAA AACCTTGGAA 420
 A 421

SEQ ID NO:507
 SEQUENCE LENGTH:413
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00567

SEQUENCE DESCRIPTION:

GATCCCANAC TGGTCNTTGA ACAGACAGAA GGANGTAAAG GNTGGAAACT ACAGCCAGGT 60
 GTGTACTGAA ATNAGGGCAG GATTAGAGGA AGGGTGGAGG GTCCTAACAG AATTGGGCAT 120
 AGGAGGTGAG GGGATAAAAC ATCCCTTGCC CCTCCTCTG AATCCAGGNC CTAGCCAATG 180
 GNCTGGACAA CAAGCTCCGT GAAGACCTGG AGCGACTNAA GAAGATTCGG GCCCATAGAG 240
 GGCTGCGTCA CTTCTGGGGG TGAGTGGGGG GTCTCATCTC CCTGCCTACC TCGACTCAGC 300
 ATTCTCTCTA CTCGNTCTTC TTNTTTTCCC AACCTTTTGG TTTCTTGCTT GTNCATGACC 360
 TNGTGACTTN TTCNTNTTTT TACCNTGCAN GCCTTTNGTN GTCCTAGGGN CAN 413

SEQ ID NO:508
 SEQUENCE LENGTH:407
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00568

SEQUENCE DESCRIPTION:

GATCTNAGGG TGAACCACTT CATTCTGCAG GGTCTCCCT CCCACCTTAA AGAAGTCCCC 60
 CTTATGTGGG TTGCCTGGTG AATGGCCTTC CTTCCCGCCA NAGGGCTTGT AAACAGACCG 120
 GAGAGGACAG TGGATTGTTT ATACTCCAGT GTACATAGTG TAATGTAGCG TGTTTACATG 180
 TGTAGCCTAT GTTGTGGTCC ATCAGCCCT CACATTCCTA GGGGTTTNG AGTGTGTAGG 240
 TGGTATGTGA CACCAAAGCC ACCTCTGTNA TTTGTNGTGA TGTCTTNTCT TGGCAAAAGC 300
 CTTGTGTATA TTTGTATATT ACACATTTGT ACAGAATTTN GGAAGATTTT CNAGTCTAGT 360
 TGCCAAATCT GGCTCCTTTA CCAAAAGGAN ATTACCCTTG NGGNAAA 407

SEQ ID NO:509
 SEQUENCE LENGTH:402
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00569

SEQUENCE DESCRIPTION:

GATCAAACAG TTTCTGGAGT GTGCCAGAA CCAGGGTGAC ATCAAGCTCT GTGAGGGTTT 60
 CAATGAGGTG CTGCANCAGT GCCGACTTGC AAACGGATTG GCCTAATGAA GAAGTTCAAC 120
 CTGGAGAGAT GGAATATCAG CTCTCATAAC TANGTTAATT TAGTATAAAA NTAGAATTGA 180
 TAGTGAGGGT ATAAAGTGTA ACCATCAGTT AAACCTCTCC TGTATTCTCT GGCTTCCTTG 240

CTTCAGANTT GAAATGGAAG TGGGGGTGTC CCTACTCTGT AGAATCTGGG NCTGGGCAAA 300
 TGTGTTGTTG GCCTCCTTAA ACTAGCTGTT ATGTTATGAT TTTTNTTCTT TGTGAGTTAA 360
 TTAGGAATAA AGTCATTTTC TTTCCAAGGG TATGGTTCCA AA 402

5

SEQ ID NO:510
 SEQUENCE LENGTH:396
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00571

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SEQUENCE DESCRIPTION:
 GATCATGAGA AGGAATGGAA ACTAGGCCGG TGCATTTTAC GGTTCCTGA GATTCTGCAA 60
 AAGATTTTAG ATGACTTATT TCTCCACACT CTCTGTGATT ATATATATGA GCTGGCAACT 120
 GCTTTCACAG AGTTCTATGA TAGCTGTAC TGTGTGGAGA AAGATAGACA GACTGGAAAA 180
 ATATTGAAGG TGAACATGTG GCGTATNCTG CTATGTGAAG NAGTAGCTGC TGTGATGGCC 240
 AAGGGGTTTG ATATCCTGGG AATAAAACCT GTCCAAAGNA TGAATCCTT CATAGGTTTG 300
 AACTGTGTG TTTTACCCAA GTGGCCATTG GNACTGTTG CTTTTTTACA ATCATGTGGG 360
 CACAAGCNTA AGAAAGGAAA TTNGCAACCA GGGAAA 396

20

SEQ ID NO:511
 SEQUENCE LENGTH:384
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00572

25

SEQUENCE DESCRIPTION:
 GATCCAATCA GATGCAGAGA ATGTGGATAC AGAATAATGT ACAAGAAAAG GACTAAAAGA 60
 TTGNGCGTTT TTNATGCTCG ATGAATGCTG GGAATTCAGA GGAATGTNTT CACTTATACT 120
 TGGATTTGCT CTCTTCCCAT TTCTGATTGT NGTATAGCTT TCGATTTTNC TTACAGTAGT 180
 TCCCCCTTAT CTNCGGGAGA TACATTCCAA GGCCCCCAGT GAACTCCTGA AACCTCAAAC 240
 AGTACCAAAC CTTTATACAC TGTTTTTTCC ATATATATAT ACCTATGATA AAGTATAATG 300
 TATANNTTAA GCATAGCAAG AGATAATAAT AATGTNATAG NCCATTGNTA CNANCTATAN 360
 TAANNGGTTA TGTGANTGTG AAAA 384

35

SEQ ID NO:512
 SEQUENCE LENGTH:383
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00573

40

SEQUENCE DESCRIPTION:
 GATCAGAGCA AAACATGCAG AGCCCTTAGC AGAAACCCAC TTTAATGCAT TTTCTTCATA 60
 TCCCTAAAGT TCCTTAAAAA TATGTGACAA TGCATCAGGA AGAGGAGAAC TGAAGAGTAG 120
 AAGTTCCCTT GCAGATTTTT TTATCAGTGA CATGTAATGA GCAATTCACA GATGAGCGCA 180
 GGCAGAGCTC TGTGTGCCGT GTACATATGG ACCGTGCTAT GATGTGTCTC ACATTGGATG 240
 ATATTCCACT TTGGGAATTT TAGTATTTGT ATATAGAAAA TGGGTTTAAT AACTCACCAT 300
 GGTTTTNATT NGTCTTATAT TCGTTATTTT TTAATACTCT NGTATGTGTT TTTATAATAA 360
 ANAATAAAAG TAAGCCATGG AAA 383

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SEQ ID NO:513

SEQUENCE LENGTH:381

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00574

SEQUENCE DESCRIPTION:

GATCCAAAAT CATACTGTCA AGACCATCAA ACAAACAAA GAAGCTTAAG TGAAC TAAGC 60
ACAGGGAAAA GTTGT TTTT CACTCGTTCA TTTTGT CATC TGCTTCTAGA TGCTGCAATC 120
AAGAAGTAGC AAATGCCCAA GTTGCCATAG TGTTCG CAGG AAAAAAGAG AAAAAATAAT 180
AAAAATAAGG AAGGAGCAAT GCCAAAAATT GAAGGAAATA TTATATAATT AANGCAAGAA 240
GNTATCTATC CATTGAGNGA AACAA TTTT ATATTATTG CTTT TAGCNG CAAAGCATT A 300
GGAATTCTGA GATTGT TATA GCACTAAGAA GGTTT NATT CTGTGTACAC ACTGGAAAAAT 360
TAAATTCTG GGTAAAGGAA A 381

SEQ ID NO:514

SEQUENCE LENGTH:381

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00575

SEQUENCE DESCRIPTION:

GATCCCCCTG GAAGAGGGAC TCCAATGGGC ATGCCCCCTC CGGGAATGCG GCCTCCTCCC 60
CCTGGNATGC NAGGCNTTCT TTNACCCTTG GCCACAGAGT ATGGAAGTAG CTCGCAGAG 120
GCGTGGGCTC GATTCTCAG GGCCACGTTA CCACAGACCT GTTTGTTTCT NATGCTGTTG 180
TTCGTGGAGT CTCATGGGAT TGTNTGGTTT CCNTTACAGG GCCCNCTCCC CNGGGAATGC 240
GCCCACCAAG GCCNTAGACT CATCTTGGCC NTCTCAGCT CCTGCCTGT TTCCGGTAAG 300
GCTGTACATA GTNCTTTTAT CTNCTTGTGG CCTATGAAAC TGGTTTATAA TAACTNTTA 360
AGAGAACATT ATAATTGCAA A 381

SEQ ID NO:515

SEQUENCE LENGTH:377

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00576

SEQUENCE DESCRIPTION:

GATCTGCGTG GGGCTGGTGG TGGTTGGTGT CCTGCTCATC ATCCTGATTG TNCTGCTGGT 60
CGTCTTTCTC CCTCAGAGCA GTGACAGCAG TAGTGCCCA CGGACCCAGG ATGCAGGCAT 120
TGCTCAGGG CCTGGGAAC TACCCAGCTG GTCCTGAAGG AGAAGCCAAA TGGCTGCACT 180
GGCCGATTCT GGTCTCCAGA GGACCTTGGT GTTGCTCTC CCTTGACCCA CCCCAGTNAG 240
TGCCAAAGGG CAGCCCCAAC ATGTGCACCC CTGCATTTC TGTCATGCCA CAGACTGGCC 300
CTTGAGGGCA GCCTGCTGTA CTGGCCATGC TGGGCCAGCC NCACCTGGAG CTCAGTAAAA 360
ACTGCTGTTT GATTAAA 377

SEQ ID NO:516

SEQUENCE LENGTH:375

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00577

SEQUENCE DESCRIPTION:

GATCACACCA GTTCAGAGAG CTACACTTTA TGGGTAACAG TTTCACCTGT NATACAGTTC 60
 CCTAGAACAT TTTCCCAAAA GTAGTGAAGT GCAAAGTGCT TAGGTTTGAC ATTTATTGTA 120
 GCAGAACAGT AATATCACAG TATGGGACAA AGGTTTACAC TTTCAGGGT ATTCTTTGGG 180
 GGAATGTAA ATACTGTAAT AAAAACATGT TCAATCATGG TAAATGTTT AACTNGTTAA 240
 ANTTACAAAT GGNCAAAAAA NATTTTTTTC CTNATATATN GCCTAANTAC CAAATGAAGN 300
 GCTTAANCTT AAGNTTCAAT GTGAAANCGA GTAAATNTGT TCCTAAATTT GCAGNAATAA 360
 NAGATANCCN GTANN 375

SEQ ID NO:517

SEQUENCE LENGTH:374

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00578

SEQUENCE DESCRIPTION:

GATCCATGTA CTGTCATGTT TTTTTCAGG AACAAGCACA TCATGATTGA TTTGGGGACT 60
 GGCAACAACA ACAAGATTAA CTGGGCCATG GAGGACAAGC AGGAGATGGT GGACATCATC 120
 GAGACGGTGT ACCGCGGGGC CCGCAAAGGC CGCGGCCTGG TGGTGTCCTC CAAGGACTAC 180
 TCCACCAAGT ACCGCTACTG AGGCGCCTCA GTCTGCGCGG ATAAATGTCG TGGAGCCCTT 240
 TTTGTATGGA AACGTTTAA GCTATTTAAA GCCTTTGGAA AATACAGGAN GTNCAGGGCT 300
 GGAGCACCTC TGAGATGGAA TTGATAACAT GGTCTTAACT CACCGAAATA AACAAGCACG 360
 TNGTGAGNGG NAAA 374

SEQ ID NO:518

SEQUENCE LENGTH:374

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00579

SEQUENCE DESCRIPTION:

GATCTCACCG TGGGTCCGAT TAGCCTTNC TCTGCCTTGC TTGCTTGAGC TTCAGCGNAA 60
 TTCGAAATGG CTGGCGGTAA GGCTGGAAG GACTCCGGAA AGGCCAAGAC AAAGGCGGTT 120
 TCCCGCTCGC AGAGAGCCGG CTTGCAGTTC CCAGTGGGCC GTATTCATCG ACACCTAAAA 180
 TCTAGGACGA CCAGTCATGG ACGTGTGGGC GCGACTNCCG CTGTGTACAG CGCANCATCC 240
 TGGAGTACCT NACCGCAGAG GTACTTNAAC TNGGCAGGNA AATTGCATCA AAANGACTTA 300
 AAGGTNAAAN GGTTTTACCC CTNGGTNANT TGCAACTTTG GTTATTNGN TGGGGGATGA 360
 AGGNTTTGGG TTNN 374

SEQ ID NO:519

SEQUENCE LENGTH:372

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00580

SEQUENCE DESCRIPTION:

GATCAGAGAG ATTAGGATTG TATTTTGACA TAGGATTGG AACCCATCTA AATGTTGAAG 60
 TTCCCTGAGA CAGCTCTCCA GCTGCTNNGC CTGCGCCAGG GGCTANGCAG CCCCTAATGA 120
 GAGGGCTCTGC TCCCTTTCCC ACCTCGCCAA TGTGTTGTT GCTGCCTTTT TGATTTGTAT 180
 CCTCTGTTAT AGACATTTTT NAAAAACGAT TTCCTCTTC ATTGTGCACA AGTGCTGAGA 240
 GTCTNAGGCC CCATTCTGC TGTGTATATA TATCCTGACT CGGGGCTTTT ATTCAGCAAA 300
 CTGTTTCATTG TTCTGTCAGA CAATGTCATA TTCAACTCTG TTCATATTAA ACCACTTGTN 360
 AAGCANTNNA AA 372

SEQ ID NO:520

SEQUENCE LENGTH:371

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00581

SEQUENCE DESCRIPTION:

GATCTGGTCG CTGCCCCAGG GGGACTGATG GGCAGNGTCG CCCCTGTGGC TGGACTGTNA 60
 CCATCCCTGA TGGGGCTGA CCGCGGGAGC TGAGGAAGCG CCGCTCCACC GTCTGCCCTC 120
 CAAGGACCCG CATGGAGGCA GTGGGCTGGC AGCTTCCTGC TGCTCCGTGT NAGAGTCAAA 180
 GCACAAATCC TCAGGACGGG CTCAAGGGCC AGGGCAGCCG AGGGAAGTNC AGGTGGGGAC 240
 CACGTCTTCC TGAGGTTGGT GCCACTGCTT GGNACCGTTT GCAGTGGGGT GGCCTCCCTC 300
 CTGTTTGCNT GGTGNAGNNA GCGTGGCGTG GGGACGTGAC TGAATAAAGC ACCATGGGTG 360
 ATGTGTTGAA A 371

SEQ ID NO:521

SEQUENCE LENGTH:382

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00582

SEQUENCE DESCRIPTION:

GATCTNTGGG ACGTCAGCTG CTGAGAGGAG CAAGCGGTAG TACCACCCTC TAGTTGAGGG 60
 AGTCAGCACA GTCCTTTCTG CAGCTTCTAA CCCAGGACCA TGAAGTCAAG TGCCTAGAGA 120
 AGCCAGGCAG CNNAAGGACA AGGAATGCTG GGGGCTGTGG GAACAGGAAT GCAGATACCC 180
 TTTGAAGGAG CATTCCTGCT AAAAGAAGCT GAAAATGTAG ACCTATGTGA AGTGCTCTGA 240
 TTTCTAAATA TTGTGAAGGT TAAGAAAAAC ATANATTTTN GGGTCTATGG GCTAGGATTN 300
 AGNCCCACAG TTGGCCANTT TNTAGNGGT NCCCAAATGG ANTGGTTAA CCNNNGGTTT 360
 NGNTTCCTAG CCTAGGGGTA AA 382

SEQ ID NO:522

SEQUENCE LENGTH:382

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00583

SEQUENCE DESCRIPTION:

GATCAAGAAC AATGCCTCCA CTGACTATNA CCTATCTGAC AAGAGCATCA ACCCTCTGGN 60
 TGGCTTTNTC CACTATGGTG AAGTGACCAA TGAAGTTTNTC ATGCTGAAAG GCTGTGTGGT 120

5
GGGAACCAAG AAGCGGGTGC TCACCCTCCG CAAGTCCTTG CTGGTGCAGA CGAAGCGGCG 180
GGCTCTGGAG AAGATTGACC TTAAGTTCAT TGACACCACC TCCAAGTTTG GCCATGGCCG 240
NTTCCAGACC ATGGAGGAGA AGAAAGCATT CATGGGACCA CTGAAGAAAG ACCGAATTGC 300
ANAGNGAAGA AGGAGCTTAA TGCCAGGNAC AGATTTTGCA GTTGGTGGNN GTCTCAATTA 360
AGNGTTATTT NNCCACTGGA AA 382

10
SEQ ID NO:523
SEQUENCE LENGTH:367
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00584
15
SEQUENCE DESCRIPTION:
GATCTCCAAG CNAACTCAGC CTCCANCCAA NCTCCCTGTG GGTCTAGCC ACAAGCTCTC 60
CAACAATTAC TATTGCACTC GCAATGGCCG CCGGGAATCT NTGCCCCCTT CCATCATCAT 120
CNCGTGCGAG AAGTCGCTGG TGTCAGGCAA GCCAGCAGAG AGCTCTGCTG TAGCTGCCAC 180
TGAGAAGAAG NCGGTGACTC CAGCTCCTCC CATAAAGAGG TGGGAGCTGT CCTCGGACCA 240
GCCTTACNG TNAACTGCA CCCTNACGGC ACCNGACTAC TTTGCCTGCT TGGATTTCCT 300
20
CCAGGGGAAT GTGACCTAAT TTATGNCAAA TACGTAGAGT CAGGTATCAC TTCTAGTTTA 360
CTNTAAA 367

25
SEQ ID NO:524
SEQUENCE LENGTH:365
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00585
30
SEQUENCE DESCRIPTION:
GATCAAGAGG AAAGAGAAGC TAACAACCAG AACCCCTGGA CATTTGAGCG AATAGCCACT 60
GCCAATATGC TGGGCATACG GAAAGTACTG AGCCCATATN ACTTGACCCA CAAGGGGAAA 120
TACTGGGGCA AGTTCTACAT GCCCAAACGT GTGTAGTGAG TGTAGGAGAT AACTGTATAT 180
AGGCTACTGA AAGAAGGATT CTGCATTCTT ATTCCCTCA GCCTACCCAC TGAAGTCTTT 240
35
GGGTAGCTCT TAAGCCATAA CTAAGGAGCA GCATTTGAGT AGATTCTGA AAAACAATGT 300
TATTTGTTGA TTAAAAAGA AAAGTGTATT NTTATTAAAT AAAATTAAAA CATCACTTCA 360
GGAAA 365

40
SEQ ID NO:525
SEQUENCE LENGTH:396
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00586
45
SEQUENCE DESCRIPTION:
GATCTATGGG TTGACTAATT AAACAATAAT TCAAGTAGAG TGTCCCAGAA AAAAACCCT 60
TGGGCTCCCT GTTTGGAGTC TGGCTGGCTC TGAGCATTGC CAATGGCCCC TACTCACCTG 120
ACTTTGTATC CTCTCCTTTT AGAGGCTTTG CATTCTGCAC CCAGCTTCAC TAACAGTGGG 180
50
CTGAAAACAT CCTTGGGTTG AGTGTTCAT TTGGGAGTTA TTTGGCCAGG GCCTTTTGAA 240
CAGTAGTGTC CCCATGAAGT GCTAGATAAT ATATGTGTAA GAGTCAGCTT TTTTTTTTTT 300

55

TAAACTNTAA CACCNTTNAG AANTTTCTAA CTACTIONGNA ACTGNATGGT TTANCCCGGN 360
 GNTAAAAGCN GTTTTAAAA GTNTANGTTT TCCAAA 396

5 SEQ ID NO:526

SEQUENCE LENGTH:360

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

10 CLONE:HUMGS00589

SEQUENCE DESCRIPTION:

GATCCGCGGG CTCCACTNC ACCATCGGAT GTTTGCCACT CAGACTGAGG GGGAGCTCAG 60
 AGTGACCCAA ATTCTCAAAG AAAAGTTTCC ACGAGCTACA GCTATAAAG TCACTGACAT 120
 TTCAGGCACT AAAAGAAGAA ATCAAAGAGA TGCATGGATT GCGGATATTT ACCTCTGTCC 180
 15 CCAAACGCTG ACCACGGCCT GGCTGCATAG ATGCTGCTGC TTAAGACCTT GGATGAACTT 240
 CACTGACATC ATTCTTCCCT AAGCAGTCAC CAAAAATTT ATATATNTNG CTCATATACA 300
 NTNCCATATN ATANTTATAG AAGATGTATA ATCTATTTTA GATGTNANTN AAAGGGTAAA 360

20 SEQ ID NO:527

SEQUENCE LENGTH:267

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS00590

SEQUENCE DESCRIPTION:

GATCGGGTTT GGGCCCCAGC CCGGCTCAG CCAGTCCCTC TTCCTCTGCC GGGAGGGTGT 60
 TTTCAACTCC AAACCCAGAG GAGGGGTGT AGATTGGGTC CAGCTTTGCT TCAGTGTGTG 120
 GAAATNTCTC GTGGGGTGGC ATCGGGGCTG CGGGGTGGGG ACCCAAGGC TTTCTGGGGC 180
 30 AGACCCTTGT CCTCTGGGAT GATGGGCACT GCTATCCACA GTCTCTGCCA GTTGGTTTAA 240
 TTTNGAGGTT TNTGGGCTTT TTTTAAA 267

SEQ ID NO:528

35 SEQUENCE LENGTH:352

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00591

SEQUENCE DESCRIPTION:

GATCAATCAC CTTCTGCTGC TTGGATGGGT GGATTTGGTG CTCAGCCTCC CCAAGGACAA 60
 GCTCCTCCCC CTGTAATACC TCCTCCTAAC CAAGCCGGAT ATGGTATGGC AAGTTACCAA 120
 ACACAGTGAG CCGGGACTCT AAAAAAAAAAT TGTAATTCAT GATAGGCTTC GATTCCTGT 180
 GACACTCTGA AGACATGAAA GTAGACATCG GAAATGNAA ATATTTATTT TAAAAATTGA 240
 45 AATGTTTGA ACCTTTAGCA CAGATTGCT TTGGTGAAGG ACACGTGTCT TCTAGTTCTG 300
 CCTTTTAAA GTTNTTGT CATGNTGGAT NTTGAACATN GNTTTTNTT TN 352

SEQ ID NO:529

50 SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00592

SEQUENCE DESCRIPTION:

5 GATCAAGCCT TTCTTTCATT CCCTCTCTGA AAAGTATTCC AACGTGATAT TCCTTGAAGT 60
 AGATGTGGAT GACTGTCAGG ATGTTGCTTC AGAGTGTGAA GTCAAATGCA TGCCAACATT 120
 CCAGTTTTTT AAGAAGGGAC AAAAGGTGGG TGAATTTTCT GGAGCCAATA AGGAAAAGCT 180
 TGAAGCCACC ATTAATGAAT TAGTCTAATC ATGTTTTCTG AAAACATAAC CAGCCATTGG 240
 CTATTTAAAA CTTGTAAATTT TTTTAATTTA CAAAAATATA AAATATGAAG NCATAAACCC 300
 10 AGTTGCCATC TGGGTGACCA ATAAACATT AATGCTAACC ACTTTTTTAA A 351

SEQ ID NO:530

SEQUENCE LENGTH:348

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00593

SEQUENCE DESCRIPTION:

20 GATCCAGAAT ACCCTGACCT CGCCCCAGTT CCAGCAGGCC CTGGGCATGT NCAGCGCAGC 60
 TTTGGCCTCG GGGCAGCTGG GCCCCTCAT GTGCCAGTNC GGTCTGCCTG CAGAGGCTGT 120
 GGAGGCCGCG AACANGGGCG ATGTGGAAGC GTTGCCAAA GCCATGCAGA ACAACGCCAA 180
 GCCCGAGCAG AAAGAGGGCG ACACGAAGGA CAAGAAGGAC GAAGAGGAGG ACATGAGCCT 240
 GGACTGAGCC ACGCGCCGTC CTCCGAGGAA CTGGGCGNTT GCAGTGC GTT GCACACCTTN 300
 25 ACCTTCNACN TACTGATTAT TAATAAAGTT TTTTCTTTA CCTGCAA 348

SEQ ID NO:531

SEQUENCE LENGTH:347

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00594

SEQUENCE DESCRIPTION:

35 GATCCTGAAG AGATTGAAAA AGAAGAGCAG GCTGCTGCTG AGAAGGCAGT GACCAAGGAG 60
 GAATTTGAGG GTGAATGGAC TGCTCCCGCT CCTGAGTTCA CTGCTACTCA GCCTGAGGTT 120
 GCAGACTGGT CTGAAGGTGT ACAGGTGCCC TCTGTGCTA TTCAGCAATT CCCTACTGAA 180
 GACTGGAGCG CTCAGCCTGC CACGGAAGAC TGGTCTGCAG CTCCCACTNG CTCAGGCCAC 240
 TGAATGGGTA GGAGCAACCA CTGACTGGTC TTAAGCTGTT CTTGCATAGG CTCTTAAGCA 300
 40 GCATGAAAA ATGGTTGATG GAAAATAAAC ATCAGTTTCT ATTTAAA 347

SEQ ID NO:532

SEQUENCE LENGTH:346

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00595

SEQUENCE DESCRIPTION:

50 GATCCGGTNT TGGTGCCAAT GTCTCCAAC TCACTTTTGC TCCTAGCACG ATTATATTTC 60
 ACCTGGGACA TGCTGCTATG CTGGGACTCA TGTATGTCTA CTGGACTCAG CTCAACATGT 120
 TCCAGACCTT GAAGTACCTG GCCATCTTGG GCAGTGTGAC GTTCTGGCT GGCAATCGGA 180
 TGCTGGCCCA GCAGGCAGTC AAGAGAACAG CACATTAGTT CCAGAAGAAA GATGGAAATT 240

55

CTGAAACTG AATGTCAAGA AAAGGAGTCA AGAACAATTC ACAGTATGAG AAGAAAAATG 300
GAAAAAATA CCTTTATTTA AAAANGAAAA AAGTCCAGNT TGTAAA 346

5 SEQ ID NO:533
SEQUENCE LENGTH:346
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00596

10 SEQUENCE DESCRIPTION:
GATCTTGTAG CCTAGATAGG ATAGTNTGAC CTTCTAGCAT AGTCTTTTGG CCAAATNATT 60
TGTTGTTTCA GTGTGTGGGG AAGCTGTCTT GGGGGCTGGG GCGACAGATA GCACATAGGC 120
TGTTTCTGGG GCTGCAGGGG CTTCCNTGAG CTGGATGTTG TGGGTNTTGC CGTGCTTCAG 180
15 GAAGTNTGGC GACCAGAAAG CGTAGACCCG GGGCCCAGGG TGTGCCCGCC CCTGCAGCNT 240
GGCTCCCCG CACAGGCTGT GGCTTGCACT CCAGCCGNTC TAGTNTCTNA GGAATTTNCT 300
TGTNACTTGT ACTGTGTAAA TAAAGCTTCC TGGTTCAATA CCNAAA 346

20 SEQ ID NO:534
SEQUENCE LENGTH:345
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00597

25 SEQUENCE DESCRIPTION:
GATCCTATGG CCATGACCCA GAAGTATGAG GNGCATGTNC GGGAGAGCAG GCTCAAGTAG 60
AGAAGGAGGA CTTCACTGAC ATGGTGGCTG AGCAGGCTGC CAAACAGAAG CAAAAAATC 120
GGAAAGCTCA GCCCCAGGAC AGCCGTGGGG GCAGCAAGAA ATATAAGNG TTCAAGTTT 180
AGGTCCCCC AACTAGCCC TTTTGTGGC CCTACGCTG GATGCCCTGGG CTTACACAA 240
30 GAACACCTC TCCCGCAGTT CCAAGGNTC TGTATTTC TGTCTTATT TTAGACCTGT 300
TTTGAAATA AAGCTGTTT CCAAGGAAAG AGATGAATAT TTAAT 345

35 SEQ ID NO:535
SEQUENCE LENGTH:354
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00598

40 SEQUENCE DESCRIPTION:
GATCGTGTG ATGGTGAATC CAAGTTGGGA GGAATGAAA TAGTATCTT NTTGAAAGGA 60
ATATTGACTC TTTTGTCTAC TACATAAAG AAAGATACTC ATTTATAGT ACGTTCATT 120
CAGGTAAAC ATGAAAGAAG CCTGGTACT GATTGTATA AAATGTACT TTAAGTATA 180
AAATATAAG TAAGTAAAT TTCATGCATC TTTTATGAA GACCACCTAT TTTATATTC 240
45 AAATTAATA ATTTAAAGT TGCTGGCCTA ATGAGCAATG TTCTCAATT TCGTTTTCAT 300
TTTGCTGTAT TGAGACCTAT AAATAAATGT ATATTNTTT TTGCATAAG TAAA 354

50 SEQ ID NO:536
SEQUENCE LENGTH:343
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00599

SEQUENCE DESCRIPTION:

5 GATCCGTGAC AAGCGCACAG GCAAGACCAA GGGCTACGGC TTCGTCAGCT TCAAGGACCC 60
 CAGCGACTAC GTGCGCGCCA TGGGTGAGAT GAATGGGAAG TATGTGGGCT CGCNCCCCAT 120
 CAAGCTTCGC AAGANCATGT GGAAGGACCG GAATCTGGAC GTGGTCCGCA AGAAGCAGAA 180
 GGAAAAGAAG AAGCTGGGCC TGAGATAGGG TCTGTGGCCA GGCACCCGCT CCCACCTGGC 240
 10 CGGGCGCTGG CTCTCCCTC AGTTCTCTTT GGGAAAACCC CCAGCTNGTC CACCCATCCN 300
 NTGCCCCAAA ACCAGTTTCA GTAAATTAC GTTCATTTC AAA 343

SEQ ID NO:537

SEQUENCE LENGTH:341

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00600

SEQUENCE DESCRIPTION:

20 GATCGAACGG ACTGTGAAAT CCGCTCTTTG TCGGAAGCTG AGCAAGCTGT GGCTTTTTTC 60
 CAACTCCGTG TGACGTTTCT AAGTGTAAGT TGGTAGGACC CCGGCGGGTG TGGCAGCAAC 120
 TGCCCTGGAG CCCAGCCCC TGCNTCCATC TGTGCTGTGC GCCCCACAGT AGACGTGCAG 180
 ACGTCCCTGA NAGGTTCTTG AAGATGTTA TTTATATTGT CCTTTTTAC TGGAAGACGT 240
 ACGCATCTC CATCGATGTT GTATTTGCAG TGGCTGAGGA ATTCTTGAC GCAGTTTTCT 300
 25 TTGGCTTTAC GAAGCCGATT AAAAGACCGT GTGAAATGAA A 341

SEQ ID NO:538

SEQUENCE LENGTH:339

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00601

SEQUENCE DESCRIPTION:

35 GATCCTCGGG TGTCTTTCC ATCAGATAAA ATAGTTCAC ACAGACAGAT GTTTTTATCT 60
 ACTGAACTAC AAAGAGTAGA AGAGCTTTAT GATTCATTAT TACAAGCTGT TGCCTTCTAT 120
 GANTTAGCAG TGTTTGACTC TCAGCCTTAG AATTCTGAGG TTAACGTGCT AAAGTATAAT 180
 TTTAGCTCT AACGTAACAC CAACTGTTGT GAACATCCAT GTTATTGGAA AAGAACACAT 240
 TTTAGTGTA TTTTAGATGT TTAANTTCTG ACTTTTGGCT ATTAAATGGT TTACACAATA 300
 40 AGCCAAGACC AAATCAATAA ACATTTNTG AGAACGAAA 339

SEQ ID NO:539

SEQUENCE LENGTH:339

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00602

SEQUENCE DESCRIPTION:

50 GATCATCATC CGAGTGCAGA CCACGCCGGA CTACAGCCCC CAGGAAGCCT TTACCAACGC 60
 CATCACCAGC CTCATCAGTG AGCTGTCCCT GCTGGAGGAG CGCTTTCGGG TGGCCATAAA 120
 AGACAAGCAG GAAGGAATTG AGTAGGGGCC AGAGGGGGCT CTGCTCGGCC TGTGAGCCCC 180

55

5 GTTCCTACCT GTGCCTGACC CTCCGCTCCA GGTACCACAC CGAGGAGAGC GGCCGGTCCC 240
 AGCCATGGCC CGCNTTGTGG CCACCNTCA CCCTGACACC GACGTGTCCT GTACATAGAT 300
 TAGGTTTTAT ATTCCTAATA AAGTATAGCG GAAGAGAAA 339

10 SEQ ID NO:540
 SEQUENCE LENGTH:339
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00603
 SEQUENCE DESCRIPTION:
 15 GATCGTTATG AATATCAAAT GTCCATTCT ATNGTAATGA ATTCAGTGA ACCATCACAC 60
 AAAAGCACAC AAAGACCTCC TCCTCCACAG GGGAGACAGA GGTGGGGAGG CTCTCTTGGC 120
 TCACATAATC GTGTCTGTGT CACAAATAAT CATTAAATTA GCTATTTCA GCTAACACAT 180
 TTGTNGTTGC ACTTGAAAAA GAGTTAGTGA GCCTGTCTTG GAGTTTAAGT AGTTTCAAAT 240
 AAAAAAAGGC TACAGTGCCT CACAAAGGAT GTTCCCAGCA AGTNGTTTAA ATTCCCAGCA 300
 AGTTGTGTTAA GTGTAAATAN AANTATATGA ANTTGTAAA 339

20 SEQ ID NO:541
 SEQUENCE LENGTH:355
 SEQUENCE TYPE:nucleic acid
 25 TOPOLOGY:linear
 CLONE:HUMGS00604
 SEQUENCE DESCRIPTION:
 GATCCTGAAA TCTACTAGAG ACACCCCTAA GCCATGAATG AACTACATCC AAATACCTGA 60
 NTTTTTGAA TCTGTTTCAT GGATTTTCA TCTTCTACCG TATGTNAAAT TGCAAGTNTT 120
 30 TGAAGATTTA TAAGTACAAA TTTGGGAACA TACAAATCTT TTAGGTAGTA GAGTTTAAAG 180
 TGTATAAGCT AAAAGTGAAG GTAAGTGAAG GTTCTCTTGT TTCTTTGCAT TAATGTAAGT 240
 GTGTGGTTTG CCTTTGTCCC CCTGGATAGA ACGTGCATTT AAAGAATATA TTGTACTTAC 300
 TGTGACAGCA GATAATAAAC CAGTCTCTTG GAGGGCACAA CCCTTATTTG ACAA 355

35 SEQ ID NO:542
 SEQUENCE LENGTH:331
 SEQUENCE TYPE:nucleic acid
 40 TOPOLOGY:linear
 CLONE:HUMGS00606
 SEQUENCE DESCRIPTION:
 GATCTTTTT ANATAAANNT TATGTATTGT GGCATAATCC TTTTTTGAG CTCTACAGAG 60
 AACAGTCTTT TGGTAATAGT GGCAGGTATT TATTCCTTCT GAATATATAC CCCATTATAG 120
 45 GAATAACTGT TACTTATTTA GGATTCATC ATTGAAAATT TTNACCCAAG GCACAGCAGT 180
 GAANTTTATA GTNCTCANTT TAGTTGNCAT TATTGACAGG CATTGGNATT ATTAGTCATT 240
 GCTAAGCAAC TAAAACTTCA TCAGTTCAAN TAAGTTTTAN TTGTCANATG GCNGTATAAN 300
 CACATGANCT TTCTAGGAAA TATTCCTCN N 331

50 SEQ ID NO:543
 SEQUENCE LENGTH:330

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00607

SEQUENCE DESCRIPTION:

GATCGGTGTG CCCCCTGCG AGGGGCCCC CATGGGGCTG NTGGCCNTC CGCAGTCAGG 60
 ACATCCCAAC CCCTGGNTGG GACTGAACCA CCCAGAGCGG AGGGCNTCCC TTTNAGCCT 120
 TGTNAGTCAC CTGGCAGGCC CCAGCTGGGC TGGCTGTCCG TGTCCCTCAG CCTGGNTGGT 180
 GATTCCCTTG AGGCCAGAAA TNAAGAGTCC CTGTAGGTTT TGGTTTGTG TGTTTTATTT 240
 TGTTCCTTCA CCTTTTTTCC TCATTAATAA AAAAANGNCC CTGNGGAGTG TACTNATTNA 300
 TTTTTTGATN AAAGGGANGT AAAATGNAAA 330

SEQ ID NO:544

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00608

SEQUENCE DESCRIPTION:

GATCCAGACT GTAAGATGTT GTTTTAGGGG CTAAAGGGGA GAAACTGAAA GTNTTTTACT 60
 CTTTTTCTAA AGTGTGGTC TTTCTAATGT AGCTATTTN NTTGTTGCAT CTTTCTACT 120
 TCAGTACACT TGGTGACTG GGTAAATGGC TAGTACTGTA TTGNCNCTGT GAAAACATAT 180
 TTNTGAAAAG AGTATGTAGT GGCTTCTTTT GAACTGTTAG ATGCTGAATA TCTGTCCACT 240
 TTTCAATCCC AATTCTGTCC CAATCTTACC AGATGCTACT GGACTTGAAT GGTAAATAAA 300
 ACTGCACAGT GCTGTTGGTG GCAGTNAAA 329

SEQ ID NO:545

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00609

SEQUENCE DESCRIPTION:

GATCACTAGA TTTATGGAGG AATTNGTCAC AAATNACTN TAGAAAAATG CTGTCATATA 60
 GTTCATTTC TCAATTTCTG TTGCAGGAAG CCACTCCACC ACAGAATGCT AATATGCCAG 120
 TGGTACCCAG TACCTCTTGT ATATAGGTTA TTGCAAATAT TGTNCTGAAA TGCTTAACCT 180
 CAGAATTACA TTTTAAAG TAAATAATTG TTTTAAATCT ATTTTGTAAG GNTATAAAGT 240
 ACAATAGAAT TTCTGGAGTA CAGATTAAAC TATTTGCACT AACACACGTG CCGTGCATGA 300
 TTTAATAAAA TACTNNACT CTCNTAAA 329

SEQ ID NO:546

SEQUENCE LENGTH:328

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00610

SEQUENCE DESCRIPTION:

GATCACCGTG TGCTCAGGCC AGGTGTGAAT CCTGAGGTCC ATGGAGGTGC AGAGATGAGA 60
 TTACTCCTAT TCACGTTGAA GTGATTTGCT TTGTAAACAA AAAATTGCAG CTATTGTCTA 120

GCTTTCATTT TTTTACTGAG AACTTTAAAT TAGTCCCCTA TTAGAATAGG GTTGCTACTC 180
 ANCNTNTTTN AAAAACCGAA TTTTCATCATT TATCTAAAGA GNAATATGC AGANTAACGT 240
 GTCTTGTTAA GAGTGCAATA TTATATNNNN ANGTAAGAACT AAAANTNAAT TTGGGGGGAT 300
 TATTTATNCA GCATGANACC TANTNTGN 328

SEQ ID NO:547

SEQUENCE LENGTH:328

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00611

SEQUENCE DESCRIPTION:

GATCCCNNGG ACGTGAGACT TANNCTTCCA GCCAGTGTGA ATCATTGTAT TTTGTCTCAT 60
 AATCACAGCA CNCCTGCATG ACACAACAAC GTGCAGCATT TTTACATAA AAATATGGTA 120
 GANTTAATTT ATGACATGGA AATGCCCTTAC GTGGTATCAC ACTTAGTCTT GAAAAAACA 180
 CCNAGGTGAC GTTTAAATTT TTTAGTACAT ATCCTCAAAT TGGAGCTAAG TTATACTTCT 240
 TTTATAACCT TTTGGGCATC TGGTCGAGAG AAGACAAGAT TTTNTCTATT TACAGTGATG 300
 CAATAAATAT GTTTGCCACC TTTGAAA 328

SEQ ID NO:548

SEQUENCE LENGTH:322

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00612

SEQUENCE DESCRIPTION:

GATCTTGAAG AGACCGCTGG CAGCACCAGT ATTCCCAAGA GGAAGAAGTC TACACCCAAG 60
 GAGGAAACAG TTAATNACCC TNAGGAGGCA GCCACAGAAG TGGCTCCAAG AAAANAGGA 120
 ATTNTCCAAA GAGGAGCCGG TCAGCAGTGG NCCTGAAAGA GCGGGCTGGC AAGANCAGCT 180
 CCAAGAAGAA GAAATGTTC CATAAAGCAT CCCAGGANGA TTAGAATCAA ATGGACANTC 240
 TCTNGGAGGT GGGNATACCA TAGNCCAAGG TNCATTTCCC ACCNTGTGCC GTGTTCCCAA 300
 TAAANACAAA TTCACAAGGA AA 322

SEQ ID NO:549

SEQUENCE LENGTH:318

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00614

SEQUENCE DESCRIPTION:

GATCCACCTA GCCTCAGCCT CCCAAAGTGC CGCCGGGATT ACAGGCGTNA ACACCATGAC 60
 TGGCCTTCAT TATCTCTNTT TAAAAATGA AAAAGTTTAT AATTACATT CAGTAAATC 120
 ACCCTTTTGA GTGTCTAGTC TGTGAATTTT GACAAATGCA TGGTTTTGTA ACCAATCGAT 180
 AGGNCAGTTC TGCCACCCAG GACATTCCCN TCTGTTCTC TGTTCCTCTC TTCTCCTGCC 240
 CCCTAGCAAC CACTGGTGTG TTCTGTCCNT CTGGTTCATT TGACATTAT TTTAAATAA 300
 AATATTTTAA AATCTAAA 318

SEQ ID NO:550

SEQUENCE LENGTH:318

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00615

SEQUENCE DESCRIPTION:

GATCCTCACC GTGGAGGACC ATNATAATNA AGGTGGCATT GGTGAGGCTG TGTCCAGTGC 60
 AGTAGTGGGC GAGCCTGGCA TCACTGTAC CCACCTGGCA GTTAANCGGG TACCAAGAAG 120
 TGGGAAGCCG GCTGAGCTGC TGAAGATGTT TGGTATCGAC AGGGATGCCA TTGCACAAGC 180
 TGTGAGGGGC CTCATNACCA AGGCCTAGGG CGGGTATGAA GTGTGGGGCG GGGGTCTATA 240
 CATTCCTGAG NTTCTGGGAA AGGTGCTCAA AGATGTACTG AGAGGAGGGG TAAATATATG 300
 TTTGNGNAN AATGCAAA 318

SEQ ID NO:551

SEQUENCE LENGTH:314

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00616

SEQUENCE DESCRIPTION:

GATCCCTCT CTGAAGAGAA AGGAGGAAAG AAAAGAAAA AACAGAAACA GAAGCTCCTG 60
 TTCAGCACCT CAGTCGTCCA CACCAAGTGA CACTACTGGN CCAGGCTACC TTCTCCATCT 120
 GGTTTTTNTT TTTNTTTTT TTTCCCAT GCTTTGTTT GGNTGCTGTA ATTTTAAAGT 180
 ATTTGAGTTT GANCAGATTA GCTCTGGGGG GAGGGGGTTT CCACAATGTG AGGGGGAACC 240
 AAGAAAAATTT TAAATACAGT GTATTTTCCA GCTTCCTGTC TTTACACCAA AATAAAGTAT 300
 TGACACAAGA GAAA 314

SEQ ID NO:552

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00617

SEQUENCE DESCRIPTION:

GATCCCTACT TGGNAGTTAA CCCTAACTAC TTGCTCGAAG ATTGAGATAG TGAAAGTAAC 60
 TGACCAGAGC TGAGGAACTG TGGCAGCA CCTCGTGGCC TGGAGCCNGG CTGGAGCTCT 120
 GCTAGGGACA GAAGTNTNC TGGAAGNAT NCTTCCAGGA TTTNTTTTC AGAAACAAGA 180
 ATTGAGTTGA TGGTCCTATG TNTCACATTC ATCACAGGTT TCATACCAAC ACAGGCTTCA 240
 GCACTTCCTT NGGTGTGTTT CTNTCCAGT GAAGNTGGAA CCAAATAATG TGTAGTCTCT 300
 ATANCCANTA CCN 313

SEQ ID NO:553

SEQUENCE LENGTH:310

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00618

SEQUENCE DESCRIPTION:

GATCTTAGCT AGTTCATCAC TTCCTCAGGG AAACATTCCC TAATTCTGT CACAGAGTAA 60

GACCCGTTGT TATACGTCTC ACCTGACCAT GTACCTCTAC TTAGCATTTA ACACGTGTAA 120
 TTTTGTATGT ATTGGTTTGA TTAATGTCAG ANCCACTAGA TTGTAAACTC CATGAGGACC 180
 GGAATTTNGT TTCTGTCAAT GTCATTGTTT AACTTTGTAT TTTTATGCCC TCATACAGTG 240
 CCTGGCACAT AGTAGGTGCT CAATTAACTT NATTGGAAAG AATAAAATGA ATGGATGAGG 300
 TATCAAGAAA 310

SEQ ID NO:554

SEQUENCE LENGTH:310

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00619

SEQUENCE DESCRIPTION:

GATCTGGGGG CCACCACCCT GTGCCGGTGG CCTCTGGGCT GCCTCCCGTG GTGTNAGGGC 60
 GGGGCTGGTG CTCATGGCAC TTCCTCCTTG CTCCCACCCC TGGCAGCAGG GAAGGGCTTT 120
 GCCTGACAAC ACCCAGCTTT ATGTAAATAT TCTGCAGTTG TNACTTAGGA AGCCTGGGGA 180
 GGGCAGGGGT GCCCCATGGC TCCCAGACTC TNTCTGTGCC GAGTGTATTA TAAATCGTG 240
 GGGNAGATGC CCGGCCTGGN ATGCTGTTTG GAGACGGAAT AAATGNTTTC TCATTGAGTC 300
 TNCAGTCAAA 310

SEQ ID NO:555

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00620

SEQUENCE DESCRIPTION:

GATCCNGTGC TGAAGAGAA ACCAAGAAAA AAGATGACAT TCCAGAAGAA GACAAAGGAA 60
 ATGTAAAACA ATGTGAAATC AATTATGTAA AGAAATTTCAGAGCTTCAA GACCACAAAC 120
 TTAAATAAG TAAAGANGAC AGTAAATTN TAAAAAGGC TCGGAAAGAT GGATTTTTC 180
 ATGAGACGCT TCTGGACAGG NGAGCCAAAT TGAAGCCGA CAGATACTGC AAGTNACTGG 240
 GATTTTNTT TCTGCCTTAT CTTNCTGTNG TTTTCTGA NTAAATATT CAGAGGAATG 300
 CTTTTAAA 308

SEQ ID NO:556

SEQUENCE LENGTH:300

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00621

SEQUENCE DESCRIPTION:

GATCTTCCTG AAGTNTCTCC CCGTTTNGTG CAGCTGGCCA TACCCAGGT GGACATNATG 60
 AGTCAGGCTG ACTTAATTNC TCATGAGCAG ACCATCCCAG TGAATGCAA GGGCATGGGC 120
 TCCACAGCCT GGACCCTGGC ATGGAGTCCA GCNNCCTGCT CACCGGCCAG GAGGCCTGGG 180
 GGGGGGTAC TTACCCCTNT NAGCCTCANT TTCTNTTCT GGAAGCGGAG ATGGTAATAG 240
 CTTTACATT NGAGGTGAAT GTNAGAATTA AACTTGGGCA CATGGAGGAA TACACCTAAA 300

SEQ ID NO:557

SEQUENCE LENGTH:299

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00622

SEQUENCE DESCRIPTION:

GATCACTTGT CCTATTACCC TATACCTAGC ACTTGTGACA CCACCCCTAA ATCACTTTGA 60
GCCTGGGAAA TAAGCCCCCT CAACTACCAT TCCTTCTTTA AACACTCTTC AGAGAAATCT 120
NCATTCTATT TCTNATGTAT AAAACTAGGA ATCCTCCAAC CAGGCTCCTG TGATAGAGTT 180
CTTTTAAGCC CAAGATTTTT TATTTGAGGG TTTTGTGTT TTTAAAAAA AATTGAACAA 240
AGACTACTAA TGACTTTGTT TGAATTATCC ACATGAAAAA AAAGAGCCAT AGTTTCAA 299

SEQ ID NO:558

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00623

SEQUENCE DESCRIPTION:

GATCTGCTTC TCCAGTTTTT GAGGAGCCAG CCAGGGGTCC AGCACAGCCC TACCCCGCCC 60
CAGTATCATG CGATGGTCCC CCACACCGGT TCCCTGAACC CCTCTTGGAT TAAGGAAGAC 120
TGAAGACTAG CCCCTTTTTC TGGGGAATAA CTTTCTCCT CCCTGTGTTA ACTGGGGCTG 180
TTGGGGACAG TGCGTGATTT CTCAGTGATT TCCTACAGTG TTGTTCCCTC CCTNAAGGCT 240
GGGAGGGTGN TAAACACCAA CCCAGGANTT CTCAATAANT TTTTNATTAC TAAACCTGAA 300
A 301

SEQ ID NO:559

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00624

SEQUENCE DESCRIPTION:

GATCAGATTT TGCTAAATGG AAATAATATA ACAATGCTGG TTCCTGGAGG AGAAGGACCT 60
GAAGTGTGAA TGAGTTTCCT TGACTTACAC TAGATTTTGT TTTGGCTTAT AATGACAAGA 120
AAATGGAATT TTTTTTCCC ACTTTCTAAT GTTTAAATCC CATAAAGCTA AGTTTCCCGT 180
TAAAGGGAAG TGCTTTGAAG ATGTGTACCC ATTTTGTAA GTTAATCATG ATTATCCTGG 240
AAAAAGAAGA AAAGAGCTTC TTCTTTGCAG ATGAAAAATA AGGTGTTTTT GGTAAAA 297

SEQ ID NO:560

SEQUENCE LENGTH:304

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00625

SEQUENCE DESCRIPTION:

GATCTATTTG TAGATTAGGA TTAATGGA TTTAATCCAT TTTAAGGCT GTGTGAATTT 60
TTCTAAACAA GAACCATTTG CAATATGGAT TTCTTAGAGA TTAACCAAT TATACTTAT 120
TAGCAGTCGC GAGCACATGT TCATATAGTC AATGTAAAAA TACACTAATG AGTATTGGT 180

AAATCCCAGT AGGCTTTTAC CATTAGCATA ATTTTGTGTT GTACAATTAA GTTACAATTA 240
 CATCTCTAAT TTTGGATAAT ATTCATTGGT TAACANTANA GTGACAAAAG CTCATGCCTT 300
 CAAA 304

SEQ ID NO:561
 SEQUENCE LENGTH:301
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00626
 SEQUENCE DESCRIPTION:

GATCTGGAAC TTTGCACATG TCACTACTGG GGAGGTGTT CTGCTCTAGC TTCCACGATG 60
 AGGCGCCCTC TTTACCTATC CTCTCAATCA CTACTCTTCT TGAAGCACTA TTATTATTTC 120
 TTCCGCTGTC TGCCTGCAGC AGTACTACTG TCAACATAGT GTAAATGGTT CTCAAAAGCT 180
 TACCAGTGTG GACTTGGTGT TAGCCACGCT GTTTACTCAT ACAGTACGTG TCCTGTTTTT 240
 AAAATATACA ATTATTCTTA AAAATAAATT AAAATCTGTA TACTTACATT TCAAAAAGAA 300
 A 301

SEQ ID NO:562
 SEQUENCE LENGTH:294
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00627
 SEQUENCE DESCRIPTION:

GATCTNAGGA GCTTAGGGA GAAGACTTGG TGGGGCTGGA GCACACCTTG GGNCTCANTG 60
 GTTTCTGTGT CCNGTGGTG CCANTCCTTC TGGGCAGTGC AGGCGGCTGC CAGGCCCAGC 120
 CCTGACTTCC ACTCTGGCTC AGCAACCTGG TTATTTATGT GGGGCCGTGC AGGCATGGGC 180
 CCACTGCCTG TCCATCCTGT TTCTNTTATA AATTGAACT CACCATTGCC CTATCCTTGT 240
 GTCTCCACCC GCTTCCATGT GTGAATAAT AAAAGGTGGG AAAGTGCTGT CAAA 294

SEQ ID NO:563
 SEQUENCE LENGTH:296
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00628
 SEQUENCE DESCRIPTION:

GATCTGCCAT AAGAAATCT AGTCAACTC TAATTTTATG TAGTAAATAA ATTGGCAGGT 60
 AATTGTTTTT ACAAAGAATC CACCTGACTT CCCCTAATGC ATTAAAAATA TTTTATTTA 120
 AATAACTTTA TTTATAACTT TTAGAAACAT GTAGTATTGT TTAACATCA TTTGTTCTTC 180
 AGTATTTTTC ATTTGGAAGT CCAATAGGGC AAATTGAATG AAGTATTATT ATCTGTCTCT 240
 TGTAAGTACAA TGTATCCAAC AGACACTCAA TAACTTTTTT GGTGTTAAA CTGAAA 296

SEQ ID NO:564
 SEQUENCE LENGTH:307
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS00629

SEQUENCE DESCRIPTION:

5 GATCGACTAC AGAGTACTTN TTTCTTATGA TGATTGGTGT AGAAATGTGT GATTGCGGTG 60
 GGCTTTTACA TCTTGCCCTAC CATTGCATGA AACATTGGGG TTTCTTCAAA ATGTGTGTGT 120
 CATACTTCTT TTGGGAGGGG GGTGTTTTT TTCTGTTTAT TTTCTGAGAC TCCTACAGGA 180
 GCCAAATTTG TAATTTAGAG ACACTNAANT TTGTTAATCC TGTCTGGGAC ACTTAAGTAA 240
 CATCTAAAGC ATTATTGCTT TAGAATNNNC AAATAAAATT TTCCTGACCA AATTGTTTTG 300
 10 TGGGAAA 307

SEQ ID NO:565

SEQUENCE LENGTH:296

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS00630

SEQUENCE DESCRIPTION:

20 GATCTTGCTC CTTCAGACTC TGACCTGAGT GGAGACCTTT CCACCAGACA CAGCTCGGGC 60
 CTGTGTAATT GTAGGAGAAG ACACTCAGCA GTGATTGCCA TGGCACAGAG CCGTGGTCAT 120
 TGTGCTGTT ACAAGAAGA AAACCATCTG AGTTCTAACT CCTTGTTGTC TAAAAAGTAG 180
 TTCCCAAGAG TCTGAGAAGC TATTCTATT TTTAAGAGTC ATTTTTTGTA ATNTTTGTAA 240
 NACAAAAGTA CCAATCTGTT TTGTAAATAA AANTCATCCT AAAATTCGAN GTTAAA 296

SEQ ID NO:566

SEQUENCE LENGTH:288

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS00631

SEQUENCE DESCRIPTION:

30 GATCTTTNGC TAGGTGGATG ACTAGTNATA TTCAAAGCCT TTTCTCAAAG CCCTTTCAGT 60
 TACAACCACC CCACTATGGA ATCAGTATTT AGTTATACAT TTGTATAAGA NCCTGTATTT 120
 TGAAAAACAC ATTCATGTAT ATTTATTCCT GGAATTATTT GCCTGTAAAA CAGTGTCTTT 180
 35 CATGTTCTCT CCCAGATTG TAACTCTGT AAGAAGCTGC TNGTATCTGT ATCCCTTGTT 240
 GAAACTCTGA AAACACTGAA TAACTAAANT CTTCTTCTCA TCCNTAAA 288

SEQ ID NO:567

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS00632

SEQUENCE DESCRIPTION:

45 GATCTTGATA TTCTGTACAA GTTGATGTAA TACCCTGATG CGTTTTAGAG GACTTGGCAT 60
 AAAATNAAAG NTTGGCAAAG GCCCTTGAGG GGCTTGGGGA TGAGAGTATG GAACTGTCTG 120
 CATTGGACCC TAACTGGAC TAGANGAGGC ATCTTCAAGG TTCATACGTT GTCCAGCTGT 180
 AAGTTCATTT GAGTAGCAGA GCTAACAAAT ATTTGAGGTC AAAACCCTAC CATGTTAAAA 240
 50 CAAACAAAAA CTTATCATGT TAATAAAAGT ATTCATTTGC TTGANANANA AA 292

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SEQ ID NO:568

SEQUENCE LENGTH:291

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00633

SEQUENCE DESCRIPTION:

GATCCTGACA AGAAGAAAAA NAAGCTCAAA GTCAAAAAAT CTCGTGAAAA ACGGAGTTTG 60
 GCCTCTCATC TCAGTGGATA TATCCCTNCC AAAAGGAAAC AAGGGCAAGG CTTATCTTTG 120
 TGTCAAAACG GAGAGTCACC CAACTGTGTG GAAGACAAGA TGCTCTCGAC AGTTGCAGTA 180
 CTTACCCCTTG GCTAAGAACT GCACTGCTTT GTTTAAAGGN CTGCAGACCA AGGAGCGAGC 240
 TTTCTCTCAG AGCATGCTTT TCTTTATTAA AATTACTGAT GCAGANAAAA A 291

SEQ ID NO:569

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00634

SEQUENCE DESCRIPTION:

GATCANGCTG GCTGCAAAGA AGGGACTGGA CCCATACAAT GTACTGGCCC CAAAGGGAGC 60
 TTCAGGCACC AGGGAAGACC CTAATTTAGT CCCCTCCATC TCCAACAAGA GAATAGTAGG 120
 CTGCATCTNT NAAGAGGACA ATACCAGCGT CGTCTGGTTT TGGCTGCACA AAGCGGANGC 180
 CCAGCNTTGC CCCCCTNGT GGAGCCCATT ACAAGCTNGT NCCCCAGCAN CCTGGCACAN 240
 TGAGGNACCT GCACTAAATT ACTNAAAATG TGCTGTAAAG NTTTN 285

SEQ ID NO:570

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00635

SEQUENCE DESCRIPTION:

GATCACCCCTT GTAATGTGTT ACGGGTCCAT TTTTCCTGGA ATCGTTTAAAT CTAAAGCAGT 60
 TTCCCTGTGTT TTGGAGATTT TNTAGTTAAT TTTAATTTTG GCTATTGTTT GGAAAAGATG 120
 AGCTGTCTGT GTAGATATGA AGTATAGTTT TTNCCATAAA ACAGATGTTT ATTTTGTATT 180
 AAAAAATACC ACTGTACTTG TTTTACACCA TTTGTATACA TGTGGTGATA TTAATGCTAA 240
 ACTGTAAAT TCAGGAATTA AAATGTGACC CTGTAATTCC ATAAA 285

SEQ ID NO:571

SEQUENCE LENGTH:287

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00636

SEQUENCE DESCRIPTION:

GATCTAACCA TTTTCATACT CTTAACTGAT TGAAACAGAT TCAAAGAAGT ATCGAGTGCT 60
 ATGCATTGAA ACTTGTTTTT AAATGTTAGA TGGCACTATG TATATTAATG TAAANCAATG 120
 TTAATTTACT CAAGTTTTCA GTTTGTACCG CCTGGTATGT CTGTGTAAGA NGCCAATTTT 180

NGTGTATTGT NACAGTTTCA GGTNATTNAT ATTCGATGTT TTGTAAANCT CAAATANCGA 240
CTATACTNAT GGGNCCAAAT AAATGGGCAT CTGCATTCTN GGTAAA 287

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SEQ ID NO:572
SEQUENCE LENGTH:282
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00637

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SEQUENCE DESCRIPTION:

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GATCTNTGGT GGCAATGNCT GACCAGTAGA CTGGTGGCTC ACTTCTNCCC ACCTGCCGGC 60
AACACCAGTG CCAGGAAAAG GCCAAAAGAA TGTNTGTTTC TAACAAATCC ACAAATAGCC 120
CCGAGATTCA CCGTCCTAGA GCTTAGGNCT GTTTCCACC CCTCCTGACC CGTATAGTGT 180
GCCACAGGAC CTGGTTCGGT CTAGAACTCT CTCAGGATGC CTTTCTACC CNATCCCTCA 240
CAGCCTCTTN CTGCTAAAAT AGATGTTTCA TTTTNTGGA AA 282

20

SEQ ID NO:573
SEQUENCE LENGTH:279
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00638

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SEQUENCE DESCRIPTION:

30

GATCTACTGG CGAGCGATGA AAATGTTGCA GGGAGAGTCA GCAGAGGCAT TTGTAGCTAA 60
ACATGCTATG CATCAGACTG GCCATTTATG AAGATGAAGA ATACAGTCAG CTTTGTGAAA 120
TAGTATTGCA AGCAAGCCCC GTGGGCAAAT TTGTATTGAG TCCATCTGTA ATTTGCTCAG 180
TGATGGCAGA CAAGATGGCT GTCGTGTTTT GAGACACACT TTAATTTTAT GTTAACCTGT 240
TAAATCTTTT TAAAAATTAA AAAATTTTAA TGATTGAAA 279

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SEQ ID NO:574
SEQUENCE LENGTH:279
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00639

40

SEQUENCE DESCRIPTION:

GATCATTGCA TTTTCCTGTA TTTTCTAAAA TGGCTCCAAT TTTGTNTTTT AAGCTTCAGC 60
TTAAGAGGAA GTTTATGTTT TAATCTTGA CTGAGAATAC AGTATTGAGA TTCTNTGTTT 120
TACAGATAAC AACTGGTTTT TATTACTCAT TAAGTTCATT TGCATCCCGT AGCCCTCTGT 180
AAATGTTTCC CCTAGTTGTA TGTACGTAAA TGCACGCTTA TCCAGTNTAT ATTAGACATT 240
TTTGTGCTAA AATATATTAA GTGGGATTTT TGTAGCAA 279

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SEQ ID NO:575
SEQUENCE LENGTH:280
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00640

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SEQUENCE DESCRIPTION:

55

EP 0 679 716 A1

5 GATCTTTGCA AGGGCAAAAC TACAAGTAAC GAGTTTATA TAATTAATTT AAATTTNTNA 60
CAGGTTTTCA TGTTCAAGGAT AAACCATACT TCCACCTTGG GTGAGAACAC TTGCAACAGT 120
TTATTAATGA GGTGACTTTC ACCTTAGGAC AACTGTTGCA TGCCAAGTTT TTTGTGTGTG 180
TGAAACACTN TCAAACTGA TTTAAAAGAT GTAAATTTAA AATTGGTTGT ATCTAATATG 240
CCCCAGGTTT GGTAAATAAA CAATTCTTTT TAAAAACAAA 280

10 SEQ ID NO:576
SEQUENCE LENGTH:300
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00641

15 SEQUENCE DESCRIPTION:
GATCTGCCTG TCCCTTTTTC CCCTGGGGTT TGACACACAG GCTCCTCTCA GCATGAGGTG 60
GAGCAGTGAC CAGGTGGAGC AGTGACCAGG ACGCCTCTGG CCCAGTGCTG CCCAGCCTCC 120
CCGNC CGCTC CCAGGCGCCC CATGTCCTCA CAGGCCAGGA CGCCATGNCA GGATGGAGAG 180
GACTTGGTGG ATTTTGTGTT CTTGCCTGAC CTCAGTTTCA TGAAAGAAAG TGGAAGCTAC 240
20 AGAATTATTT TCTAAATAAA AGGCTGAATT GTCTGAAAAA TAAATATAT TGTATTAAA 300

25 SEQ ID NO:577
SEQUENCE LENGTH:278
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00642

30 SEQUENCE DESCRIPTION:
GATCTGGGAC GTGGTTCGGC GGANAGTCCC CAGCCCGGCC CCCTGCCTGG GACCACCAGG 60
CCCCCAGGAG AAGCCGCCTG AGCCACAACC TTGCGGCATG CAAATNAGAT GGCCGCTCCA 120
GGCCTGGAAT GTTCCGTGGC TGGGCCCCAC GGAAGCCTG ATGTCAGGG TTGGGGTGGG 180
ACGGGCAGCG GTGGGCACA CCCATTCCAC ATGCAAAGGG CAGAAGCAA CCCAGTAAAA 240
TGTTAACTGA CTTCCAGCCT CACCCGTGGG CGGTCAAA 278

35 SEQ ID NO:578
SEQUENCE LENGTH:277
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
40 CLONE:HUMGS00643

45 SEQUENCE DESCRIPTION:
GATCAGGGCC CACTGATGAT GGTGAAGAAG AGATGGAAGA AGACACAGTC ACAAACGGGT 60
CCTGAGCAGT GAGGCAGATG TATAATAATA GGCCCTCTTG GAACAAGTNT TGCTTTTNGA 120
ACATGGTATA ATAGCCTTGT TTGTNTTAGC AAAGTGAAT CTATCAGCAT TGTTGAAATG 180
CTTAAGGCTG CTGCTGATAA TTTNNTAATA TAAGTTTGA AATCNAAATG TCAATTTNCT 240
ACAAATNATA AAAATAAACT CCACTCACNA TGCTAAA 277

50 SEQ ID NO:579
SEQUENCE LENGTH:277
SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS00644

SEQUENCE DESCRIPTION:

GATCCGAGTC GTCCGGAAT CCATTGCCC GTNTTCTCAC AGTTATTAAC CAGACTCAGA 60
 AAGAAAACCT CAGGAAATTC TACAAGGGCA AGAAGTACAA GCCCCTGGAC CTGCGGCCTA 120
 AGAAGACACG TGCCATGCGC CGCCGGCTCA ACAAGCACGA GGAGAACCTG AAGACCAAGA 180
 AGCAGCAGCG GAAGGAGCGG CTGTACCCGC TCGGAAGTA CGCGGTCAAG GCCTGAGGGG 240
 CGCATTGTCA ATAAAGCACA GCTGGCTGAG ACTGAAA 277

SEQ ID NO:580

SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00645

SEQUENCE DESCRIPTION:

GATCAGGACC CACCTNCAGT NCTTCTGAAA GTGTGACAGT GTCCAGCCGG TTCTGCAGCA 60
 CTAGGGGAGG GGGCAGATGG TGGTTGCATG GGCTTCCTGG GTCTCCACTC TCCGTCTGGC 120
 CTAAAGGTGA TGTATTTGGT GTTTGGCCCT GCAGTCCCA CTCTTGAGGC TTAAGGCGCA 180
 TGTGGCAGAN CACTNCTTCC AGCAGTAGTC GCTTACTGT TACNGTTTA GGCCTAGAAG 240
 TTTCCNCA TCTGTAATG TGATTAAAA TNTAAA 276

SEQ ID NO:581

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00646

SEQUENCE DESCRIPTION:

GATCTACTTA CTCAAGTCTN ATGAATNCTG NGCCTTTCAT CACATTCCTA GCCCACTCTC 60
 ATCATTACTG CAGAAGGGTG TTGTGATGAC CAGTNTTATA CTGTGTTTG ATATGTCTAG 120
 CAATAACTTA AAGAAAAAA AACCTGGGAA ATCTTCAACA TGNNTNGGA ACATATATGT 180
 ATGTATTAAT GNATATACAT GGCTTAACTT ATACGGTTAT GGCAGCNCCT GTATACAGTT 240
 TGAACATG NACCTGAAAA ANAATTCTTA ANTTN 275

SEQ ID NO:582

SEQUENCE LENGTH:307

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00647

SEQUENCE DESCRIPTION:

GATCGCCATC ATGAACGACA CCGTAACTAT CCGCACTAGA AAGTTCATGA CCAACCGACT 60
 ACTTCAGAGG AAACAAATGG TCATTGATGT CCTTCACCCC GGAAGGCGA CAGTGCCTAA 120
 GACAGAAAT CCGGAAAAAC TAGCCAAAT GTACAAGACC ACACCGGATG TCATCTTTGT 180
 ATTTGGNTT AGAAGTCATT TTGGTGGTGG CAAGACAACT GGCTTTGGCA TGATTTATGA 240
 TTCCCTGGNT TATGCAAAGA AAANTGGAAC CCNAACATAG NCTTGCAAGT CATGGCCTGT 300
 ATGNGGN 307

SEQ ID NO:583
 SEQUENCE LENGTH:272
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00648

SEQUENCE DESCRIPTION:

GATCTGAATT TTTTCCTCCT TTTGGTTTTA TTTTGTGGT TTATTTTGTG TTTTCTTTTC 60
 TCCTTTTGG GGGGTATTCA GAGTGGGCTG GGCCCTGGG CGAGACACAG CTACCTCTGT 120
 TGGCATCTTT TTAATACCAG GAACCCAGCG GCTCTAGCCA CTGAGCGGCT AAATGAAATA 180
 AAGTGGAAAA AAAAAAANGG GAAAAACCCA AAGGNTTAAA AACCCACNGG AATTTTNTTG 240
 TNGAAANTNG AAAATAAAGG TTTCCNNGTA AA 272

SEQ ID NO:584
 SEQUENCE LENGTH:279
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00649

SEQUENCE DESCRIPTION:

GATCTATACC AATTAAACAT TITCATAGTT CTGCCTATTG TCCTTCCTG AGGCTCCATT 60
 GCTGCTTGGT GGCCATTCTC TGCCTTTTTC CAGTCACCTG AACAATGACC CATCATCTCT 120
 TGCTTGCTTG AAATCTTGCT GAAATGTTCT CATTTCTGTG TTGCTGTATG GGCTCGGGTG 180
 GGATGTTTGT TGCTCTGTT GTGTTTATTC ACCAATTGTG ACATTATTG TTGTCCTTTA 240
 CTA CTGTGTAAG CAGTAAATAT AGTTTGGTAT TCTGTCAAA 279

SEQ ID NO:585
 SEQUENCE LENGTH:273
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00650

SEQUENCE DESCRIPTION:

GATCCCAGAC TGGTTCTTGA ACAGACAGAA GGATGTAAAG NATGGAAAAAT ACAGCCAGGT 60
 CCTAGCCAAT GGTCTGGACA ACAAGCTCCG TGAAGACCTG GAGCGACTGA AGAAGATTCG 120
 GGCCCATAGA GGGCTGCGTC ACTTCTGGGG CCTTCGTGTC CGAGGCCAGC ACACCAAGAC 180
 CACTGGCCGC CGTGGCCGNA CCGTGGGTGT GTCCAGNAAG AAATAAGTCT GTAGGCCTTT 240
 GTCTGTTAAT AAATAGTTTT ATATACCTNN AAA 273

SEQ ID NO:586
 SEQUENCE LENGTH:275
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00651

SEQUENCE DESCRIPTION:

GATCTNCCAC GTCTCCATCT CAGTACACAA TCATTAAATA TTNCCCTGTC TTACCCCTAT 60
 TCAAGCAACT AGAGGCCAGA AAATGGGCAA ATTATCACTA ACAGGTCTTT GACTCAGGTT 120

CCAGTAGTTC ATTCTAATGC CTAGATTCTT TTGTGGTTGT NGCTGGCCCA ATGAGTCCCT 180
AGTCACATCC CCTGCCAGAG GGAGTTCTTC TTTTGTGAGA GACACTGTAA ACGACACANG 240
AGAACAAGNN TAAAAACAATA ACTGTGTGTG TTAAA 275

SEQ ID NO:587

SEQUENCE LENGTH:269

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00652

SEQUENCE DESCRIPTION:

GATCTTATGG ATAAACTCA GAAAGTGAAG GTGAAGAAAG AAACGGTGAA CTCCCAGCT 60
ATTTATAAAT TTCAGAGTCG TCGAAACCGT TGACGTGTTA TAGATAAGCC TTGTCATTNT 120
GTATCAAAAA TCTGTTGTCG TTTTCTAGTA ACTTCAAATT CCATTACTCC AAATGGCATG 180
GTTTTCCGGT TTGTAACCAT AACTAAATTG TCAGTCTGAC ATTTAATGTC TTTCTATGGA 240
CAACATTAATA TCNCCCTCCC TTCTGTAAA 269

SEQ ID NO:588

SEQUENCE LENGTH:272

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00653

SEQUENCE DESCRIPTION:

GATCAAGTGG CTTTCCCTGG GACCTGCCCA GCTTTGAGAA TCTCTNCTCA TCCACCCTCT 60
GGCACCCAGC CTCTNAGGGA AGGAGGGATG GGGCATAGTG GGAGACCCAG CCAAGAGCTG 120
AGGGTAAGGG CAGGTAGGCG TGAGGCTGTG GACATTTTCG GAATGTTTTG GTTTTNTTTT 180
TTTTAAACCG GGCAATATTG TGTTCAGTTC AAGCTGTGAA GNAAAATATA TATCANTGTT 240
NNCCAATANA ATACAGTGAC TANCTGAACA AA 272

SEQ ID NO:589

SEQUENCE LENGTH:268

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00654

SEQUENCE DESCRIPTION:

GATCGTCAAA TCTTTNCAA ATTTAATNTA TATGTGTATA TAAGGNAGTA TTCAGTGAAT 60
ACTTGAGANA TGTACAAATC CTTATCCAT ACCTGTGCAT GAGCTGTATT CTTACAGCA 120
ACAGAGCTCA GTTAAATGCA ACTGCAAGTA GGTACTGTA AGATGTTTAA GATAAAAGTT 180
CTTCCAGTCA GTTTTCTCT TAAGTGCCCTG TTTGAGTTTA CTGAAACAGT TTACTTTTGT 240
NCAATAAAGT TTGTATGTTG CATTTAAA 268

SEQ ID NO:590

SEQUENCE LENGTH:267

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00656

SEQUENCE DESCRIPTION:

GATCAAAAAAT AAAATGTTAT TTTTAAAGTT TCTNTTTGAG ATTTTNCTTA AGTTTGGTA 60
 GATATTCTTA AGTTTGTAGT ACCTCAGTTT GGGAAATTAAG TAAGCTAAAC ATTGTGTCCT 120
 TATTATNAGT TATATAAAAC TATGCTTTAG ACTTTGTNAG AAACCTCTGC CCCACCTTGA 180
 CTGACTGCTT TNCCATTNTT GGTGTACAA AATGAATTCA CACTTTAATG CTATGGCCAC 240
 CTTTAAATAA AGTACAGCGT GACTAAA 267

SEQ ID NO:591

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00657

SEQUENCE DESCRIPTION:

GATCTAGATT CTACATGTTA CCATTGGTTT ATTCTTGTGC TTTCTGTATT TAAACTTTG 60
 GCTGTACTAA GCAAATGCAA GGTATAATT TAGCTAATAG TAGTTTACAG ACAATTCTGA 120
 TGATTATGAT TTCATTGGT TTAACAAAGC TGTACTAGTT CATTTCATAA GGAAATGATA 180
 CTGTAGACAA ATGTAAATAA AGCCTGTGAG TCAAGCATCA AGTGGTGTGTT GTTAGAAATA 240
 ANCTAGAGAT TTTTAANCTC TGAAA 265

SEQ ID NO:592

SEQUENCE LENGTH:264

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00658

SEQUENCE DESCRIPTION:

GATCTGGGGC CAGCTCACCG CTCACGTCCT CGTCATCGAC AACTCCACCC TNTACATCAG 60
 TAGAGCATGC ACCATTTTGA ACGTGACATT TNCGGTAAAG TAAACTATGC TGATTTCTCA 120
 GACTTTAAAG ATGCTCTNNT TCTGTGTGN AAATAGGACC CAAAGTGTCT CGATTGCTGA 180
 AGTGATGAAC AAGTGGGAAA GCAGATTGA GACTATTTC TTATCTGAAT ATTTAAATGA 240
 AATACAGCAT CTTTAAAANG CAAA 264

SEQ ID NO:593

SEQUENCE LENGTH:262

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00659

SEQUENCE DESCRIPTION:

GATCTTTTAA AAAGATGATG CAGTTCTGTA TTTATTGTGC TGTGTCTGGT CCTAAGTGGA 60
 GCCAATTAAN CAGGTTTCAT ATGTATTTN CCAGTGTGA ATCTCACACA CTGTACTTTG 120
 AAAATTCCT TCCATCCTGA ATAACGAATA GAAGAGGCCA TATATATTGC CTCCTTATCC 180
 TTGAGATTC ACTACCTTTA TGTTAAAAGT TGTGTATAAT TGTTAAAATC TGTGAAAGAA 240
 TAAAAAGTGG ATTTAAATTA AA 262

SEQ ID NO:594

SEQUENCE LENGTH:260

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00661

SEQUENCE DESCRIPTION:

GATCCATCCA AAAACAAGGA CTGCAGCCTA AATTCCAAAT ACCAGAGACT GAAATTTTCA 60
GCCTTGCTAA GGGAAACATCT CGATGTTTGA ACCTTTGTTG TGTTTTGTAC AGGGCATTCT 120
CTGTACTAGT TTGTCGTGGT TATAAAACAA TTAGCAGAAT AGCCTACATT TGTATTATT 180
TTCTATTCCA TACTTCTGCC CACGTTGTTT TCTCTCAAAA TCCATTCCCT TAAAAAATAA 240
ATCTGATGCA GATGTGTAAA 260

SEQ ID NO:595

SEQUENCE LENGTH:259

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00662

SEQUENCE DESCRIPTION:

GATCCCTTTA TGAAACCTTG TGAATAGATG AATGTNTGGA GATGGCGACT AGTGGACAAC 60
AGAACAAATAT TGGAATGGTG GTAATACGAG GAAATAGTAT CATCATGTTA GAAGCCTTGG 120
AACGAGTATA AATAATGGCT GTTCAGCAGA GAAACCCATG TCCTCTCTCC ATAGGGCCTG 180
NTTACTATG ATGTAAAAAT TAGGTCATGT ACATTTTCAT ATTAGANTTT TTGTTAAATA 240
NNCTTTTGTA ATAGTCAAA 259

SEQ ID NO:596

SEQUENCE LENGTH:257

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00663

SEQUENCE DESCRIPTION:

GATCNNGGCT AAGCCAGCCA GCCCNCCCGC GCCAGGNAAA ACAGGGCTGC AGGTGTCCTG 60
TCTCCCAGCC TCATCTGGCC GGCCTCCCCA AACATTGCC TGTCCATCAG CTCTTCCTCC 120
TTTCGAGTCA TGTGGAAAGG GACAGGNCCA AGTGGCCTTG GTGTTTAAAT CTGCCCCTAA 180
ATTGTAATC ACATGATTAT TTAAAGTCAC TAGANATAAG TAAGCACAGC AATAAAGNTT 240
TAATGGAATA AAAGAAA 257

SEQ ID NO:597

SEQUENCE LENGTH:252

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00664

SEQUENCE DESCRIPTION:

GATCCCAGAA TTCAACCTGT ATTTATAAAT GTATAATGTA TTTAGCTACT TTTTGGTTTA 60
AATGAACCTTG TTGGGTTAGC TTGGTAAATG TTATAATTTT NACTATTTTC TACAAAGAAA 120
ATATTTTCTA ATTTAAGTTG GAGCTATCTG TGCAGCAGTT TCTCTACAGT TGTGCATAAA 180
TGTTTTTNC TAAAAATGAG CTAATGTATA ANATACTGCT GTATACCATA ATAANGATAG 240
TAATACTTGA AA 252

SEQ ID NO:598

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00665

SEQUENCE DESCRIPTION:

GATCATTAGT TGAATCGGTA TCATCTTCAC CAAATAAAGA AAGTAATGAA GAAGAGCAAG 60
TGTGGCACTT CCTTGGCAAG TGATTGAAAC ATCTGAAATT CTGCTGTCAA GATTCCCATC 120
TCTAAGGACT CCAAGTGCTA GAGACAAGGG GGTCTATGAG CATTACTGA CTTCTGTGA 180
AAACTTCATT TTTTCAAAC TTTTGAGCTA TGCAATATAT AANTAAACAG TAAGAATTTT 240
AAATTACAAA 250

SEQ ID NO:599

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00666

SEQUENCE DESCRIPTION:

GATCCTTCTT CCTTCACTG GTCGTGCCTC CCANNAGGTG CAGAGATTCT TAGAAGAGGA 60
GGTGTATCCC CTGTAAAAC CATATGAAAG CGTGATGAAG GTGAAAGCAG AATTATGTCT 120
GTAGAGTTGG AAGAGAATTA AACGAAAATC ATTGTTAATT GCTGAGGCAT GAAAATTGTG 180
TTACTATAAT GCCTTATTTT ACCTCGAGAA TTGTTACCTT AAATTAGTAC AGCACTTTCT 240
TCTTCCCAAA 250

SEQ ID NO:600

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00667

SEQUENCE DESCRIPTION:

GATCCTTCAG TTACATACAA TTTGTTAAT GAAATGTCAT GGCTCTGTTT ATATTTTNTT 60
NTGTNCTTC CAATTGGTAT ATACAACTTT CAGAGCCTCT TGTATTTGGA AGGCTGGAAG 120
GGCCCAGACT TTGGAATAGT GTCTTGGTTT CACTGTTTIN GTTTTGATT TTTTTTGT 180
TNGATTTTTT TAAAACTAAA GCTATATAAA GCTTGNGGAT TAANCAGANT AAATTCCTAA 240
ATTAAAA 247

SEQ ID NO:601

SEQUENCE LENGTH:246

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00668

SEQUENCE DESCRIPTION:

GATCCAGGGT GTGTGTGAGT TGAGGGTGGG TGGAGGGGTT TGCAGTGTGG GAATGTGGCC 60
CTGCAGTTGA CCTGAGCTGC TTCACATGGT TGTCATTCT GGGGCTTAA GAACTGGGAC 120

EP 0 679 716 A1

CAGACCAAGT AGAGGCCTTG GTGCTGNTTG GGGTGGGGCC TGCAGANTCT TAGTTACTGA 180
TTTCATTTTC AATAAATGTA GGTTTGTTAC ATGAGTTTCC CAATTAAAAA AAAAATGACT 240
TCTAAA 246

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SEQ ID NO:602
SEQUENCE LENGTH:284
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00669
SEQUENCE DESCRIPTION:

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GATCAGAATT TCACCAGGGA GTAAAATTAC CTGAAAACGT AAGANGTTTT AAACAGCTTT 60
TCACACAAAT TAGATGCAAC TGTTCCTCATG TCTGAGTACT TATTTAAAAG AAAGGTAAAG 120
ATTGGCCTGT TAGAAAAAGC ATAATGTGAG CTTTGGATTA CTGGATTTTT TTTTTTTTNA 180
AACACACCTG GNGNGNCAT TTGAAAACAC TTTCTTACC CTCGANCCCT GATGTGGTNC 240
CATTATGTAA ATATTTCAAA TTTTAAAAAT GTATATATTT GAAA 284

20

SEQ ID NO:603
SEQUENCE LENGTH:249
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00670

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30

SEQUENCE DESCRIPTION:
GATCGAGGTG GAGAAGCCCT TTGCCATCGC CAAGNAGTAG GGCACAGGGA CATCTTTCTT 60
TNAGTGACCG TCTGTGCAGG CCCTGTAGTC CGCCACAGGG CTCTGAGCTG CACTNGCCCC 120
GGTGTGGCA TCTGGTGGAG CGGACCCACT CCCCTCACAT TCCACAGGCC CATGGACTCA 180
CTTTTGTAAC AAACCTCTAC CAACACTGAC CAATAAAAAA AAATGTGGGT TTTTTTTTTT 240
TTAAATAAA 249

35

SEQ ID NO:604
SEQUENCE LENGTH:244
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00671

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SEQUENCE DESCRIPTION:
GATCGGAATG GTGGAGAACT TCAACCAGGC ACTCAAGGAA ATTGGGGATG TGGAGAACTG 60
GGCTCGGAGC ATCGAGCTGG ACATGCGCAC CATTGCCACT GCACTGGAAT ATGTCTACAA 120
AGGGCAGCTG CAGTCTGCCC CTTCTAGCC CCTGTTCCCT CCCCCAACC TATCCCTCCT 180
ACCTCACCCG CAGGGGAAAG GAGGNAGGCT GACAAGCTTG AATAAACAC AAGCCTCCGT 240
TAAA 244

45

SEQ ID NO:605
SEQUENCE LENGTH:244
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00672

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SEQUENCE DESCRIPTION:

GATCCCCCTT CCGTAAAAGC GTGTAACAAG GGTGTAAATA TTTATAATTT TTAATACCTG 60
 TTGTGAGACC CGAGGGGGCG CGGCGCGGTT TTTNATGGTG ACACAAATGT ATATTTTNC 120
 AACAGCAATT CCAGGCTCAG TATTGTGACC GCGGANACACA GGGGACCCCA CGCACATTCC 180
 GTTGCCCTTAC CCGATGGCTT GTGACGCGGA GAGAACCGAT TAAACCGTT TGAGAAGCTC 240
 CAAA 244

SEQ ID NO:606

SEQUENCE LENGTH:242

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00673

SEQUENCE DESCRIPTION:

GATCTTTCCC ATNTCTACCT AAGTCAGCTT TCATCTTTGT GGATGGTGTC TCCTTTACTA 60
 AATAAGAAAA TAACAAAGCC CTTATTCTCT TTTTNTTGT TCCTCATTCT TGCCTTGAGT 120
 TCCAGTTCTT CTTTGGTGT CAGACTTCTT GGTACCCAGT CACCTCTGTN TTCAGCACCC 180
 TCATAAGTCG TCACTAATAC ACAGTTTTGT ACATGTAACA TTAAGGCAT AAATGACTCA 240
 AA 242

SEQ ID NO:607

SEQUENCE LENGTH:245

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00674

SEQUENCE DESCRIPTION:

GATCCGGGTG GATGCACAGC CCGTCAAGGT CTATGCTGAC GNCTCCCTGG TCTTCCCCCT 60
 GCTTGTGGCT GAAACCTTTG CCCAGAAGAT GGATGCCTTC ATGCATGAGA AGAACGAGGA 120
 CTGAGCGGCT GCGGTCCCAG GAAGGTCTTA CCCCCTCTNC TATTTATNAA TTGCAGACC 180
 CAGCCCNCTC CCTACTTTTT GGTGAGCTAC GNCTCTAGAA TAACNCCCGG TATCTGAAGT 240
 CCAAA 245

SEQ ID NO:608

SEQUENCE LENGTH:245

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00675

SEQUENCE DESCRIPTION:

GATCTCTACC ATTTAATTAA GAAAGCAGTT GCTGTTGAA AGCATCTTGA GAGGAACAGA 60
 AAGGATAAGG ATGCTAAATT CCGTCTGATT CTAATAGAGA GCCGGATTCA CCGTTTGGCT 120
 CGATATTATA AGACCAAGCG AGTCCTCCCT CCCAATTGGA AATATGAATC ATCTACAGCC 180
 TCTGCCCTGG TCGCATAAAT TTGTCTGTGT ACTCAAGCAA TAAATGATT GTTTAACTAA 240
 ACAA 245

SEQ ID NO:609

SEQUENCE LENGTH:241

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00676

SEQUENCE DESCRIPTION:

GATCTAAAT GTCACATTCA GATTTNAGG AAGAAAATCT TCATTACAGT GGAGCACAAA 60
 TNTTCCATAC AAGACATCAT TGAGGNAGCA TGCTGTCCCC TTCTAACCTG AAACACATTG 120
 TTTCCCATCC NGGTTGGGCT TCTNTACCNC CTTATTAATT TATGAACCNG AAGTTGCTTG 180
 AAGTGTTTGGGCTTAATAA ATGGGGTGAA AGTATAGGTA GCAGTAACAC CTACATGNAA 240
 A 241

SEQ ID NO:610

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00677

SEQUENCE DESCRIPTION:

GATCTTCTGA GGTGAGGAGT TTGAGACCAG CCTGACCAAC ATGGAGAAAC CCAGTCTCTA 60
 CTGAAATAC AAAATTAGCC GGGCATGGTG GTGCACGCNT GTAGTCCCAG CTACTTGGGA 120
 GGTGAGGCA GGAGAATCGC TTGAACCCAG GAGGCGGAGG TTGCGGTGAC CCTCCAGCTT 180
 GGGCAACATG TTATGANTGA AACTCCATCT CAAAAAATAA AAAAAAAAAA GGGNNGCAAA 240

SEQ ID NO:611

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00678

SEQUENCE DESCRIPTION:

GATCTGTGAA GGCTTCCCTG ACCNNTGCCC AGGAAGAGTT CACTGGTTCG TCTGTTGTGC 60
 CCCACAGCAC TTTGTTATAC CTCTGCCACA CACTTCACGC AGCGCGTTGT AACTCATGTG 120
 TTTACATGTC TGTCCCNCCA GACTGTNAGC TCCTTGAGGG CAGGGACTGT ACATTCTCCA 180
 GCTCTGTGTC CCCAGGGCCT GGCACATTGT AGACGCTTAA TAAATTTCTG TTAAATGAAA 240

SEQ ID NO:612

SEQUENCE LENGTH:242

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00679

SEQUENCE DESCRIPTION:

GATCAGCTCC TTGACCTCTG AGGGGCAGGN GTGCTTCCTG GTGTGTGTAT TAGAATCCCT 60
 TCCTGCCTTG TTTCATGGCA GTGAAATGCC TCTTGGTCCT GTCCAAGTGT ATCTTTCACT 120
 GATTTCTGNA TCATGNTCTA GTTGCTTGAC CCTGCCANAT GGGTCCAGTG TTCATCTGAG 180
 CATAACTGTA CTAAATCCTT TTTCCATATC AGTATAATAA AGGAGTGATG TGCAATAGCA 240
 AA 242

SEQ ID NO:613

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00680

SEQUENCE DESCRIPTION:

GATCGCAACA ATNAGCCATC CACATNCGTT TTTCAGGGTC ACACCCAAGT AATTGAAAAG 60
 ACACTCCTCC ACTTATCCCC TCCNTAATAT GGCTCTNCGC ATGCTGAGTA CTGGACCTCG 120
 GACCAGAGCC ATGTAAGAAA AGGCCTGTCN CCTGGAAGCC AAAGGACTCT GCATTGAGGG 180
 TGGGGGTAAT TTTTCTTGG NGGGCCCAAGT TAGTGGGCTT NCGNANTGTN TGTATGNGN 239

SEQ ID NO:614

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00681

SEQUENCE DESCRIPTION:

GATCCAAATA AACAGACCCC GTCTGGCAAG AAATGCATTG CAGCCAAAAA AATTAAACAG 60
 TCGGTGGGAA ACAAAGCAT GTCCTTTCCA ACTGGAAAGT CAGACAGAGG CTCAGGTAC 120
 AACTGGCCAC AGAGATAGTC CTGGAAGACA CGTGGCGCCT GTGGACCGGA AGCACCAAAT 180
 GCTGGTGCTG CTTTGTACA TACATATTTT TAAACCATTA AAATTCTTCC TGAAGAAA 238

SEQ ID NO:615

SEQUENCE LENGTH:254

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00682

SEQUENCE DESCRIPTION:

GATCCATAGT CAGAAAAGTT ACTGCAGCTT AAACAGGAAA CCCTTCTTGT TCAGGACTGT 60
 CATAGCCACA GTTTGCAAAA AGTGCAGCTA TTGATTAATG CAATGTAGTG TCAATTAGAT 120
 GTACATTCTT GAGGTCTTTT ATCTGTTGTA GCTTTGTCTT TTTCTTTTTC TTTTCATTAC 180
 ATCAGGTATA TTGCCCTGTA AATTGTGGTA GTGGTACCAG GAATAAAAAA TTAAGGAATT 240
 TTTAACTTTT CAAA 254

SEQ ID NO:616

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00683

SEQUENCE DESCRIPTION:

GATCAAAGAA AGAAGGCATA CGCNGATTTC TACAGAAACT ATGATGTCAT GAAAGATTTT 60
 NAGGAGATGA GGAAGGCTGG TATCTTTCAG AGTGTAAGT AATCTTGGAA TATAAAGAAT 120
 TNCTTCAGGT TGAATTACCT AGAAGTTTGT CACTGACTTG TGTTCCTGAA CTATGACACA 180
 TGAATATGTG GGCTAAGAAN TAGTTCCTCT TGATAAATAA CCANTTAACA AATNCTTTNG 240
 ACAGAAA 247

SEQ ID NO:617

SEQUENCE LENGTH:235

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00684

SEQUENCE DESCRIPTION:

GATCTGCACC TGAGCCAAAG AAACCTGAGG AAAATCCAGC TTCTAAGTTC AGTTCTGCAA 60
 GCAAGTATGC TGCTCTCTCT GTTGATGGTG AAGATGAAAA TGAGGGAGAA GATTATGCCG 120
 AATAGACCTC TACATCCTGT GCTTTTNTCC TAGTTTCTCT CCACCCTGGA ACATTCGAGA 180
 GCAAATCAAA ACCTCTATCC AGACAAGACA AAATAAAACT CAACATCTCC TGAAG 235

SEQ ID NO:618

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00685

SEQUENCE DESCRIPTION:

GATCTGTTCC TTGGCAGTGG ACTCAGAAAG CCAACATGTG GCTCCTCCCA GCCCATAACC 60
 AGTATTTTTC CTGCTTCTAA ATACAAATNG GTTGGTTTTC ACTTCANATT GANCTTACTG 120
 TAGCCTCAAA TGATTTCCTC CCTCCGCTC CAGGAAGAAA GAATGTNACT GCCTTAATAA 180
 AAAATGAAAA GAGAATGATG CTCAAAATCT TTCCAAATAA AATGTTCCCT ATATTAAA 238

SEQ ID NO:619

SEQUENCE LENGTH:234

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00686

SEQUENCE DESCRIPTION:

GATCCGCCCT CGAATGGACA CATTACCAGT GAAGGGGCAT TTNTNGTCAA TGTAGGTGCC 60
 CTCAATAGCC TCCTTGGGTG TTTGAAGCC CAGACCGATG TTCTTGTAGT ACCGCGGGAG 120
 CTTCTCCTTG CCAGTTTCTC CCAGCAGGAC CCTCTTCTNG TTTTGAAAGA TGGTCGGCTG 180
 CTTTGTGTAG GCACGCTCAG TCTGAATGTC CGCCATCTTC CCGGCCGGCT GAAA 234

SEQ ID NO:620

SEQUENCE LENGTH:251

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00687

SEQUENCE DESCRIPTION:

GATCCCCAAG CCTGGCAAGG GAATTTNTTC AACTCCCTGC CCCCCAGCCC TCCTTATCAA 60
 AGGACACCAT TTTGGCAAGC TCTATACCA AGGAGCCAAA CATCCTACAA GACACAGTGA 120
 CCATACTAAT TATACCCCT GCAAAGCCCA GCTTGAAACC TTCACTTAGG AACGTAATCG 180
 TGTCCCTAT CCTACTTCCC CTTCTAATT CCACAGCTGC TCAATAAAGT ACAAGAGCTT 240
 AACAGTNAA A 251

SEQ ID NO:621

SEQUENCE LENGTH:241

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00689

SEQUENCE DESCRIPTION:

GATCCATCAT CCGNCAATGT TAAAAGGCC CGTGCGCGAG GCGACGTGC TCACCCTTTT 60
 GGAGTCAGAG CGAGAAGCCC GGAGGTTGCG CTGAGCTTGG CTGCTCGCTG GGTCTTGGAT 120
 GTCGGGTTTC ACCACTTGGC CGAGGGGAAT GGTCTGTCAC AGTCTGCTCC TTTTITTTGT 180
 CCGCCACACG TAACTGAGAT GCTCCTTTAA ATAAAGCGTT TGTGTTTCAA GTTAACTCAA 240
 A 241

SEQ ID NO:622

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00690

SEQUENCE DESCRIPTION:

GATCTCCTG CCTNGGCCTC CAAAAGTGCT GGGATTACAT GCATACCTGA NCTACTGAGC 60
 ACTTTNATCT TGAATGAGTG TTGGATTTTG TCAAATGCTT TTCCTGTACC TATTAATACA 120
 ATCATGATT TNNCTCTTT AGTATGTTGA TATGATGGGT TACATTAATT GATNNTCAAA 180
 TGTGGAATCA GTCTNGCATA CCTGGAATAA ATCCCACTTG GTCATAATAA A 231

SEQ ID NO:623

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00691

SEQUENCE DESCRIPTION:

GATCTATGAA ATCTGTGTAG GTTTTAAATA TTTTAAAAAT TATAATACAA ATCATCAGTG 60
 CTTTTAGTAC TTCAGTGTTT AAAGAAATAC CATGAAATTT ATAGGTAGAT AACCAGNTTG 120
 TCNCTTTTGT TTAAACCAA GCAGTTGANA TGGCTATAAA GACTGACTCT AAACCAAGAT 180
 TCTGCAAATN NTGATTGGNA TTGCACAATA AACATTGCTT GNTGTTTAA A 231

SEQ ID NO:624

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00692

SEQUENCE DESCRIPTION:

GATCCCATTT AGGAANCGGC ATTCATTCA GAAGGTACTT TTAACTGCT CAGTTTTTGA 60
 CTATTTTAAA TAGTTTGCTG AAAACTCCTG ATAACACTTG CTACATATCA TGTTTTAATT 120
 GCTTGATACG TTAACCTTTA ATTTTATTTA GTAAAGTGTA TCAAAGTAGG ACTTTTTTGA 180
 ATTGTAAATA GGTGGTTTAA TTAAATAAAA GTCAATGTAA AAATTGTAA A 231

SEQ ID NO:625

SEQUENCE LENGTH:230

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00693

SEQUENCE DESCRIPTION:

GATCCGGAGG GAAATGTGTT AGAGGGTCTG GAAAATTCAG TGCTTTTGAG TTA CTTGTTT 60
 TTATTA AAAAA TTTCCTCACA AAAGAGAGTC CTC AAGTTGT GGCTGTTCTT GGGAAAGGGG 120
 TCACCGTGTG TGACAAAGTG TAACTTTAAA AAGCACGTTG ATTTT TACA AATGTAAGTG 180
 TGCTTGGGAA TTCCTTAAAT TTTGTGCAAT AA CTA TTTT TTGGAAGAAA 230

SEQ ID NO:626

SEQUENCE LENGTH:202

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00694

SEQUENCE DESCRIPTION:

GATCCAATCA TATTNCTGT AGGGTGGAGG AGGTTTCAGA CCATCCCGCT CTGTTATATC 60
 GAAGACCACA ATGGAAGACA AAGGCTTCTA AAGTATACCC CACAGCACGT GCATCGCGGA 120
 NAGCCTNCTT GGGATAAAAT ATGTTTACAA TAACTTGCCT ATTGCTGAGA TTAAACCTTA 180
 CAGGCTGCGT TATTTTAGCA AA 202

SEQ ID NO:627

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00695

SEQUENCE DESCRIPTION:

GATCCATTGT ATCAGTACCT CACAATCAGA GTTGGCAAAT GATGGATGAG TGATTCAAGC 60
 AGTGCACCCG GTGGAAGCTG AAATCCATCT GTGAATGGAA CTGAAGTGAA CGTGAATATG 120
 CTGACTATAT CCTGGAAGCA TTTTATACC ATCTTGAAAT TTCAACANAC TGGCTTTTGC 180
 CAGTTAATCC AGCTGTCTTT CAAGAATAAA AGTTGGGGTT TTCAAA 226

SEQ ID NO:628

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00696

SEQUENCE DESCRIPTION:

GATCACCTGA GGT CAGGAGT TCGANACCAG CCTGGCCAAC AGGGTGAACC CCGTCTCTAC 60
 TAAAAGTACA AAAATTAGCT GGGCGTGGTG GCGGACGCTG TAATCTCAGC TACTTGGNAG 120
 GCTGAAGCAG GAGAGGTGCT GGAACCTGGN AGGCGGAGGT TGAAGTNAGC CGAGATTGCC 180
 CTATTGCACT CCAGCTCGGG CGNCAACTGC AAGACTCCAT CTCAAA 226

SEQ ID NO:629

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00697

SEQUENCE DESCRIPTION:

GATCTGTAA TTTCCTATCT AATAAATGCC TTNAATTGTN CTCATAATNA AGAATAAGTA 60
GGTATCCCCTC CATGCCCTTC TGTAAATAAT ATCTGGAAAA AACATTAAAC AATAGGCANA 120
TATATGTNAT GTGCATTTC AGAAATACAT AACACATATA TATGTCGTGA TCTTATATTC 180
AATTGCAAGT ATATAATAAA TAAACCTGCT TCCAAACAAC AATAAA 226

SEQ ID NO:630

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00698

SEQUENCE DESCRIPTION:

GATCAGAGTA ATTCTTTTGT ACATTGAAAT NAGGGGCTTG GTTTAAAAAA AGACCTTTCC 60
CTCTCCCTGC CCCTAGAACA ACCAGTATTA GAAGGTGCCA CCATTGGTGC TGCCTTCTNT 120
TCCCACAGCC TGTAACTCAG TGTTTTGTAC TTCACTGAAT TGTGATGGNT AGAAACTTCG 180
TGGGTAGNNN NTGGGAATCA TCCNGTTAAA CAANACGGGN TTAAAA 226

SEQ ID NO:631

SEQUENCE LENGTH:222

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00699

SEQUENCE DESCRIPTION:

GATCCTTGGT GTA CTGAGCA GTTCTTTTGG GGCTTTTCT TTCTGGGAAG CGGGAGGGAA 60
AGGAGCAAGG TGTCATCTG CTCTTCATTT GTATTTTGGT CCCAAATGT AAATACAATT 120
TNTTATGTTA CTTTTTTGTG GTA ACTACCG AGATGAATAT TTTAATTAGA TAAGTTATAT 180
GAAAAGGAAA ATCCATGTC TAAATAAAAA ACAAACTCCA AA 222

SEQ ID NO:632

SEQUENCE LENGTH:222

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00700

SEQUENCE DESCRIPTION:

GATCTTCTGG ACAAACTTCT GCGATACGAC CATCAACAGA GACTGACTGC CAAANAGGCC 60
ATGGAGCACC CATACTTCTA CCCTGTGGTG AAGGAGCAGT CCCAGCCTTG TGCAGACAAT 120
GCTGTGCTTT CCAGTGGTCT CACGGCAGCA CGATGAAGAC TGGAAAGCGA CGGGTAATGC 180
GGCATTGATG CTTNCCAATA AAACCAACCA ACCAAACACA AA 222

SEQ ID NO:633

SEQUENCE LENGTH:221

EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00701

SEQUENCE DESCRIPTION:

GATCCACCCA GTTCTTTAGG CAACCACTGA TAGCATTTTC TTAAGTATTC TTCCAGATAT 60
CGTCTATGCA TATGTAAAAG TATCTGNCTT TCTCCNTTTA AAAACACAAT TGGNAATATA 120
TCATACTNGC TGGTTTGCAC CTNGCTTTTT TTGCTTAATA TATCTAGTTT ATAATGNCCN 180
AATGNGCAAA TTTTNGCATC NGCCCTAAAT ATCTACTGGN N 221

SEQ ID NO:634

SEQUENCE LENGTH:220

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00702

SEQUENCE DESCRIPTION:

GATCACTCGT TTAAGTCCTT AGTTGTATGT NATCTCTTCT CTAGCAGGAA TTGGCAAAC 60
TTTTTGTAAG GGGGTAGAAA GTGAAGATTT TAAGGCTTTG CAGGCCATAT ATCCTCTNCT 120
GCAATNCTC AGCCCTGCTG TTGTAATGTA AAANCTNCCA CAGACACTAC ATGAACACGA 180
ATGAGTGTGG CTGGTGTTC AATAAACTT TATTACAAA 220

SEQ ID NO:635

SEQUENCE LENGTH:220

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00703

SEQUENCE DESCRIPTION:

GATCATCAAA CCAGTCCACA AGCACAGGGA GATGCGTGGG CTGACATCTG CAGGCCGAAA 60
GAGCCGTGGC CTGGGAAAGG GCCACAAGTT CCACCACACT ATTGGTGGCT CTCGCCGGGC 120
AGCTTGGAGA AGGCGCAATA CTCTCCAGCT CCACCGITAC CGCTAATATA NGTAAAGTTT 180
NGTAAATTC ATACTTAATA AACAATTTAG GACAGTCAAA 220

SEQ ID NO:636

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00704

SEQUENCE DESCRIPTION:

GATCCACATC TCAAAGAAGT GGGGCTTCAC CAAGTTCAAT GCTGATGAAT TTGAAGACAT 60
GGTGGCTGAA AAGCGGCTCA TCCCAGATGG CTGTGGGGTC AAGTACATCC CCAGTCGTGG 120
CCCTCTGGAC AAGTGGCGGG CCCTGCACTC ATGAGGGCTT CCAATGTGCT GCCCCCTCT 180
TAATACTCAC CAATAAATTC TACTTCCTGT CCACCTAAA 219

SEQ ID NO:637

SEQUENCE LENGTH:215

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00705

SEQUENCE DESCRIPTION:

5 GATCCTCTCT CGACTNGCCA TACATTCTT TCACAGCATT TACATAGTCC ATGATAGTTT 60
 ACTTGTTGGA TTATTGGTT AATCTTTGCC TTAAACACCA GGGTTCCTTG GGTGAAGGAG 120
 CTTCTTTATC TNGGTAACAG CATTATTTCA AGCATAACTN GTAATATAGT NATATTACAT 180
 ATATANCATA TATATATATN NCANANCANA TATAN 215

10 SEQ ID NO:638

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15 CLONE:HUMGS00706

SEQUENCE DESCRIPTION:

GATCTGGTTT CTTAGCAAAT TTCCAGTAG GATGTCATGT AAGTNCCTTC CCCCTCTTAG 60
 AGATTGAAGG CTGTAAGAGT CCAGATGGTG GAGCCAGGCT GTCTGGGTTT AAATGCCATC 120
 20 TTTGACACTT GCAAGCTAAA TNACATTACT CAAATTAATC GTTCTGCACT TCAGCTTCN 180
 TGTCTATCAA ATAAAAAGAA TAGTACCNGC CAAA 214

SEQ ID NO:639

SEQUENCE LENGTH:215

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00707

SEQUENCE DESCRIPTION:

30 GATCATTGTA GATGANCTGA AGCAAGANGT TATCAGTACC AGCAGCAAGG CAGAACCACC 60
 CCAGTGCAACC TCCCTGGCCT GGNCTGCTGA TGGCCAGACT CTGTTTGCTG GCTACACGGA 120
 CAACCTGGTG CGAGTGTGGC AGGTGACCAT TGGCACACGC TAGACGTTTA TGGCAGNGCT 180
 TTACATGTGG GGGAAATAACN TGGCTTTTCT GTAAA 215

35 SEQ ID NO:640

SEQUENCE LENGTH:220

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40 CLONE:HUMGS00708

SEQUENCE DESCRIPTION:

GATCAAACCA AGGCCAGGC TGCAGCCCCA GCTTCAGTTC CAGCTCAGGC TCCCAAACGT 60
 ACCCAGGCCC CTACAAAGGC TTCAGAGTAG ATATCTCTGC CAACATGAGG ACAGAAGGAC 120
 TGGTGCGACC CCCCACCCC GCCCCTGGGC TACCATCTGC ATGGGGCTGG GGTCTCTCTG 180
 45 TGCTATTTGT ACAAATAAAC CTGAGGCAGG ATTTGTAAAA 220

SEQ ID NO:641

SEQUENCE LENGTH:210

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00710

SEQUENCE DESCRIPTION:

GATCGAGAAC CACATCCTCA AGCTCTTCCA GAGCAACCTG GTGCCCCGCTA AACCCCTGAGT 60
 GAAGGCCGCGC TGCCGGGGGAC TCAGACACTC AGGGAACAAA ATGGTCAGCC AGAGCTGGGG 120
 AAACCCAGAA CTGACTTCAA AGGCAGCTTC TGGACAGGTG GTGGGAGGGG ACCCTTCCCA 180
 AGAGGAACCA ATAAACCTTC TGTGCAGAAA 210

SEQ ID NO:642

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00711

SEQUENCE DESCRIPTION:

GATCTGGTTT TATTCCTGTA ATTCAAGCCAC CTGATTTTGT GAGGGGGGGG AATAATATGT 60
 GGTTTTGTGA CAAACATGTT TCTCAGTGTG TTGTNATTTT GGAAAAATG AGGGGAGGGA 120
 GTTTGGCAAG AATGGAGAAA ATGAATGAAG AAGGCCTAAT CTCTCTCTTT TTCAGTNAAT 180
 AAATGGAACA CCATTTCTGG ATTCTAAA 208

SEQ ID NO:643

SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00712

SEQUENCE DESCRIPTION:

GATCTGTACA TTGTAAAACA CCATTCAAGT GTCAGAATCA TTATTTTCCA CCACATTATCA 60
 TGGTGCTTGA CAAGTCTTCC CAATAAATAC TGAATGAACA AATGAATGCC AGAAACATTA 120
 AAATGAACAC TATGGGGAAA GGGGAAGAGA GGCAGAATCA GAAATTATCC NGAATAAATA 180
 TTTATNCCAT TTGTCATCCN NCNAAA 206

SEQ ID NO:644

SEQUENCE LENGTH:244

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00713

SEQUENCE DESCRIPTION:

GATCTATGTG GTGAAAATGC ACAGGAGCTT GGTAGACTGC GGGGGAAAGA GAGAGCTCCT 60
 TTCGCCATGT TTTACCAGTN TGCTGTTATA ACCTCTTAGG TTGTATCCTT TAATTTCCAG 120
 CCTTTAGGT TAGTTTCTGT AACAGAACAA GTGAGTCTGG GATGAAGTCC TCAAAGTACT 180
 TCAAAATGGTA ATTTTTTGT TTTTGTAAATA GCTNAACAAA TAAACCNAGG GTTTCTATAT 240
 TAAA 244

SEQ ID NO:645

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS00714

SEQUENCE DESCRIPTION:

5 GATCTATGAA TGANAGGAGG GCAGACCACA TTGCTTTTNA CATCCATTTC CCCTCCTTCC 60
CATGGGCAGA GGACCAGGCT GTAGGAAATC TAGTTATTTA CAGGAACTTC ATCATAATTT 120
GGAGGGAAGC TCTTGGAGCT GTGAGTTCTC CCTGTACAGT GTTACCATCC CCGACCATCT 180
GATTAATAATG CTTCCTCCCA GCATAGGATT CATTGAGTTG GTTACTTCAA A 231

SEQ ID NO:646

10 SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00715

15 SEQUENCE DESCRIPTION:

GATCTACATC TTTTCTAAA GAAAAGTGGA GCTTGCCTCC AGTTCAATTC ACAAGAGCAT 60
TTTCCCTCCC ATGCCACCT TTTCTGTGG CTGTCGCTAG GAAGGATGCA GAGGCTGTGT 120
GGTTTACCAA ATGCCTTAAC TTAGCAGTGA ATGACAACAT TCAAACACAT GTTGAGGGGA 180
AATTTTACT GATTCACAAA 200

SEQ ID NO:647

SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS00716

SEQUENCE DESCRIPTION:

30 GATCTGCCGC AAGTGCTATG CTCGCCTTCA CCCTCGTGCT GTCAACTGCC GCAAGAAGNA 60
GTGTGGTCAC ACCACAACC TCGTCCCAA GAAGNNGGC AAATAAGGT GTTCTTTCCT 120
TGAAGGGCAG CCTCTGCCC AGGCCCCGTG GCCCTGGAGC NTCAATAAAG TGTCCCTTTN 180
ATTGACTGGG GNNGNANAAA 200

SEQ ID NO:648

35 SEQUENCE LENGTH:199

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00717

SEQUENCE DESCRIPTION:

40 GATCCAGAAG GGGTTTGGTC TGGGACTTCC TTGCTCTCCC TCTTCTCAAG TGCCTTAATA 60
GTAGGGTAAG TTGTTAAGAG TGGGGNAGAG CAGGCTGGCA GCTCTCCAGT CAGGAGGCAT 120
AGTTTTTACT GAACAATCAA AGCACTTGA CTCTTGCTCT TTCTACTCTG AACTAATAAA 180
TCTGTTGCCA AGCTGGAAG 199

SEQ ID NO:649

SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50 CLONE:HUMGS00718

55

SEQUENCE DESCRIPTION:

GATCTTTTGT CCTCACTGCT TTCTAATGGG GAGGGCTGAG GGTTCCTGT CCCCACAGCA 60
 GGTATGTTGG GNTCTGCCCC AGCCCCACAC TTGCTCTGAA AACCAAGTGN NAGAGCCCCCT 120
 TCCCCTTGT TTTATTTTAC TGTATAATA ATTATTAAC TCCTTGTAAT AGAAATAAAG 180
 TTTGTACTTG GAGTTCAGCT CAGAAA 206

SEQ ID NO:650

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00719

SEQUENCE DESCRIPTION:

GATCCTCGTT TTCTNGGTTT TGGTGATGTT GGAGGAGTAC CCCCCAGCCC ACCGCCCCGA 60
 TTCCTTTTGG CTCTGGTTT GGAGCTCCGG ACCAGGACCT TCGTCTGGT CAGTTTTTAA 120
 ATAATNATT AGCAGTGTA CTTTTAAACC TCGTGACAT CTACANNNG CCAATAAAG 180
 AAAGAGGAAG CCACGGTCAA A 201

SEQ ID NO:651

SEQUENCE LENGTH:198

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00720

SEQUENCE DESCRIPTION:

GATCTGTTAT CTAGCTGAGT TCATTTCATC TCTCCCTTTT TTATATCAAG TTGAATTTG 60
 GGATAATTTT NCTATATTAG GTACAATTTA TCTAACTGA ATTGAGAAAA AATTACAGTA 120
 TTATTCTCA AAATAACATC AATCTATTTT NGTAAACCTG TTCATACTAT TAAATTTTGC 180
 CCTAAAAGAC CTCTTAAA 198

SEQ ID NO:652

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00721

SEQUENCE DESCRIPTION:

GATCTTAAAC ATCGGTCAGA TGAGTCATAC ATTGGGTTAT TTTTATATA CATGTATACA 60
 CAAAATATTT CAAATTGAAA GCAACATCTT AATGGATTCA AAATATTAC AAGCTGTTGT 120
 CTAACACAGG TGAGAAAAAA ATTTATAACT GTAAANCAA ATGCACATAT TGATATTTAA 180
 AATGCGTAAT TAAGAAA 197

SEQ ID NO:653

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00722

SEQUENCE DESCRIPTION:

5 GATCTGGACT GTCCTGGCAT CGAACTCTCC CTCTGTGTGT AATTGGAGGA GACCACAAGC 60
 TGTGTGTTTG GGTGACTGAA GTATAAAGTG TTNCTGTAC CTTAGATTCA CAAACTTTGT 120
 ATTTTNAAGTA CATATTNNNA AGAATTTCTA TAGTACATAT NTNNAAGAAT TTNATATCA 180
 AATATACCGT ATACTNN 197

SEQ ID NO:654

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00723

SEQUENCE DESCRIPTION:

15 GATCACCGCC GCGAGTAAAA AAGGCTCCAG CCCAGAAGGT TCCTGCCAG AAAGCCACAG 60
 GCCAGAAAGC AGCGCCTGCT CCAAAAGCTC AGAAGGGTCA AAAAGCTCCA GCCCAGGNNN 120
 GCACCTGCTC CAAAGGCATC TGGCAAGAAA GCATAAGTGG CAATCATAAA AAGTAATAAA 180
 GGTTCTTTT GACCTGTAA A 201

SEQ ID NO:655

SEQUENCE LENGTH:199

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00725

SEQUENCE DESCRIPTION:

25 GATCTGCAGT TTAAGTTGCC ATGCTGCTAG GAAATTGTCC TTTTNCCTTC TAGCTGTAA 60
 CCTACTTCCT GGA AAAAGTA GTAGCTCTCT GTAGCATTAT GGAGTTTCAG TGGAACCAAA 120
 TTTTGGCAT TAAAACTGG CATTATACTG AACTATACAT TGAGAAATCA ATCAAAATAA 180
 30 AANTTTTAC TTTCACAA 199

SEQ ID NO:656

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00726

SEQUENCE DESCRIPTION:

40 GATCTGGTTT CTAGCAAATT CCCAGTAGGA TGTCATGTAA GTCCTTCCC CTCTTAGAGA 60
 TTGAAGNTGT AAGAGCCAGA TGGTGGAGCA GGCTGTCTGG GTTCAAATGC ATCTTTGCAC 120
 TTNAAGCTAA ATGACATACT CAAATTAATC GTCTGACTCA GTTCCTTGCT ATCAAAATAA 180
 AAGATAGACC TGCAAA 196

SEQ ID NO:657

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00727

SEQUENCE DESCRIPTION:

50 GATCTGCCTG CCTCAGCCTC TCAAAGTGTT GAGATTACAG GCGTGAGCAN CCGCTCCCTG 60

CCCAACACAT ATACCATCTG AAAATGTTAG AATTCTGAGT TGTGATTTTA TTGACTTGTT 120
 GCTTGCTTTT CCTNAGGCTT TGTAACCTGT AATATGTTAA AGTGACTAT CCTAATAAAC 180
 TGAATACTTT GGTATCTTAA A 201

SEQ ID NO:658

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00728

SEQUENCE DESCRIPTION:

GATCCTCCAT TGGAGTGGCC CAAATCTTTC CATCTAGGGC AAGTCCTGAA AGGCCCAAGG 60
 CCCCTCCCC AGTCTGGCCT TGGCCNCCAG CCTGGAGAAG GGCTAACATC AGCTCATTGT 120
 CAAGGCCACC CCCACCCAG AACAGAACCG TGTCTCGAT AAAGGCTNTT GAAGTGAATA 180
 AAGTTTAAAA ANCTAAA 197

SEQ ID NO:659

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00729

SEQUENCE DESCRIPTION:

GATCGTNTTT GTTTTGT TAAAGAAAGG TGAGATTGGC TTGGTTCTTC ATGAGCACAT 60
 TTNATATAGC TCTTTTCCTG TTTTNCCTTG CTCATTTCTG TTTGGGAAG AAATCTGTAC 120
 TGTATTGGGA TTGTAAAGAA CATCTCTGCA CTCAGACAGT TTACAGAAAT AAATGTTTTT 180
 TTTGTTTNNC AGAAA 195

SEQ ID NO:660

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00730

SEQUENCE DESCRIPTION:

GATCTCAAAC TCCAGGCTCA GAACTGTGAA GACTGTTTCC AGCCTGGCTG TGAGCCAAGA 60
 CCTGGTTCCT GGTGGACCCT GAGGACAAAG TGTGATAAAA CCTCTGGCTC AGACTTGCTC 120
 TACTGAAGGC TTCTTGTTA TAAGATGCAT AAAGTCACTG GGGCTAGCTA AACAATAAAG 180
 AGTTTATTGT GAGAAA 196

SEQ ID NO:661

SEQUENCE LENGTH:194

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00731

SEQUENCE DESCRIPTION:

GATCTAATGT ACTGTAACCTT TATCAGTGAA AGGTAAAATC TCAAATAACA AGTACAAACA 60
 TTGAACAATT ACCTATAAAG ATTTNTAAAA GTAAAATTTT TCCAATAGAT TTCATTCTTG 120

TCATTTTGTA AGACGACCCT GCAGTCCACC NGTTTGTAAC TTTTAAATA AAATAGACAT 180
CTGTATTACT GAAA 194

5 SEQ ID NO:662
SEQUENCE LENGTH:246
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
10 CLONE:HUMGS00732
SEQUENCE DESCRIPTION:
GATCAAGAAA ATAAGGACAA CGTGAAGTTT AAAGTTCGAT GCAGCAGATA CCTTTACACC 60
CTGGTCATCA CTGACAAAGA GAAGGCAGAG AAAGTGAAGC AGTCCCTGCC CCCC GGTTTG 120
GCAGTGAAGG AACTNAATAA ACCAGACACA CACAGAACAG GCGATTATTT ATTTGTTTTT 180
15 AATTTATTTT GTCATATTTT TGTAAAACGG CAGAAATGCA ATAAAACCTA TATTTCAACA 240
GTGAAA 246

SEQ ID NO:663
20 SEQUENCE LENGTH:192
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00733
SEQUENCE DESCRIPTION:
25 GATCATATTT TATACATGTG TAATAGATAA AAATAAACCA GATTGCAAAT CCTTTTAA 60
AATCCTAAC CATGTACCAA GTTTTGGTC CAAATTATGT AGGATAAGTT AAAGTAAAT 120
TGCATTCTAT TAACCAATAT GAGTGTATTT CTGTAAGCAT AGTTATGTTG AAATAAAGTT 180
TTAAAAACCA AA 192

30 SEQ ID NO:664
SEQUENCE LENGTH:191
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
35 CLONE:HUMGS00734
SEQUENCE DESCRIPTION:
GATCTTCACA CTAATGATGA GTGTGTGGCT ACATACAAAG GAGTTCCTT TGAGGTGAAA 60
GGGAAGGGAG TATGTAAGGG CTCAAACCAT GAGCAACAAG TGAATCAA TAAATGCTT 120
40 CCACNACCAA AAGACATTAG AGAAAACCTT AAAAGTAATA AAGNGAAATA TATTTNTCAC 180
TTATACCTAA A 191

SEQ ID NO:665
SEQUENCE LENGTH:188
45 SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00735
SEQUENCE DESCRIPTION:
50 GATCTGAATC TNCCGGGGCC CCAGCCCACT CCACCCTGCC AGCAGCTTCC AGCCAGTCCC 60
CACAGCCTCA TCAGTCTCT TCACCGTTTT TTGATACTAT CTCCCCCAC CCCCAGCTAC 120

55

CCATAGGGGC TGCAGAGTTA TAAGCCCCAA ACAGGTCATG CTCCAATAAA AATGATTCTA 180
CCTACAAA 188

5 SEQ ID NO:666
SEQUENCE LENGTH:186
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
10 CLONE:HUMGS00736
SEQUENCE DESCRIPTION:
GATCTNAAAC CCAAGGTCT GAGGCCAGGG CCGACTGCCG TAAGATGGGT GCTGAGAAGT 60
GAGTCAGGGC AGGGCAGCTG GTATCGAGGT GCCCATGGN AGTAAGGGGA CGNCTTCCGG 120
GCGGATGCAG GGCTGGGGTC ATCTGTATCT AAAGCCCCTC GGAATAAAGC GCGTTGACCG 180
15 NCGAAA 186

SEQ ID NO:667
SEQUENCE LENGTH:184
20 SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00737
SEQUENCE DESCRIPTION:
GATCTGTAAA TAATCATTGC CAGTNTGACT TTTGTTCAAC AAAAGGATTG TACTGTATTA 60
25 AGAACCAGATG AAAAAAATTN TCCTGTAACA TTTTTTAAAG AAAACTTTGT TTGTTTAAAG 120
AAAAAGTATT GTATAANTNA TAATTTAAT TTAAATAAAC CTAAAATGCT TTGTGCTAAG 180
GAAA 184

30 SEQ ID NO:668
SEQUENCE LENGTH:180
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00738
35 SEQUENCE DESCRIPTION:
GATCCCAGAA AAGTTCTAAT TTTCATTAGC AATTAATAAA GCTATACATG CAGAAATGAA 60
TACAACAGAA CACTGCTCTT TTTGATTTA TTTGTACTTT TTGGCCTGGG ATATGGGTTT 120
TAAATGGACA TTGTCTGTAC CAGCTTCATT AAAATAAACA ATATTTGTAA AAATCATAAA 180

40 SEQ ID NO:669
SEQUENCE LENGTH:179
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
45 CLONE:HUMGS00739
SEQUENCE DESCRIPTION:
GATCTATCCA AGGTTTTGAC ATGTATCGAG AGTTTATTCC TTTTATTGC TGAATAGTAT 60
TAATATTCTA TAGTATGGAT GTAACATAGT GTGTTTAAAC ATTCGCCTGT TGAAGGACAC 120
50 TTGGGTTGTT TCCAGTTTCA GGTCTTACA AATAAAGCTA CTCTGTGTGT TCATGTAAA 179

55

SEQ ID NO:670

SEQUENCE LENGTH:179

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00740

SEQUENCE DESCRIPTION:

GATCAAATGC CAGTGTCAAT TTGTACTTAA GTTCCAAAGT AGGAACATTN TATACTTTTT 60
NCTGTATTGT AATAGGTAGT TTTGTATGAA ATCTTTTCTC CTCTCCCGTT GTACCGCATT 120
CTTTCCAGCA TTGTGCTTTT TCCCTGGNCT TATTGAAAA TTTTACTGTT TTATACAAA 179

SEQ ID NO:671

SEQUENCE LENGTH:177

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00741

SEQUENCE DESCRIPTION:

GATCCAAGAA ACCAGGGCCA TGACCAGGTC CACTGTGGAG CAGCCATCTA TCTACCTGAC 60
TCCTGAGCCA GGCTGCCGTG GTGTCATTTT TGTCATCCGT GCTCTGTTTC CTATTGGAGT 120
TTCTTCTCCA CATTATNTTT GTTCCTGGGG AATAAAAACT ACCATTGGAC CTAGAAA 177

SEQ ID NO:672

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00742

SEQUENCE DESCRIPTION:

GATCTGCAAG TCCCGGAGAG CAACAGCACA GCTCTGCCTG ACGCTCTCAT TAAATCTAT 60
GCAGCCAAGC TCGGCACCTT GTAGCAGCCG GCCTTGCGAA GCCTCCTCAG CTCGGGGGGC 120
CGGGGACCCA GTGAGCCGAG AGCCCTCTGG NCTCCACTTA TGCATATGCA CCAAA 175

SEQ ID NO:673

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00743

SEQUENCE DESCRIPTION:

GATCCGGAGA ATAGGGCENN AATATGTGCC GCCAGTGTTT CCGTCAGTAC GCGAAGGATA 60
TCGGTTTCAT TAAGTTGGAC TAAATGCTCT TCCTTCAGAG GATTATCCGG GGCATCTACT 120
CAATGAAAAA CCATGATAAT TCTTTGTATA TAAATAAAC ATTTGAAAAA ACCCTTCAA 180

SEQ ID NO:674

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00745

SEQUENCE DESCRIPTION:

GATCTATTCA GATGGTTCTG ATGAAGTGAA ACGNGCCATG AACAAATCCT TTATCNNNGT 60
 CGGGTGGTAC AGTTTGTAGT ACCAACTGGT CTGATGTAGG TAAAAGGAAA GTTGAAATCA 120
 ATCCTCCTGA TGATATGGNN NGGAAAAAGT ACTAAATAAA TTAATTTGCT CTCAAA 176

SEQ ID NO:675

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00746

SEQUENCE DESCRIPTION:

GATCAAAACC AGTTTGATTG GGAATCTTC CCCTTTCCAA ATGAAATAGA GATGCAGTAC 60
 TTAACCTTCC TTGGTGTGTTG TAGATATTGC CTGTGTATT CCACTTAAAA CCGTAATCTA 120
 GTTTGTAAAA GAGATGGTGA CGCATGTAAA TAAAGCATCA GTGACACTCT AAA 173

SEQ ID NO:676

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00747

SEQUENCE DESCRIPTION:

GATCCTAGCA TCCCTTTTCA CATGGTTTCT CCATGTATAT AACAGAATCA AGAAACAAAT 60
 TTNAATTAAA CAATCTGTAA CAGAATCAAG AAACAAATAC ATTTTAATTA AACAACTCTAT 120
 ATGGAACAAA CATTCCCAA TNCTAAGAAT AANTNTTCNT NTAAGTTTTC AAA 173

SEQ ID NO:677

SEQUENCE LENGTH:182

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00748

SEQUENCE DESCRIPTION:

GATCCAAATA ATTTATTTAA TGACTGGTCT CAGAACTGA ACTCATTAAAT GTCTCTGGTT 60
 AACAAAATA CGCATCTCAT AGCCAAAGAG GAGATGATAC ATAATCTACA ATAAGGGTCT 120
 TAGTGCTTTA GAAAAAGTT AAAATTGGAA GTCATTAAAA AAAGACTGTT ATAATGGTGA 180
 AA 182

SEQ ID NO:678

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00749

SEQUENCE DESCRIPTION:

GATCTTATGA GAAGAGGAAG GAGAGANGTC TCTNCCTATG CTCACACACA AAGGAAAGTC 60
 CACATGAGGA CACAAGGAGA AGCCAAGAGN GCCCTTACCA GGANTTAAAC CTGCTAATCC 120
 CTATTTTAAAT TAGAACAGTG AGAAANTAAA TATCTGTATT TAAGCCTCAC AAA 173

SEQ ID NO:679

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00750

SEQUENCE DESCRIPTION:

GATCCAGAGA AAGCCAAAGC TCTTAGTAAA CACTTGCCAT CGTCAGTNTN ATGTCTCTAA 60
AAGTAGATGT TGAGGCTCTT NAAAATNCTC CTGGTGCTAC ATACATTCGG AAGAAGGGTG 120
GAAAAGTTAC TGGAGATAGT CAACCAAAGG AACAAGGACA GGNAGATTG AAA 173

SEQ ID NO:680

SEQUENCE LENGTH:172

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00751

SEQUENCE DESCRIPTION:

GATCCAATCC ATTCAAGCAGT CCATTGAAAG GCTCTTAGTC TAAACCTGTG GCCTCTGCCA 60
CGTNGCTCCC TGCCAGCTTC CCCCCTGAGG TTGTGTATCA TATTATCTGT GTTAGCATGT 120
AGTATTTTCA GCTACTCTCT ATTGTTATAA AATGTAGTAC TAAATCTGGA AA 172

SEQ ID NO:681

SEQUENCE LENGTH:170

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00752

SEQUENCE DESCRIPTION:

GATCAAATTT AAACCTCATT TTGGGGGGTA TTTTGGTACT GTAATGGGGT CATCAAATNA 60
TTAATCTGAA AANAGCAACC CAGAATGTAA AAAAGAAAAA ATTGGGGGGA AAAAGACCAG 120
GTCTACAGTG ATAGAGCAAA GCATCAAAGA ATCTTTAAGG GAGGTTTAAA 170

SEQ ID NO:682

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00753

SEQUENCE DESCRIPTION:

GATCGGAACA GCTCCTTACT CTGAGGAAGT TGATTCTTAT TTGATGGTGG TATTGTGACC 60
ACTGAATTCA CTCCAGTCAA CAGATTCAGA ATGAGAATGG ACGTTTGGTT TTTTTTGT 120
TTTGT TTTTTCCTT TATAAGGTTG TCTGTTTTT TTTTNAAAA AATNGCANCA 180
GTNCATGGCC CCCATCATT ANANGNGAGG ANTNCANCAG AAAATAAAAT ATNCACTCN 239

SEQ ID NO:683

SEQUENCE LENGTH:170

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00754

SEQUENCE DESCRIPTION:

GATCCAGACA GCCATCAGGG AAAGCTTGTN TTTAACCGAA CTGTCACACT GAAGGAAGAC 60
CCAGGAAAGG TGTGAGCTGG AAGCACTGAA CCTACCTCAT CCTCCTGGAG GGTGTGGCTA 120
CCCTCGCCAC CCCAAATTCC ATGTCAATAA AGAACAGCTA AATTCTCAAA 170

SEQ ID NO:684

SEQUENCE LENGTH:168

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00755

SEQUENCE DESCRIPTION:

GATCTTTCCA TTGAAATAA CTGGAAGTGA AGAGGTTTGTG TTGCTTGTA AGTGTCAGAT 60
GAGGAACACC ACTATCTTAA TTTTGTGATA CACTGCATT GCTGGTGCTA TTTTNATACA 120
GTGAAGCAAC AGCTTTCAG CAAAATAATA AAATACTTCT ANGTTAAA 168

SEQ ID NO:685

SEQUENCE LENGTH:169

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00757

SEQUENCE DESCRIPTION:

GATCCATCGT NATGCTTAT TTAAGGGGAA CGTGTGGNCT ATTTAGGCTT TATGGCCCTG 60
AAGTAGGAAC CAGATGTCGG ATACAGTTCA CTTTAGCTAC CCCCAAGTNT TATGGGCCCC 120
GAGCGAGGAG AGTAGCACTC TTGTNCGGA TATTGATTTC ACGGAGAAA 169

SEQ ID NO:686

SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00758

SEQUENCE DESCRIPTION:

GATCTGCTAC TAAACAGAGT TCAAAAACCT TCCAGAGTAA TTAATATGTA AAGCCANGTA 60
ACTAACAAAN GATTTGCTTT AGAGATAATT ATTTGGAATT TTTATAGCTN ACTTCACAAT 120
GTGCCCAGGT CAGCTGTATA AAATAAATAC TGCATTNTNG TTTCTTTCAA A 171

SEQ ID NO:687

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00759

SEQUENCE DESCRIPTION:

GATCCTGACA CTAAGGAAAT GCTGAAGCTT TTGGACTTCG GCAGTCTGTC CAACCTTCAG 60
GTCACCTCAG CTACAGTTGG GATGAATTC AAAACGCCTC GGGGACCTGT TTGAATTTT 120

NCTGTAGTGC TGTATTATTT TCAATAAATC TGGGACAACA GCAGAAA 167

5 SEQ ID NO:688

SEQUENCE LENGTH:166

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00760

10 SEQUENCE DESCRIPTION:

GATCAGCGAT GAAGAGGAAG AAGATGATGA TTGAAGTATG AAATATGAAA ACATTTTATA 60

TATTTNATTG TACAGTTATA AATATGTAAG CATGAGTTAT TTTGATTGAA ATGAATCGAT 120

TTGCTTTTGT GTAATTTTAA TTGTAATAAA ACANTTTAAA AGCAAA 166

15 SEQ ID NO:689

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

20 CLONE:HUMGS00761

SEQUENCE DESCRIPTION:

GATCTATTTG GTCTTTCTCA TGTCCCCAC TGGTCTGTAC CCCAGGGAGC GGGTGCTTGT 60

ACTGTGTGAA TCCAGTGTTT ACATTCACAC TTAATGACTT CCTTGGCACC AATCATGTAT 120

25 TTCACCGTTT GCACTTNTTG TATTTCAATA AAAATGTTGA TGCAAAACTG CTAAA 175

SEQ ID NO:690

SEQUENCE LENGTH:165

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS00762

SEQUENCE DESCRIPTION:

GATCGACTCT ATCATCCAAC GCTCCGAGGA CAGCCCATGT CCCACCCCN GNGACCCGGA 60

35 CCCGGCCAGC AGGACCCACT GAGANGGGCT GCCCGGGNCT NCTCAGCTGC CCACACCCAC 120

ACTGTCCAGC ATCTGGCACA ATAAACATNC TCTGTTTTGT AGAAA 165

SEQ ID NO:691

SEQUENCE LENGTH:164

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00763

SEQUENCE DESCRIPTION:

45 GATCAAGAAA TAAACATAAA CATCTCAGAA TGCTCCTTCA TTACCAGAGT CACTACCTGA 60

TTATGTCTTA ATGGGTTACA TAATGACAGA GGGTATCTCA TATATGTNCT TTTCCAAACA 120

TAAAATAACT TTTTGTTTTG TTTGATTGAA AAAAAATTTA GAAA 164

SEQ ID NO:692

50 SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00764

SEQUENCE DESCRIPTION:

5 GATCCAGATT CTCACTTAAT GGGGTTTATA TGGACTTTCT TCTCATAAAT GGCCTGCCGT 60
CTCCCTTCCT TTGAAGAGGA TATGGGGATT CTGCTCTCTT TTCTTATTTA CATGTAAATA 120
ATACATTGTT CTAAGTCTTT TNCATTAAAA ATTTAAAACT TTTCCCATAA A 171

SEQ ID NO:693

10 SEQUENCE LENGTH:164

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00765

15 SEQUENCE DESCRIPTION:

GATCGACTCT ATCATCCAAC GCTCCGAGGA CAACCCNTGT CCCCACCCCC GGGACCCGGA 60
CCCGGCCAGC AGGACCCACT GAGAAGGGCT GCCCGGNTCA CCTCAGGGGG NCACANTTTA 120
CACTCTCCAG CATCTGGCAC AATAAACATN CTCTGTTTTG TAAA 164

20 SEQ ID NO:694

SEQUENCE LENGTH:168

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS00766

SEQUENCE DESCRIPTION:

30 GATCTAATGG TCTAAAACT GGAGTTTCCG GACACAAGCT CTCCCTTTNC CTGCAACCAT 60
CCATGCAAGA TGTNACTTGC TCCTCTNTGC TTTCTGCCAT GATTGTAAGG CCTCCCCAGC 120
TACATGGAAC TNTAACTCCA TTAACCTCT TTNTTTTGTA AATTGAAA 168

SEQ ID NO:695

SEQUENCE LENGTH:160

SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear

CLONE:HUMGS00768

SEQUENCE DESCRIPTION:

40 GATCCGCCCA CCTCAGCCTC CTAAAGTGCT GGGATTACAG CTGTGAGCCA CCCTGCCCGG 60
CCACTTTTGT ATGATTCTA ATGTATTGT AATTACCTA ACAAATTGCC TAATCTGCTA 120
TGTTAATGTA TTTATGAATT AAAATAAATA CGACTGCAAA 160

SEQ ID NO:696

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS00769

SEQUENCE DESCRIPTION:

50 GATCCGTAGC GGCATGTTCT GGCTGCGCTT CTAGGCGGGA AGCCTATGTA AGCAAGAGGG 60
CAGGGCCGGG GTTTGTGGTC CCCCCCCAC CACAAACACA GCACTTCGGC TCCTCTAACC 120

55

TGTGCCACAG GTGACCACCA ATAAAATCCT CTGCTGAGAA A

161

5

SEQ ID NO:697

SEQUENCE LENGTH:159

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00770

10

SEQUENCE DESCRIPTION:

GATCTCCCTG CCCCCACCC AGTTCCCCAA CCCACTCCCT TCCAACAACA ACCAGTCCA 60

ACTGACTCTG GTCTTGGGAG GTGAGGCTTC CCAACCACGG AAGACTACTT TAAATGAAAA 120

AANGAAATTG AATAATAAAA TCAGGAGTCA AAATTCAAA 159

15

SEQ ID NO:698

SEQUENCE LENGTH:159

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

20

CLONE:HUMGS00771

SEQUENCE DESCRIPTION:

GATCTTTTNN TTTTTTTTAA GTCTCACAAG ACATGGGGCA TCTCCACAAA TTTAAGTTCC 60

TGTCCATTG GAAATTTGTT TCTATGTGTA CAGTTTGTC GAGAAAAACA AAGTTTTTGT 120

25

ATGANTACAG AATGTGATT ACGCAAGATT TGACAGAAA 159

SEQ ID NO:699

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

30

TOPOLOGY:linear

CLONE:HUMGS00772

SEQUENCE DESCRIPTION:

GATCTACCTA TCTTCAGGAT GGAACCTTGG GGAAAAATAA AATTGAGGGG AAGTAAAAAG 60

35

TATGTAACAC TTCCAGTTGT GAGCCAAGAT TGTAACCAGA GAGCAGCCAG GAGCTTCCTG 120

TCAGTAACCA TTTTTCAAT AAATACTCTT TCATGTACAA A 161

SEQ ID NO:700

SEQUENCE LENGTH:157

SEQUENCE TYPE:nucleic acid

40

TOPOLOGY:linear

CLONE:HUMGS00773

SEQUENCE DESCRIPTION:

GATCCTCTCA CCTCAGATT CCAAAGTGTT GGATTATAGG TGTAAGCCAC TGAGCCCAGT 60

45

TTGAATGCTT TTTTATATAT TTTTGGCCA TTTGTATGTC ATCTTTGGAG AAATGTCTAT 120

NCAAATCCNT TGCTCATTAA AATNATTNC TGATAAA 157

SEQ ID NO:701

SEQUENCE LENGTH:160

SEQUENCE TYPE:nucleic acid

50

55

TOPOLOGY:linear

CLONE:HUMGS00774

SEQUENCE DESCRIPTION:

GATCTGGCCG TNAGCCGCGA NCCGCTGNGA ACTCCACTCG GGGAACTCCT TTCCAAGCTG 60
ACCTCAGTTT TCTACAAGA ACCCAGTTAG CTGATGTTTT ATTGTAATTG TCTTAATTTG 120
CTAAGAACAA GTAATAAGTA AATTTTAA AAGCCTTAAA 160

SEQ ID NO:702

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00775

SEQUENCE DESCRIPTION:

GATCAAATTG TGCAGTACTT TGTGCATTCT GGATTTTAAA AGTTTTTNAT TATGCATTAT 60
ATCAAATCTA CCACTGTATG AGTGGAAATT AAGACTTTAT GTAGTTTTNA TATGTTGTAA 120
TATTNCTCCA AATAANTCTC TCCTATAANC CACCAGGGAA A 161

SEQ ID NO:703

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00777

SEQUENCE DESCRIPTION:

GATCAGAGCT TATACTTAAT TAAGGTTTTA TACACACCAG TTCCCCAGTA AATNCAAATT 60
TAACAAGAAA ATCAGACATG TCATATGTNC AAAATGCTCA TGGCAACAA TCATTTTGCA 120
TTCCTGCAAA TAAAATTGTT TTATACTGTA GAAA 154

SEQ ID NO:704

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00778

SEQUENCE DESCRIPTION:

GATCTGTTTG TTCCCTGAGC TTTTAAATA CCCTGTGAAA ATTTTNTTC CTCCTTGGT 60
CATCATGCAT CTAATTGTGG GGAAATGTTT GTCAAACCA CCTGCAAAGC AGCATGGTGT 120
AGTTGAGAAG AATAACAGA GAAGACTGGG AAA 153

SEQ ID NO:705

SEQUENCE LENGTH:152

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00779

SEQUENCE DESCRIPTION:

GATCTTTGGA CAGAAGCAGC TCTTTCCCGA ACACTTGTGG CGTCTGGNAC GGCCCCACCC 60
NTCCCCCAC ACTCCCTCCC ACGGGGCTCC GGGAGACAGG CCGGCCCTGC ACCTNACCCC 120

ACCGTGACCT CAATAAACGT TGAAACTNCA AA 152

5 SEQ ID NO:706
SEQUENCE LENGTH:152
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00780
10 SEQUENCE DESCRIPTION:
GATCTATCCT TTA CTTGAAA GCTTTTGAAA AGTGGAAAGG TCATTTTGTT GCATTCCCC 60
ATTCTTGTT TTTAAAAGAC CAACAAATCT CAAGCCCTAT AAATGGCTTG TATTGAAGTT 120
TTACATTGA ATTAAGATG TTAACATGA AA 152

15 SEQ ID NO:707
SEQUENCE LENGTH:151
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
20 CLONE:HUMGS00781
SEQUENCE DESCRIPTION:
GATCTAGTAT GCTCCTGGTC TAATGCATTT ACATTGTTA GGTAAGTGGT TCCTAATAAA 60
AAGAATTATA AAATACCCTC AAATTAACAA TTCAATNGCA TATAATAGCC TAACTCAGTA 120
25 AGANTATTAA AACTTACTAT TATNCTTCAA A 151

SEQ ID NO:708
SEQUENCE LENGTH:152
SEQUENCE TYPE:nucleic acid
30 TOPOLOGY:linear
CLONE:HUMGS00782
SEQUENCE DESCRIPTION:
GATCTANTCT GTGCTACCTG ATTAACCTAC AGCAGGCTTA CTGANTGGCT TCATTTCAGA 60
35 TTTAGTTGAT TTCTCCACCA AATNCATGTC ATGTATTCTC AATAGGCTGT ATTCCCAGCA 120
GNCAATAAAT GGAACACCCG TANAANCNCA AA 152

SEQ ID NO:709
SEQUENCE LENGTH:147
40 SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00783
SEQUENCE DESCRIPTION:
45 GATCCCCAGG GTTCTTTTGT CTTATTTATG GAGAAAAACC GGTCACCTTG TCCAGCGCAC 60
TGTGAGGCC CCACTCAGGC CAGCCCTGGC CCCCCTTGG TACTTGGAAC CGAAGTTACA 120
GATTATATTA AAATAATAAT GTACAAA 147

50 SEQ ID NO:710
SEQUENCE LENGTH:146
SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS00784

SEQUENCE DESCRIPTION:

5 GATCTTATAA AAGGAAATTC TAGCAGTTT AGAAATAGGT GGGAAAACT CAAATATTCC 60
 TCCTATCTGC ACCAAAAAGT TTATTTGTGG TATATAAAT GAATATTGTT TTATAATAAC 120
 TTGTTAATAA AGTACTTTCT AATAAA 146

SEQ ID NO:711

10

SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00785

15

SEQUENCE DESCRIPTION:

GATCAATGAA GTGAGAAATT GTTGAGAAG ATACAGTTTG TTTTAGATG TCCTTTGTCC 60
 AATGTGAACA TTATTCATA TTGTTTGTAT TACCCTCGTG TTAACAAG ATGGCAATAA 120
 ATACTATGGG ATTGTTTGT TAAA 145

20

SEQ ID NO:712

SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25

CLONE:HUMGS00786

SEQUENCE DESCRIPTION:

GATCTCCCTT CAGCAACTTA TTTTGCTTAA ATTGCTTTAA ATCTTAAGCA ATATTTTAA 60
 TTCAGTAAAC AAATCTTTC ACAAGGTACA AAATCTTGCA TAAGCTGAAC TAAAAATAAA 120
 NTGAAAAGGA GAGATTAANG GTAAA 145

30

SEQ ID NO:713

SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

35

TOPOLOGY:linear

CLONE:HUMGS00787

SEQUENCE DESCRIPTION:

GATCTAGAAG CAGAGGAATC CCAGCGCCTT TAAAAGTTG TTATGTGGTT TTCTTTTAA 60
 AAGCTCCTGT TTTTGGAAG TAGAATTAT GGGTACAACG TATGTTCAAT ATTTGTACAT 120
 AAAATAAAC CATTTAATAA GTAAA 145

40

SEQ ID NO:714

SEQUENCE LENGTH:154

45

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00788

SEQUENCE DESCRIPTION:

GATCTATGCC TAACAGAGCC CCAGTACAAC TATTTNCAG AATGGCTGTT ACCCTAGAAT 60
 TACTATAGCA CATATTGAGA TATAGTTGTA CTCCCTAGTA GATAGGAAC GACCCAACA 120

50

55

ATAAACTTTG ATAATAAAGA AAAAAAANCG NAAA

154

5

SEQ ID NO:715

SEQUENCE LENGTH:144

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00789

10

SEQUENCE DESCRIPTION:

GATCAACCTT AAAGGAAACT GCTATCCGAA CTTGGCTATC TCACAGCAGA GCCAGTTTGA 60

CGAATGGGTA AACCTAAGG ACATGCTGGG TCCAAAGTGA TTTACATAAA TNTATAATGA 120

AAATAAACAT GTATAANATT TAAA 144

15

SEQ ID NO:716

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

20

CLONE:HUMGS00790

SEQUENCE DESCRIPTION:

GATCCGTGAT GCCACTTACC TGTGTGTTTG GTAACAACAA ACCAACATCA TGGAGGTCCC 60

TGGATTGAAA AAGGAGCCTC TCCCACTCCT CCTACCACCA AAGTGGTTAG GACNCTATAT 120

25

AANTAAAAAC AAGGCTTTTG GAAAATAAA 149

SEQ ID NO:717

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

30

TOPOLOGY:linear

CLONE:HUMGS00791

SEQUENCE DESCRIPTION:

GATCTGGCTG AACCACTTCC ACAAGGTTAC TGTATACATA GCCTGAGTTT AAAAGGCTGT 60

35

GCCCACTTCA AGAATGTCAT TGTTAGACTT TGAAATTCT AACTGCCTAC CTGCATAAAG 120

AAAATAAAAT CGTTTTAAAT CAAGAAA 147

SEQ ID NO:718

SEQUENCE LENGTH:115

40

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00792

SEQUENCE DESCRIPTION:

45

GATCTGGGGC AGCCACCTTG CTACCATGAA GGAAAGGCCA AGACAATCAT CCACAGCTAT 60

TCCCTCCAGC ATCTGGTTCT GTACAAAAAT TAAATGCTTA TTTNTTTAAG TCAAA 115

SEQ ID NO:719

SEQUENCE LENGTH:142

50

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

55

EP 0 679 716 A1

CLONE:HUMGS00793

SEQUENCE DESCRIPTION:

5 GATCGCCACT GTAAAGGTCC TAGAGTTGCC TGTGTGTCTC TGGAGATGGA ATTAAACCAA 60
ATAAAGAGCT TCCACTGGAG GCTTGATTG ACCTTGTAAC TATATGTTAA TCTCNTGTTA 120
AAATAAAATA TAGCTTGTGA AA 142

SEQ ID NO:720

10 SEQUENCE LENGTH:142

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00794

SEQUENCE DESCRIPTION:

15 GATCTGTGCC TACNTTTTAC CACCCTCTTG ATTGGAGCTT TTGTNATGCA GCTACCATNN 60
TTCAAAAAA TTAATAATTA AAAAAAAAAA ATCTGCCACT TATCCAAGTC CACTAGAGGC 120
CACTGTCTTC AAAGNTTNTN TN 142

SEQ ID NO:721

20 SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00795

25 SEQUENCE DESCRIPTION:

GATCCAGGTG ACTCTGAACA TCATTAGAAG CATGCCAGAA CAGACTGGTG AAAAGTAAAC 60
CTTTTCACCT AAAAAATTTC ACCTGCAAAAC CTAAACCTG CAAAATTTC CTTAATAAAA 120
ATTTGCTTGT TTAANAACA NNNGAAA 147

30 SEQ ID NO:722

SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35 CLONE:HUMGS00796

SEQUENCE DESCRIPTION:

40 GATCCAGAGC CTCCGGGCC TTCTCCGGTG TCCTGTACCA ACTCTTCTAT TTAAGAGAAC 60
CTCAGATGAT GTACCTGAGC CTCAGGGTTT TGTTTCAGAG GGATATAAAT NATTTAAAAA 120
TTAAATGAAA ACGTTGCAAA 140

SEQ ID NO:723

SEQUENCE LENGTH:150

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS00797

SEQUENCE DESCRIPTION:

50 GATCGGCCAC TACCTGGGCG AGTTCTCCAT CACCTACAAG CCCGTAAAGC ATGGCCGGCC 60
CGGCATCGGG GCCACCCACT CCTCCGCTT CATCCCTCTC AAGTAATGGC TCAGCTAATA 120
AAGGCGCACA TGACTCCAAA AAAAAATAAA 150

55

SEQ ID NO:724

SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00798

SEQUENCE DESCRIPTION:

GATCAGGGTA AGGCAGTCAG GCGGGTGTTC ACCACTGCCT TTCCTTCCTC TGAGCGTGAG 60
 AACACTGAAC CCAGCCACTG CCCCTGGGTC CCTGTCCTGG AAATNGTCTA ATAAATCCTT 120
 TNCCCTTCTT GAGCTACAAA 140

SEQ ID NO:725

SEQUENCE LENGTH:141

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00799

SEQUENCE DESCRIPTION:

GATCCGAATC GAGGCCAACG AGGCCCGGGA TGAAGGCCCN GGAGTAGGCG AGCCAGACGA 60
 CAAGGTTGAC CTCAGCTTCG GAGCCACCTC TGGATGAACT GCCCCAGCC CACGNCCNAT 120
 TAAAGACCCG GAAGCCTGAA A 141

SEQ ID NO:726

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00800

SEQUENCE DESCRIPTION:

GATCAGCTTT ACCTATGGTG CTTTGCCTTT AACTAGAGTG TGTGATGGTA GATTATTTCA 60
 NATATGTATG TAAACTNTT TCCTGAACAA TAAGATGTAT GACCCGGAGC AGAAATAAAT 120
 NCTTTTCCTA ATTAAA 136

SEQ ID NO:727

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00801

SEQUENCE DESCRIPTION:

GATCATGTCA TTCAATTCCA GTCACCTCTT CTGCAATCAT GACCTCTTGA TGTCTCCATG 60
 GTGACCTCCT TGGGGGTCAC TGACCCTGCT TGGTGGGGTC CCCCTTGTA CAATAAAATC 120
 TATTTAAACT TTAAA 135

SEQ ID NO:728

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00802

SEQUENCE DESCRIPTION:

5 GATCTTAAAC ATTGTTTGT AGTGTATATT ACTTGTCAT TCCTTTAAGG GGAGCAGCCT 60
 GCACTCTTTT GTAGATTACT TTTGGGGGAT ATATTNNAG AATNATGAAA CGGAATAAAA 120
 TTGTAATAAAA CTAAA 135

SEQ ID NO:729

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00803

SEQUENCE DESCRIPTION:

10
 15 GATCATGTTA CCATATCAAG CTGAAAATGT CACCACTATC TGGAGATTTC GACGTGTTTT 60
 CCTCTCTGAA TCTGTTATGA ACACGTTGGT TGGCTGGNTT CAGTAGGGGG NTATTNNAGG 120
 CCTTTCTTTT TAAA 134

SEQ ID NO:730

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00804

SEQUENCE DESCRIPTION:

20
 25 GATCTANGTT GCCTACCTTG AATTTTTTTT TAAATATATT TGATGACATA ATTTTGTGT 60
 AGTTTATTTA TCTGTACAT ATGTATTTTG AAATCTTTA AACCTGAAAA ATAAATAGTC 120
 ATTTAATGTT GAAA 134

SEQ ID NO:731

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00805

SEQUENCE DESCRIPTION:

30
 35 GATCTCACTA AAGGATTCTT ATTTGCTGTC AGTTAAAAAT AAAGCCCTAA ATACATTTTT 60
 ATTCTTTCTA CTGAGGGCAT TGTCTGTTTT CTTTGTAAT GCCGTACAAT AAACAAATTA 120
 40 TTTAATAACC TAAA 134

SEQ ID NO:732

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00806

SEQUENCE DESCRIPTION:

45
 50 GATCTTGCA CTCTCATGT TCTCTACAAG AAGCTGTGGT GATTGGCCCT GTGGTCTATC 60
 AGGCGAAAAC CACAGATTCT CCTTCTAGTT AGTATAGCG ACTTAATAAA AGAGGAAAAA 120
 ACTCTTGCTT CAGTAAA 137

5 SEQ ID NO:733
 SEQUENCE LENGTH:134
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00807
 SEQUENCE DESCRIPTION:
 10 GATCCTCGAA CGGAAAGCCA AATCTCGCCA AGTAAGGAAA GGAAAAGGGC AAATACAAGG 60
 AAGAAACCAT TGAGAAGATG CAGGAATAAA GTAATCTTAT ATACAAGCTT TGATTAAAC 120
 TTGAAACAAA GAAA 134

15 SEQ ID NO:734
 SEQUENCE LENGTH:132
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00808
 SEQUENCE DESCRIPTION:
 20 GATCACTGGC TTTGAATGAA ATACAGATGC ATTATCCAGA ACTGAAGTTG CCCTACTTTT 60
 AACTTTGAAC TTGGCTAGTT CAAAGATAGA CTCTTCTTTT GTAAAGTAAA TAAATTCTTC 120
 AAAATGCTTA AA 132

25 SEQ ID NO:735
 SEQUENCE LENGTH:132
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00809
 30 SEQUENCE DESCRIPTION:
 GATCNNAACC TTTTCAATAA AAGGCAAAAC AAACCAATNT CCNAACATAG CATTACAGCC 60
 TTAAAAACCA TTCACTNCTC ATAGTGATTC ACAGAGGACA AGAGATTAAA GTGCTGGATT 120
 TTAAATGTCA AA 132

35 SEQ ID NO:736
 SEQUENCE LENGTH:131
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 40 CLONE:HUMGS00810
 SEQUENCE DESCRIPTION:
 GATCANATGC AACCNACAA CCTCGGCTGA GTCTTGAGAC TGAAAGATTA AGCCATAATG 60
 TAAACTGCCT CAAATTGGAC TTTGGGCATA AAAGAACTTT TTTATGCTTA CCATCTNTTT 120
 TTTTCTTAA N 131

45 SEQ ID NO:737
 SEQUENCE LENGTH:383
 SEQUENCE TYPE:nucleic acid
 50 TOPOLOGY:linear

55

CLONE:HUMGS00811

SEQUENCE DESCRIPTION:

5 GATCATACAC CTGCTCACAG GCGAGAACCC TCTGCAGGTC CTGGTGAACG CCATCATCAA 60
 CAGTGGTCCC CGGGAGGACT CCACACGCAT TGGGCGCGCC GGGACTGTGA GACGACAGGC 120
 TGTGGATGTG TCCCCCTGC GCCGTGTGAA CCAGGNCANN TGGCTGCTGT GCACAGGCGC 180
 TCGTNAGGCT GCCTTCCGGA ACATTAAAGAC CATTGCTGAG TGCCTGGCAG ATGAGCTCAT 240
 CAATGCTGCC AAGGGCTCCT CGAACTCCTA TGCCATTAAG AAGAAGGACG AGCTGGAGCG 300
 10 TGTGGCCAAG TCCAACCGCT GATTTTCCCA GCTGNTGCCC AATAAACCTN GTCTGCCCCT 360
 TTTGGGGGAA GCCCCGAAGC AAA 383

SEQ ID NO:738

SEQUENCE LENGTH:128

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00813

SEQUENCE DESCRIPTION:

20 GATCCAGCTG CCAGAGGATG AGTGACCAGT TGCTAAGTGG GGCTCAAGAA GCACCGCCTT 60
 CCCACCCCC TGCCTGCCAT TCTAACCTCT TCTCAGAGCA CCTAATTAA GGGGCTGAAA 120
 GTCTGAAA 128

SEQ ID NO:739

SEQUENCE LENGTH:128

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00814

SEQUENCE DESCRIPTION:

30 GATCTGGATT ACNATGTAA TTCACAGCAG TAAGATAATA TAAATTTTGT TGAATGTATT 60
 AACATCATAT GGTCTGAAAA TGTGGGTTTT NATTTGGCAC ATTAAATAA AATGTTTCTA 120
 ACTAGAAA 128

SEQ ID NO:740

SEQUENCE LENGTH:128

35 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00815

SEQUENCE DESCRIPTION:

40 GATCAAGAAT GAAAAAGACA TCATATGAAN NGGGAGAAAC TATTGCACA CCATCTATCT 60
 CATGGTTTGG TTAATATTCA AACTATATNA GCAGAATGTG TAAGGATATC CTACAACTCA 120
 ATAGCAAA 128

SEQ ID NO:741

SEQUENCE LENGTH:138

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50 CLONE:HUMGS00816

55

SEQUENCE DESCRIPTION:

GATCCAAGGG GAAACTGCAG GTCAAGGGCT GATAACGGCC ATGCAGGATG CTTGATGCTG 60
 CGTCCCCCGC TGCTTGCCGC CCCCCACCCC GCCATTTTGT ATAATAAAGC TCCCTGTGTA 120
 TTCTCAAAAA AAANCAAA 138

SEQ ID NO:742

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00817

SEQUENCE DESCRIPTION:

GATCCCTGAG ACTGAGGGGT TTACGGGCTG TGAATGGACC TTCAGCCCTN CCCACCCTCC 60
 CTCCCCACTG CTGCTGAGTC TGTCTGATGT TTTGGTTGTG TGAATAAATA TAATCCCTCT 120
 CTGGAAA 127

SEQ ID NO:743

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00818

SEQUENCE DESCRIPTION:

GATCGGGTAG CTCAAAAGAA GGCAAGCTTC CTCAGAGCTC AGGAGCGGGC TGCTGAGAGC 60
 TAAACCCAGC AATTTCTAT GATTTTTCAT GATATAGATA ATAAACTTAT GAACAGCAAC 120
 TAAA 124

SEQ ID NO:744

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00819

SEQUENCE DESCRIPTION:

GATCAGAAAT TCTCTTGCTT GAGAGATTTT TTTTGTCTT CTGTTGACTA CATAGTTTCA 60
 AATCTCTCTN TATTTCTATG TGATATATAA ATNGCTTTTA ATTATATNAA ATNTTAATTN 120
 NCCN 124

SEQ ID NO:745

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00820

SEQUENCE DESCRIPTION:

GATCTCATTG CCTGTTTCC GAATTCTGCC GTGTGTATCC CCAACCCCTG ACCCAATGAC 60
 ACCAAACACA GTGTTTTTNA GCTCGGTATT ATATATNTTT TTCTCATTAA AGGTTTAAAA 120
 CCAAA 125

EP 0 679 716 A1

SEQ ID NO:746

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00821

SEQUENCE DESCRIPTION:

GATCCGTGGC TTAAGACAGG AGATTATCTC TNTACTCCAG TGGCATCTCC TTAGCCAAGA 60

TGTGAAATTA AAATCATAGT TCGCCTCATT TAAAAATNCT AATAAAGCAC TCAAACTTTG 120

AAA 123

SEQ ID NO:747

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00822

SEQUENCE DESCRIPTION:

GATCCAAATC TGGTTCAAAC ATTCAAACT TCAAAGATAA TTCATCTTTC AGCTAATGCT 60

TGTGGTTCGT TTGTTCCCTT GAAAAAAAT AAAACAGTT GCCTTCNGGG AAAANTTNA 120

AA 122

SEQ ID NO:748

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00823

SEQUENCE DESCRIPTION:

GATCTTGTGT TTTAGGNTGG GCATTTTCAC TCTTCTGCCT TAAATCCCTA ACCCCATGGA 60

GCTGACATTC TAGTGCGGCT GAGGGGAGGG GAAACATTGT AAAATAAATC ATAAAAATTA 120

AA 122

SEQ ID NO:749

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00824

SEQUENCE DESCRIPTION:

GATCTCTGGG CTGGGGACTG AATTCCTGAT GTCTGAGTCC TCAAGGTGAC TGGGGACTTG 60

GAACCCCTAG GACCTGAACA ANCAAGACTT TAAATAAATT TAAAAATGCA AAAACTCGGA 120

AA 122

SEQ ID NO:750

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00825

SEQUENCE DESCRIPTION:

5 GATCNTAGAA GGGCTTCCCA ACCNNATTTG CAACATCCAA ATTGTCTTCA ATTNAAGGAA 60
 GGCCCTTATCA GTTCATAGAT GANCTTCATT GTAAAAATAA ATGTACTTTG CACCACTTCA 120
 AA 122

SEQ ID NO:751

SEQUENCE LENGTH:273

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00826

SEQUENCE DESCRIPTION:

15 GATCCACTTC TGTNATTANG TAAATGGATG TNTCGTGATG CGTCTACAGT TATTTATTGT 60
 TACATCCTTT TCCAGACACT GTAGATGCTA TAATAAAAAT AGCTGTTTGG TAACCATAGT 120
 TTCATTGTN CAAAGCTGTG TAATCGTGGG GGTACTATCT CAACTGCTTT CGTATTCATT 180
 GTATTAAAAG AATCTGTTTA AACAACTTTT ATCTTCTCTN CGGCTTTAAG AAACGTTTAT 240
 TGTAACAGTA ATTAAATGCT GCCTTAATTG AAA 273

20 SEQ ID NO:752

SEQUENCE LENGTH:144

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS00827

SEQUENCE DESCRIPTION:

30 GATCAAAAAG AAACCTTTGTT TTTCCGCAAT TGAAGGTTGT ATGTAAATCT GCTTTGTGGT 60
 GACCTGATGT AACAGTGTC TTCTTAAAAT CAAATGTAAA TCAATTACAG ATTAAAAAAA 120
 AAAGCCTGTA TTAAAGAAC GAAA 144

SEQ ID NO:753

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear

CLONE:HUMGS00828

SEQUENCE DESCRIPTION:

40 GATCAGAGGA AAAATCCAGT GTGACAGAGT GCAAGTNAGA AGACCTGGCT TTNATCCCA 60
 GCTTTGAAAC TTGGAACCTT TTGATTGACA AATTAATAAA CCTCTCTATG CCTCAGGCTC 120
 CTCATCTGTA AA 132

SEQ ID NO:754

SEQUENCE LENGTH:117

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00829

SEQUENCE DESCRIPTION:

50 GATCTAGGCT TGAGCTTGGT TGGGATTGCT NTTTTCTTCT TCTTCTTTAT AAACGATTCT 60
 NTGTAACNT TTGTATTGAC AGTTTCAAAC TTACAGTAAA ATTGCAACAC GAGTAAA 117

55

SEQ ID NO:755

SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

5

TOPOLOGY:linear

CLONE:HUMGS00830

SEQUENCE DESCRIPTION:

10

GATCAGTACA TAGCATTGG CTCNTGAACN NAATTNTAAA CTTTCAGGTA TTTTGTACA 60
AATAAGGGAC TGATGTTCTG TTTCTGTAA TTAGAAATAA ACATTAATAC AGTGAAA 117

SEQ ID NO:756

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

15

TOPOLOGY:linear

CLONE:HUMGS00831

SEQUENCE DESCRIPTION:

20

GATCTATCAT TACTGCAAAA ACCTGCTCTG TTGTGCTGGC TGGNAGGCCC TGTGGCTGCT 60
GGCTGAGGGT TCTGCTGTCC TGTGGCACCC CATTAAAGTG CAGTTCCTC CGGGCCAAA 119

SEQ ID NO:757

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

25

TOPOLOGY:linear

CLONE:HUMGS00832

SEQUENCE DESCRIPTION:

30

GATCTGAAAT TAAATACTCA ACAGACTCCT CCTTTTTTAG CTGTATTTT CAGGTACTGT 60
GTGGTGACCG CCCCACTGGT GTCTATTACA GGCCACTTTG GTAGTTGTGT ATCTGNTCAT 120
GTATGTGATT TGACAAACCA GTTTTTTAAA ATAAATGGCT TTTTAAA 167

SEQ ID NO:758

SEQUENCE LENGTH:379

SEQUENCE TYPE:nucleic acid

35

TOPOLOGY:linear

CLONE:HUMGS00833

SEQUENCE DESCRIPTION:

40

GATCCAATA GAAATGAATG GAAGATGATG GGAAATATGA CTTACCAAG GAGCAATGCT 60
GGGATTGCAA CTGTAGGGAA CACCATTTAT GCAGTGGGAG GATTGATGG CAATGAATTT 120
CTGAATACGG TGGAAGTCTA TAACCTTGAG TCAAATGAAT GGAGCCCCTA TACAAAGATT 180
TTCCAGTTTT ANCAAATTTA AGACCTCTC AACTANCAG GCTTAGTGAT GTAATTATGG 240
TTAGCAGAGG TACACTTGTG AATAAGNGG GTGGGTGGGT ATAGATGTTG CTANCAGCAC 300
CACAANGCTT TTCCATATTN GCNTCCTNTT AACCATGCNT GTCCATAAAC CCNGGGANGN 360
NNANTTGNGG GGTNAANN 379

45

SEQ ID NO:759

SEQUENCE LENGTH:121

50

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00834

SEQUENCE DESCRIPTION:

GATCTACTAC TNGGCCTTCA GTGCGAAGAG CCACATCCAG GCCTGAGGGC GGCACCCCAG 60
CCCTGCCCTT GCTTCCTTCA ATAAACATCA CAGGACCTGG GACTGCACAG GNCCTGGGAA 120
A 121

SEQ ID NO:760

SEQUENCE LENGTH:303

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00835

SEQUENCE DESCRIPTION:

GATCGAAGCA ATTGANGTAT CATGGATTGG ATTGTTACTG ATTCAGTAA AGTATGTTTT 60
GCCAATTAGA TACATATATA CAAGATAAAG GAATAGGATG GTAATATATT TGTNTGAAAT 120
TAAATTACTG TTTTATTAA AAAAATACTGC TTCATTGGGC TGATTTTGTA AAATGTAATG 180
AGTAAAAATGA ATTACTGTAT TTNCCCTTTT ATGTCCACAG AATGAGAGTC ATATGTNGTN 240
ATATNCTAAA TTNCAATTA ATATTCATGT CACCTTGAGT TGTCATGATA AGTATGTTTT 300
AAA 303

SEQ ID NO:761

SEQUENCE LENGTH:373

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00836

SEQUENCE DESCRIPTION:

GATCTACTAT GTNATGTCAG GGCCTGCGTG GCAACTCATG CAGCAATTCC AGAACCCCTGA 60
CTTCCCACNC GAAGTAGAGG AACAGGATGC CAGCACCTG CCTGTGTCTT GTGCCTGGAA 120
GAGTGGGATG AAACGCCACA GAGCAGCCTG TGCTTCGGCT AGTATTAATG TGTAGATAGC 180
ACTCTGGTAG CTGTAACTG CAAGTTTAGC TTGAATTAAG GGATTTGGGG GGACCATGTA 240
ACTTAATTAC TGCTAGNNNN GGAATGTCTT TGTAAGAGTA GGGTCGCCAT GATGCAGCCA 300
TATGGAAGNC TAGGGTATGG GTCACACTTT ATCTGTGTTT CTATGGAAC TNATTTNGNA 360
TATTTNGNTT TGN 373

SEQ ID NO:762

SEQUENCE LENGTH:406

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00837

SEQUENCE DESCRIPTION:

GATCTAGGGA GATGTGGAAG AAAGTGTGAC TACTATAGAA ATTGATGAAG AAACATATGA 60
AGAGATATAT AAATCAACGN AACGGAATAT TCCAATGCTC TTTGTCCGGG GAGATGGCGT 120
TGTCCTGGTT GCGCCTCCAC TGAGAGTTGG CTGAAACAAA GAATTTGTCC TGTATGGAAA 180
NCGNNNNNNN GGTGTACAGT GGCCTCTCTA AAAGTACAAA ACATTCATAA GAGAAACCCG 240

CATACATTTT GATATTAAGA AATAATCCG GGGATTCTTC CACTCCTGAA ATGAGTTGAT 300
TTGCAGATAA CTCACAACCT CTTAAGCTAA ATGGTATTTT CATTTTCTC AAGCTCTCCN 360
ATAANTATGG CCACCNNNGG NNANNGNGTG GGGAAAAAAA NAATTN 406

5
SEQ ID NO:763

SEQUENCE LENGTH:120

SEQUENCE TYPE:nucleic acid

10
TOPOLOGY:linear

CLONE:HUMGS00839

SEQUENCE DESCRIPTION:

GATCCCCACG CCACAGCCCT TTTGTCTCTG CAAACTGCCT TCTTCGGAAA GAAGAAGGTG 60
GGAGGNTGTN AATTGTTAGT TTCTGAGTTT TACCAAATAA AGTAGAATAT AAGACGNAAA 120

15
SEQ ID NO:764

SEQUENCE LENGTH:115

SEQUENCE TYPE:nucleic acid

20
TOPOLOGY:linear

CLONE:HUMGS00840

SEQUENCE DESCRIPTION:

GATCTTGATG GTGTTTCTTT CCCCAAAAAT TGACTTAGAT ATTAAAAATT GGTGCTTATA 60
AGAGAGAGTT AAAAAAAAAT AGGATTGCTT CAATTAATAA TACAAAAGAG NCAAA 115

25
SEQ ID NO:765

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

30
TOPOLOGY:linear

CLONE:HUMGS00841

SEQUENCE DESCRIPTION:

GATCCAGTGA CAGCAGGTGT CATGGGTCAA GCATAAATCA TATATAGCAT TTTCAGGCAT 60
GTTCTTGTA GTTCTTTTGA GTCTGACATT CTAATAAAAT AATTTGTAGG AAA 113

35
SEQ ID NO:766

SEQUENCE LENGTH:112

SEQUENCE TYPE:nucleic acid

40
TOPOLOGY:linear

CLONE:HUMGS00842

SEQUENCE DESCRIPTION:

GATCTTTGTG AGGATTAGGA ATTAGGTAA AAGAAATTAA GAACCATCTT CAAGCAAAAN 60
TTAAACTTTA TTCTNCTTA ANCAATAAAT ACACCTGANT TAGTTTTCCA AA 112

45
SEQ ID NO:767

SEQUENCE LENGTH:112

SEQUENCE TYPE:nucleic acid

50
TOPOLOGY:linear

CLONE:HUMGS00843

SEQUENCE DESCRIPTION:

5 GATCAAAGAC CCAAAGGAAT GCAACANTTT ATCTNTTATC TACCTATNAC CTGCGAGCTG 60
 CCCACCACCC CCANGTTGTN GCGCCTTTCC AGACAGAACC AGTGATACATC TN 112

SEQ ID NO:768

SEQUENCE LENGTH:130

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00844

SEQUENCE DESCRIPTION:

15 GATCCAAAAC TTAATACAT CTATGAATTT CCTGGGGCTA TTGTGAGTAC TGTGTATGTA 60
 TTTAGCAAAT ATTTAAGACC TAGTAAGTGC TCAATAAATT GTAGCTGTTA TTGCTGTTGT 120
 NGTTTGTAAA 130

SEQ ID NO:769

SEQUENCE LENGTH:111

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00845

SEQUENCE DESCRIPTION:

25 GATCGTGCCA CTGCTCTCCA GCCTGCATGA CGGGAGTNAG ACACCATCTC AAAAAATACA 60
 TATAATAATA TAAATAAAAA TATCTTTTNN GAAAAATAATT TAATATNNCN N 111

SEQ ID NO:770

SEQUENCE LENGTH:110

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00846

SEQUENCE DESCRIPTION:

35 GATCNAGTAN TGNAGGGGCT GTTAGGAGCT TCCTGCAAAT CCCTGAGAGG GCAGAAGATA 60
 GCTTCTGTTA ATTCATTATT CTTCCAATAA ATGTTGATTG AGTACCTAAA 110

SEQ ID NO:771

SEQUENCE LENGTH:109

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00847

SEQUENCE DESCRIPTION:

45 GATCACCGNC CAGTAATGGG CTCAGAGCAG GTCTTCATCA TGCCTTGTCCT TTTTAACT 60
 GAGAAAGGAG ATTTTTTGAA AAGAGTACAA TAAAAGGAC ATTGTCAAA 109

SEQ ID NO:772

SEQUENCE LENGTH:109

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

55

CLONE:HUMGS00848

SEQUENCE DESCRIPTION:

GATCTTCTTC AATATGTGAA TTTGGGCTCA CAGAATCAAA GCCTATGCTT GGTTTAATGC 60
TTGCAATCTG AGCTCTTGAA CAAATAAAAT TAACTATTGT AGTGTGAAA 109

SEQ ID NO:773

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00849

SEQUENCE DESCRIPTION:

GATCAACAAG GTTGGCCACT GCTTGTATTA CCAGGGACTG GTTACAACCA TTATTTCTNT 60
TCATTGCTT GGCTTATCTC ATATTAAGT GAGTTTGGAG TTCTCCAA 110

SEQ ID NO:774

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00850

SEQUENCE DESCRIPTION:

GATCCAGTTC TAAACTTTGG GATATTTTTT TTCAATTTTG AAGAGAAAAT GGTGAAGCCA 60
TANGAAAAGT TACCCGAGGG AAAATAAATA CAGTGATATT CTTACGCAA 110

SEQ ID NO:775

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00851

SEQUENCE DESCRIPTION:

GATCTGTGTG CTCTTATCAC CAATCAGTTC AGACCTGGTT GATTTTGTAC TTTGGAAGTG 60
TACCTTGGAT GGTTTGTGTT ATTAAAAGAG AAACCTGAAG TACTCAA 108

SEQ ID NO:776

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00852

SEQUENCE DESCRIPTION:

GATCACCATC TTAAATTTA CTTCAAAATA AAAGCATGTA AGTNACTGTT TTCAAGAAG 60
AAATGTGTTT CATAAAAGGA TATTTATATC TCTNNGCTT TGACTIONN 108

SEQ ID NO:777

SEQUENCE LENGTH:106

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00853

SEQUENCE DESCRIPTION:

5 GATCCCCCTC GGAAGAGGGA CTCCAATGGG CATGTCCCCT CCGGAAATNC GGCCTCCTCC 60
 CCCTGGAATG CNAGGNCCCC CTCCCCCGGN AATNCGCCCA CCAAGN 106

SEQ ID NO:778

SEQUENCE LENGTH:130

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00854

SEQUENCE DESCRIPTION:

15 GATCCCATCA TGAATTCATT GGAATTTGTG TTGCATGTAA GGCAATCTTT TCCNTGTTGT 60
 AAATCTTCCG TTTTITAATG TACATATATT TTGAAAAATA TGAATAACA TGAAATTTTA 120
 AAAGCTGAAA 130

SEQ ID NO:779

20 SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00855

SEQUENCE DESCRIPTION:

25 GATCATGGTG GGTGAGCTGT ACTGATTGTN ATCCTGACTT TGGCATTGGC AGCTCTTATA 60
 TNCCGACGAA TATATCTGGC AAACNNATAC ATATNTAACT TTAN 104

SEQ ID NO:780

30 SEQUENCE LENGTH:107

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00856

SEQUENCE DESCRIPTION:

35 GATCTTTTTA CAGTATCCAT TTATTATGTA ATNCTTNTNA GAAAAGAATC TTATAGTACA 60
 TTTTANTATA TGCAACCAAT TAAATGTAT AAATTAGTGT AAGCAAA 107

SEQ ID NO:781

40 SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00857

SEQUENCE DESCRIPTION:

45 GATCAAAATG AAAGAAAATC ACAGAAATTA TCCTATGTGT ACTCCTCATC CCTCCTGCTG 60
 TATATNTTCT NATTTTTTGC GTAATAAATN ATGTTAATTA CCAAATAAA 109

SEQ ID NO:782

50 SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS00858

SEQUENCE DESCRIPTION:

GATCTCCAAT GTTTTGGGGA TGCTTTGAGT CTCAAAAAA ATTGATAATC AGAAAAGTAA 60
TTTTTGTTTG TTTGTTTAAT GTATCCCTGT TCTGTTTTTA ATTAACTCC AAGTCTCATT 120
TAAA 125

SEQ ID NO:783

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00859

SEQUENCE DESCRIPTION:

GATCGAGGTG ACAAATANTC AGTCNTANG TCCCCACAAT GACCTACCA NNATGGCTTT 60
GGGGAGCTCT TCACCCTAAA GATTGGGTCT GGTGCTAA TGN 103

SEQ ID NO:784

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00860

SEQUENCE DESCRIPTION:

GATCTGGAGG CAAGATGCCA GGCCCCACAG GTGTTCTCAG GGCAGTTCTT GGTGCTGCT 60
TCTCAGATAC CAAGGACTGG AATAAAACC TTCCTGGGA AA 102

SEQ ID NO:785

SEQUENCE LENGTH:99

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00861

SEQUENCE DESCRIPTION:

GATCACAGCC GAAGAGTGAA AGGTGCTGCA ATGAATGTTA GCTGTGGCCA CTGTGGATT 60
TTCGCAAGAA CATTATAAAA CTAATAACTT CATGTGAAA 99

SEQ ID NO:786

SEQUENCE LENGTH:94

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00862

SEQUENCE DESCRIPTION:

GATCAAGTTA TTTTNAATTT GGTTCACACA TTGGAACAA GTCAGTCATT CAGATATGAT 60
TCAAATGTCT ATAAACCGAA CTGATGTAAG TAAA 94

SEQ ID NO:787

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00863

SEQUENCE DESCRIPTION:

GATCTCTTCT TCTCCCTGTG GCCCCTGCGC TGTGCCCCG TCCCCGTCAC CCCGCCGNN 60
ACTGAAATNT ATAATCTGAC TTCCTGTACA GAAACCTGCA AA 102

SEQ ID NO:788

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00864

SEQUENCE DESCRIPTION:

GATCTTGTTA GCAATGCTGT TTTTCTGTT AGTCGGGTTA GAGTTGGCTC TACGCGAGGT 60
TTGTTAATAA AAGTTTGTTA AAAGTTTAAT AAA 93

SEQ ID NO:789

SEQUENCE LENGTH:100

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00865

SEQUENCE DESCRIPTION:

GATCTTCAAG TGAACATCTC TTGCCATCAC CTAGCTGCCT GCACCTGCCC TTCAGGGAGA 60
TGGGGGTCAT TAAAGGAAAC TGAACATTGA ACCCTTTAAA 100

SEQ ID NO:790

SEQUENCE LENGTH:92

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00866

SEQUENCE DESCRIPTION:

GATCAGAATT TAAATGTGT GATTCTTTTT CTTTCTGTAA GTATGTATTG CTATGATAAA 60
TAAAAAATGG CAGGACCATT NTTTTATNA AA 92

SEQ ID NO:791

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00867

SEQUENCE DESCRIPTION:

GATCTCCAAC CAGGCCAGAG AAGATTCTCA CAGAAGGTTT TGAACCTAA GAAATAAATT 60
GGTTTGTTAA TAAATGGCTT CTGGTCAGAT AAA 93

SEQ ID NO:792

SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00868

SEQUENCE DESCRIPTION:

GATCTTGAT CTTTGATAA CGGATGTAT TTGTACGAAG GGCAGTTCGT AAACAGCACT 60
TGTCCTTTA ATAAAAGAAT GTTTTGCAAA AAAAAAAAAA AAANCCCNAG GAAA 114

SEQ ID NO:793

SEQUENCE LENGTH:90

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00869

SEQUENCE DESCRIPTION:

GATCTGTTTT GTACTTTTA TACTGTTGGA TACTTATAAT CAAAACTTT ACTAGGGTAT 60
TGAATAAATC TAGTCTTACT AGAAAATAAA 90

SEQ ID NO:794

SEQUENCE LENGTH:88

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00870

SEQUENCE DESCRIPTION:

GATCCATTTC ATAAAGTATG ATTTGCCCAA ACCTGTACCA TTTCCGTATT TCTCCTGTAG 60
AAGTAAGAAA TAAATTCCT TAAATAAA 88

SEQ ID NO:795

SEQUENCE LENGTH:89

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00871

SEQUENCE DESCRIPTION:

GATCTGGCGC TTGGGGGTAA GTGGNATGAT TTGCTAATAT TGAGNATCTG TTGTATCAAA 60
CATAATAAAC TTTTTTTGA GATGTGAAA 89

SEQ ID NO:796

SEQUENCE LENGTH:89

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00872

SEQUENCE DESCRIPTION:

GATCAGGGTG TCTCCTTGTG CTTCTNAGAT GTGGAGAAGA GGCTGCTGGC TACCCTAAAA 60
NTTGAAATAA AAGATTTTGT CCTTTGAAA 89

SEQ ID NO:797

SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00873
SEQUENCE DESCRIPTION:
GATCCATTGA GCCCAGCAGT CCAACCTGGG CAAAATAAGT GAGAGACCCT GTATCTGAAA 60
GTAATAATAA AAATAAAAAA TATAAA 86

10 SEQ ID NO:798
SEQUENCE LENGTH:86
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00874
SEQUENCE DESCRIPTION:
GATCCTTTTT GATAATCTCA TTCCTAGAAA TTAAACCTTA ATGAAATCCC TAATAAAACT 60
CAGTGCTGTG TTATTTGTGC CTCAAA 86

20 SEQ ID NO:799
SEQUENCE LENGTH:87
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00875
SEQUENCE DESCRIPTION:
GATCGAACAT TTCACCTCTC ATATTAAGTC TGGCAATGAT GACTATATGT ATTCCTGCCT 60
AAATAAATCA TCTATTAATC ATTAAAA 87

30 SEQ ID NO:800
SEQUENCE LENGTH:86
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00876
SEQUENCE DESCRIPTION:
GATCTCCGAG TCAGGACGGT CGGCCAGACC CACGGGGTAA CGGGTCTAAT CGGTAGGAA 60
TAAAGCTGTA TTCCAGTGCT TCCAAA 86

40 SEQ ID NO:801
SEQUENCE LENGTH:84
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00877
SEQUENCE DESCRIPTION:
GATCCCCGCG ATACTTCAAC GCCTTCTGAC TTCCAGGTGA TGACTGGGCC CCCAATAAAT 60
CCCGTCTTTG GGTCTCTCTG CAAA 84

50 SEQ ID NO:802
SEQUENCE LENGTH:84

55

SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
5 CLONE:HUMGS00878
SEQUENCE DESCRIPTION:
GATCCCTCAA AACCTCACTA ACTGGAAGGA TGATTTTGTC TCAGTTTGTA CTCCTAAATA 60
AAAAGTAAAC ATGACACCTC TAA 84

10 SEQ ID NO:803
SEQUENCE LENGTH:88
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
15 CLONE:HUMGS00879
SEQUENCE DESCRIPTION:
GATCTGTGAA GAAATGAAAT AAAATGGTAT TTAGTAAGAA ATCTCTATTT TAAGAAAAAA 60
AGTAAACCT GTTATAACA CATGCAAA 88

20 SEQ ID NO:804
SEQUENCE LENGTH:82
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
25 CLONE:HUMGS00880
SEQUENCE DESCRIPTION:
GATCGTGCCA TTGTGATATG AATATGCCTT ATATGCTGAT ATGAATATGC CTTAAAAATA 60
AGTGTTCCCC ACCCCTGCCA AA 82

30 SEQ ID NO:805
SEQUENCE LENGTH:81
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
35 CLONE:HUMGS00882
SEQUENCE DESCRIPTION:
GATCTTAAGT CATAATTN AATTGTNTAG AGGTTGTCA ACTGAAGGAA TAAATGTCTA 60
TNAANCTAAA ACAAATGGAA A 81

40 SEQ ID NO:806
SEQUENCE LENGTH:78
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
45 CLONE:HUMGS00883
SEQUENCE DESCRIPTION:
GATCAAGTTT GTACATAACA CTAGTGGCAT TTCTTATCAA AAGGATTGGA TAATAAAAAAT 60
AAGTTTCTAC TGGGTAAA 78

50 SEQ ID NO:807
SEQUENCE LENGTH:78

55

SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00884
 SEQUENCE DESCRIPTION:
 GATCCCCCA GCAAGGATAN CATTCAAAGG AGCTCACATT TATGGAATGG ATGAATCAAT 60
 AAATTAATTC ACTTTAAA 78

SEQ ID NO:808
 SEQUENCE LENGTH:77
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00885
 SEQUENCE DESCRIPTION:
 GATCCCATTT CTGATGGATG TGTACACCT TTTCTGTCAA AATAAAATGT CTTGGAGGTT 60
 ATGACTCCTT GGTGAAA 77

SEQ ID NO:809
 SEQUENCE LENGTH:77
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00886
 SEQUENCE DESCRIPTION:
 GATCTGTGTT AATCTGAGTA ACTTATTGCC TAGCCTATAA ATAAATTCCA AAATATCCAA 60
 TTCATTCTT CTTGAAA 77

SEQ ID NO:810
 SEQUENCE LENGTH:75
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00887
 SEQUENCE DESCRIPTION:
 GATCATCCTT CCTGGCAAAT AAATCCCCTT TTCTATCCAA AAGAGCAATA AAAAGTTTTC 60
 AGTGAAATGT GCAAA 75

SEQ ID NO:811
 SEQUENCE LENGTH:76
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00889
 SEQUENCE DESCRIPTION:
 GATCTGAAAG CCTGAGTGTG TGTACGTGCG CGCGTGCGTG AAGGCCCTGC CACGATTAAA 60
 GACTGANACC GGCAAA 76

SEQ ID NO:812
 SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00890
 SEQUENCE DESCRIPTION:
 5 GATCTTTAAT ACAATATAGA AATTGTGTAA TAGTTATTAT AAATGTTAAT ACACAACTTT 60
 CAGGTAATTT TAACTGATTA TTTCTTTTGC TCTTTTAACT TAAGTTATTA AAGTTTAAAA 120
 GTTCGTAAA 129

10 SEQ ID NO:813
 SEQUENCE LENGTH:74
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 15 CLONE:HUMGS00891
 SEQUENCE DESCRIPTION:
 GATCTGGTCT CGGTGGTCCT TCCCCGCAGG CAGGTGTCAG GACCGGCCTA ATAAACATGT 60
 GTGGCCTCCT CAAA 74

20 SEQ ID NO:814
 SEQUENCE LENGTH:82
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 25 CLONE:HUMGS00892
 SEQUENCE DESCRIPTION:
 GATCCAAATC CCATTACAGT TGTATAAAGA AATAAAATTT TGTACTNATA TTATTAATAA 60
 TCACATTTT AATATTGTA AA 82

30 SEQ ID NO:815
 SEQUENCE LENGTH:72
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 35 CLONE:HUMGS00894
 SEQUENCE DESCRIPTION:
 GATCCCCAGA GACCCCATTT GCCTCTCAAC ACTCAGACCT TCAACTGTTT TTNAATAAAT 60
 CTACTTTTAA AA 72

40 SEQ ID NO:816
 SEQUENCE LENGTH:72
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 45 CLONE:HUMGS00895
 SEQUENCE DESCRIPTION:
 GATCCTACAC CCNGAGCCTC AGAGCACTGC TACTTTTTAA AATACTTCTT TCTCTTAAAA 60
 GTCTTTACCA AA 72

50 SEQ ID NO:817

55

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00896

SEQUENCE DESCRIPTION:

GATCAGATGT TAAGACTGAC ATTTCCAAGG TTGGCTACTA TGTAAAATTA AAATTACACA 60
AATTGTGCAA A 71

SEQ ID NO:818

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00897

SEQUENCE DESCRIPTION:

GATCTGAAGT AATTGTGCTG TATTTATGTT TATTCACCAG TCTTTGATTA AATAAAAAGG 60
AAAACCAGAA A 71

SEQ ID NO:819

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00898

SEQUENCE DESCRIPTION:

GATCTAGCTC TCTGATTCCA TACATTCCAG ACTTCTCAGT GGATTGTAA TAAACTATAA 60
ATAAAAATAG CTCTCATTTA TAAA 84

SEQ ID NO:820

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00900

SEQUENCE DESCRIPTION:

GATCATGTCT TTTCATGTG TACCTGTAAT ATTTTCCAT CATATCTCAA AGTAAAGTCA 60
TTAACATCAG AAA 73

SEQ ID NO:821

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00903

SEQUENCE DESCRIPTION:

GATCTGATTA TTACTTTGT TTATTGTCTA TATGCCTTTT AAAAAATAA ACTTGTTATG 60
CAAAATAAA 69

SEQ ID NO:822

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00904

SEQUENCE DESCRIPTION:

GATCCAGTTG TAGCTGCCAT CAGATGCCGG AGACTCGCCC NTCAATAAAA AAATCTCTTC 60

TAGCTGAAA 69

SEQ ID NO:823

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00905

SEQUENCE DESCRIPTION:

GATCACTGTA AATGGTAATC AGTTGGAATT CTCCTAAATG TCTCCAGAC ACTAGTAAAA 60

AACGACCTGA AA 72

SEQ ID NO:824

SEQUENCE LENGTH:68

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00906

SEQUENCE DESCRIPTION:

GATCTTTCTA CTGCCTTTC CATGTCATGA GAGGAAGAAA CAAGAATGAC AAGTGTATGA 60

CTNCCAAA 68

SEQ ID NO:825

SEQUENCE LENGTH:67

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00908

SEQUENCE DESCRIPTION:

GATCACGTAC CTGTGCAGAA ACCGCCTCTG TGGCTGCATT TGAATAAAA CCCGACCCAG 60

CAGCAAA 67

SEQ ID NO:826

SEQUENCE LENGTH:342

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00910

SEQUENCE DESCRIPTION:

GATCATATTT TATGAACAGA AAGACTCAGG ACATATTAAA AAATAAACTG AACTAAAACA 60

ACTTTTGCCC CTGACTGATA GCATTTTCTT TGAAGGGCTA TGATACCATT 120

TATTAATAG TGTTTTATTT TAAAAACAAA ATAATTCCAA GAAGTTTTTA TAGTTATTCA 180

GGGCACTATA TTACAAATAT TACTNNGTTA TTACACAAAA AGTGATAAGA GTAACATTG 240

CTATACTGAT GNTTGTNTAC TCAAAAACCT CNGNTNAAACN GTATGTAATC TNAGTTCACT 300
GCACTTAAGT TCACCNAACA TNNATNAATG TCAATGNAGA AA 342

5

SEQ ID NO:827
SEQUENCE LENGTH:72
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

10

CLONE:HUMGS00911
SEQUENCE DESCRIPTION:
GATCTAAGAA GTTGTGAATG TTGTTAATCA TTTAGCCGTT GCAATAAATG TAGAGGAAAT 60
GCAGTGTGCA AA 72

15

SEQ ID NO:828
SEQUENCE LENGTH:65
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

20

CLONE:HUMGS00912
SEQUENCE DESCRIPTION:
GATCACCTGA GGCCATGAGT TTNAGACCAG TCCTGGTAAC ATAGCAAGAC CTCCATCTCT 60
ACAAA 65

25

SEQ ID NO:829
SEQUENCE LENGTH:65
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

30

CLONE:HUMGS00913
SEQUENCE DESCRIPTION:
GATCCTAGAC AGCGCCTTAT CTATGATTGA GTGTCCGTGT AAATAAATTC CTACTTAGAC 60
TTAAA 65

35

SEQ ID NO:830
SEQUENCE LENGTH:65
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

40

CLONE:HUMGS00914
SEQUENCE DESCRIPTION:
GATCTGGGAA CTTTTNCTG TACAAATCTG TTTAAAAAAA AAAAAAGGNA CCNCATTGAT 60
TTAAA 65

45

SEQ ID NO:831
SEQUENCE LENGTH:63
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

50

CLONE:HUMGS00915
SEQUENCE DESCRIPTION:

55

GATCCAAATT AAAACCTGGT AGAATCTAAT ACATTGACTG CAATTAAAAAT GTTGCCTGG 60
AAA 63

5 SEQ ID NO:832
SEQUENCE LENGTH:68
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00917
10 SEQUENCE DESCRIPTION:
GATCCAGTTC TAAGTGTCAT CTTTATNAT NAAGACAATA AAATCTTGAG TTTATGCTC 60
ACTNAAA 68

15 SEQ ID NO:833
SEQUENCE LENGTH:63
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00918
20 SEQUENCE DESCRIPTION:
GATCCACGGT TGTNACCATG TATTACCACA AATTAAACAA TAAAAAATTG TTTAAGAGT 60
AAA 63

25 SEQ ID NO:834
SEQUENCE LENGTH:109
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00919
30 SEQUENCE DESCRIPTION:
GATCTACTGT CATTGNATG CAATTCCTG TTACCTTGAA AAAATAAAAA TGTTAACAGG 60
AATGCAGTGT GTCATTCTC CCNAAATAGT AAANCCCACT GTATACAAA 109

35 SEQ ID NO:835
SEQUENCE LENGTH:62
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00920
40 SEQUENCE DESCRIPTION:
GATCCAATTA CACACATTG TTCACAAC TC AACACAAATT CCTATTAAAT ATTAAGTA 60
AA 62

45 SEQ ID NO:836
SEQUENCE LENGTH:61
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00922
50 SEQUENCE DESCRIPTION:

55

GATCTTAAAC ATAGGAAAAC CATACGTGTT CATGATAATA AAATGCTTTC TATGAAATAA 60
A 61

5 SEQ ID NO:837
SEQUENCE LENGTH:56
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00924
10 SEQUENCE DESCRIPTION:
GATCATACCA CTGCTCTCCA GCCTGGCTAT CAGAGTGAGA CTCTGTCTCA CAGAAA 56

15 SEQ ID NO:838
SEQUENCE LENGTH:56
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00925
SEQUENCE DESCRIPTION:
20 GATCAGACAC TTAACCCCTTA TAANTTAAAG TCAATAAAGC ACCTTTTAA AGGAAA 56

25 SEQ ID NO:839
SEQUENCE LENGTH:57
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00926
SEQUENCE DESCRIPTION:
30 GATCAAAGTG AAACAATGTT TGGATGCAAC GCAGAATAAA AGAATATAAG AAATAAA 57

35 SEQ ID NO:840
SEQUENCE LENGTH:52
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00929
SEQUENCE DESCRIPTION:
GATCTAATTA AAAGACCTTC TGCACAGCAA AAGAAACTAA CAACAGAGTA AA 52

40 SEQ ID NO:841
SEQUENCE LENGTH:52
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
45 CLONE:HUMGS00930
SEQUENCE DESCRIPTION:
GATCCCGGCA GAAGCTATGA AAGGGAATAA AGAGAAAAGA AGTACCCAGA AA 52

50 SEQ ID NO:842
SEQUENCE LENGTH:52

55

SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00931
5 SEQUENCE DESCRIPTION:
GATCTTTTAG TTTCAACTCA GCTTTTACAA TAAAANGGAT TTGTATTGCA AA 52

10 SEQ ID NO:843
SEQUENCE LENGTH:58
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00932
15 SEQUENCE DESCRIPTION:
GATCTCTTTT CAGAAGTGTCTATAGAACAA TAAAAATCTT TNACTTCTGA CCTTGAAA 58

20 SEQ ID NO:844
SEQUENCE LENGTH:53
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00934
25 SEQUENCE DESCRIPTION:
GATCCTAAAT CATGACTTAC CTGCTAATAA AAACCTATTG GAAAAGTGAG AAA 53

30 SEQ ID NO:845
SEQUENCE LENGTH:52
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00935
35 SEQUENCE DESCRIPTION:
GATCAAGCTG TAAAAAACN AAAAAATTAA TAAAAATTC GAGAAATANA AA 52

40 SEQ ID NO:846
SEQUENCE LENGTH:51
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00936
45 SEQUENCE DESCRIPTION:
GATCAGCATT GTGACTTGGA GATAATAAAA TTTAGACTAT AAACCTTGGA A 51

50 SEQ ID NO:847
SEQUENCE LENGTH:62
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00937
55 SEQUENCE DESCRIPTION:
GATCTGAGGT AAACTTTGAA GTAAAAATAA AGCTGTGTTT GAGCATCATT TGTATTTGGA 60

AA

62

SEQ ID NO:848

SEQUENCE LENGTH:59

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00938

SEQUENCE DESCRIPTION:

GATCCTCCCT CCCCTAATTA AAGTCTCTTT TTGCCCCCTT GGGCTGNCAT GAGGTCAAA 59

SEQ ID NO:849

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00955

SEQUENCE DESCRIPTION:

GATCAGAATT TTAAATNAAA GGTTTTTTCT TTAAATNATT TGTATTACTT TATTAAAACT 60
CTGATATTAA A 71

SEQ ID NO:850

SEQUENCE LENGTH:661

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00972

SEQUENCE DESCRIPTION:

GATCCGGTTC TGGGACAGCA GGGGGCCCCA CTGCACCCAG GTCATCCCTG TGCAGGGCCG 60
 GGTCACTCC CTGAGCCTCA GCCACGACCA ACTGCACCTG CTCAGCTGTT CCCGAGACAA 120
 CACACTCAAG GTCATCGACC TGCCTGTGAG CAACATCCGC CAGGTGTTCA GGGCCGATGG 180
 CTTCAAGTGT GGTTCGACT GGACCAAAGC TGTGTTGAG CCGGACAGAA GCTATGCACT 240
 GGCAGGCTCC TGTNATGGGG CCCTTTACAT CTGGGATGTG GACACCGGGA AACTGGAGAG 300
 CAGACTACAG GGACCCCAT TGCCTGCCGT CAACGCCGTG GCCTGGTGCT ACTCCGGGAG 360
 CCACATGGTG AGCGTGGACC AGGGCAAGGA AGGTTGTGCT TTTGGCAGTA GGGCCACGAC 420
 CTGCCTGCTT GGGNTGGAGN TTTTNCCTG AAGCTNAAAG TTTCTTNGG GGCAATGAAG 480
 GGGTTTGGGG TTTGGGATTN GAGNTTNGNC TTGGGATTTA ATTGGGNAAG AAGGCTTGA 540
 AAGACCTTGN CTTTTTTNTT TAAAANTNAA GTATTGGTTT GGGGGNTTAA GGTAATTTT 600
 TTTTNGAATT TTAANTTNAT NTCTAAATTT TTTTCCAAAT TTTGAAAAAT TTTTTTTNAA 660
 A 661

SEQ ID NO:851

SEQUENCE LENGTH:641

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00973

SEQUENCE DESCRIPTION:

GATCTTGGAT GTCTATTATA GGAGAAGTAT GTCCTGCCAA TGTACAAGAA GGCAGCATTG 60

TAGGATTAAC ATTCTTGTCT ACTGTATATT ATCTTGAAG GCTCTTGTTA ATATGTTACA 120
 CTTAATATTC TCCACAGTTA CCTTTAGAGA GAATTTATGA GAAGTTAGTT TCTGATGCAG 180
 AGGTTTTTAG GCTGTGATTT CATCAAAAGT CCTAATAGCA TTCTACCTCA AAGGGACACT 240
 TAGNATGCCT AAAATTTATT CACTTAGTTT TCCTTTTTTA TTTGAAAAA TACATGACAT 300
 GTAATCTTTT TTTCTGAAT TCTTCTCAG ATTTTAAAGT ACTATATTAA AGAAAAAAT 360
 TAATGTCTAA AGGCCTAGCA TTCCTTGCAG GACCCCTATA CTAACCATGG TAATGGGGGA 420
 GAGGGGTGGG GCAGNTNNGT AGGGGNACCA GGTTCAGGC CTCAAGCTTC CCAAAGCCAT 480
 TTTTNTAAA TGGGAAATCC NTNAANTTNT GGAACCCGCT TTGNTATNGG NGCCCTTTT 540
 TTTAAATTC CNGGCCTTTT TTTNNTTGGT AATGGGGGTT NCTGTTTGNG GTTTTAACCT 600
 NANCCTGGNC CGGGGGGGT TAAAGGAATG CTGNCCTGCAA A 641

SEQ ID NO:852

SEQUENCE LENGTH:627

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00974

SEQUENCE DESCRIPTION:

GATCTGCTNC AGTGCTCTGA GCCCTAGGAT TCATCTNTCT TTTCACCGTA GNGCGCNGGA 60
 CTGGCATTGT ATTAGCAAAC TCATCACTAG ACATCGTACT ACACGACACG TACTACGTTG 120
 TAGNTCACTT CCACATATGTC CTATCAATAG GAGCTGTATT TGCCATCATA GGAGGCAACA 180
 TTCACTGATT TCCCTATTC TCAGGCTACA CCCTAGACCA AACCTACGNC AAAATCCATT 240
 TCACTATCAT ATTCATCGGC GTAAATCTAA CTTTNTCCC ACAACACTTT CTCGGCCTAT 300
 CCGGAATGCC CCGACGTTAC TCGGACTACC CCGATGCATA CACCACATGA AACATCCTAT 360
 CATCTGTAGG CTCATTCAAT TCTCTAACAG CAGTAATATT ANATAATTTT CATGATTGA 420
 GAAGCCTTCG GTTTCGAAGC GAAAAGTCTT AAATAGGTAG GANGAACCTT TCCATTAAAC 480
 CTGGAGTGAC TATATGGNTT GCCCNTACCC TTACCANACA TTCNGAGGAN CCCGTATACA 540
 TAAAATTNTN GNNAAAAAAN GGANGGNTT GNACCCCCA AAGTTGGTT TNANGNCAAC 600
 CCCCNTGGGC TCNATGGTTT TTTTAAA 627

SEQ ID NO:853

SEQUENCE LENGTH:617

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00976

SEQUENCE DESCRIPTION:

GATCAGANTG CCCCTCCACT CATGAGACTC TTCATTTTGT CCACCTTGAC AGGAAAAGTG 60
 GGAATGTATG CAGAGCTCTC AAAAGAAACA AAAAAGGCCA AAACGCTGCC TTCAGCCACA 120
 TCCTCTGAAT TGGCCCTGAC TTGGACTAAA NCCNCTAATG CAAAATCCCT TGACAAAAGC 180
 GCATAGGTTA TTTCAAACCA GCATTGTTTT TTATGTAACC TGTTTTACCG CATCTTCTCA 240
 GCAGTTCTG ACCACTGCTC AATTTTTTCC TTTACAGCCA TTGTTCTGGT GGACAAATAA 300
 CCTAGGTACT CCAATCCTG GCAGGAAAAA TATACAGCAT TATGAAACAG CACTCAGTAA 360
 TCCTAAAAATG GATTTTCCAA AGCTGGTTAC ACATGNCCTG CAAAGTCTTA TTAAATTTA 420
 AAAGGCCTTT CTCATTACC AGGGGTTTAG GTCAACGNG GCAAACCCCT GGGGGAATTT 480
 AAATGGGAA GTTTANTTNC CTTTNGTAAA TTCATAGGNG CAAAANGCN GGGNAGTTAA 540
 TTTTCCATN GGGTTGGTGG CNCCCGGGNT TCATTGGTNT TNGGCCCAN GGAATTTAAT 600

TTTTTTAAAN CCTTAAA

617

SEQ ID NO:854

SEQUENCE LENGTH:602

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00977

SEQUENCE DESCRIPTION:

5 GATCCCGTGC GGC GCGCTGC CCGAGGGGAG CAAGGACAGC TTG CAGTTC TCCTGGAGTT 60
 CGCTGAGGAG CAGCTGCGAG CCGACCATGT CTT CATTTCG TTCCACAAGA ACCGCGAGGA 120
 CAGAGCCGCC TTGCTCCGAA CCTTCAGCTT TTTGGGCTTT GAGATTGTNA GACCGGGGCA 180
 TCCCCTTGTC CCCAAGAGAC CCGACGCTTG CTT CATGGCC TACACGTTG AGAGAGAGTC 240
 10 TTCGGGAGAG GAGGAGGAGT AGGGCCGCCT CGGGGCTGGG CATCCGGCCC CTGGGGCCAC 300
 CCCTTTTINAG CCGGGTGGGT AGGAACCGTA GACTCGCTCA TCTCGCCTGG NTTTGTCCGC 360
 ATGTTGTAAT CGTGCAAATA AACGNTCACT TCCGAATTAA GCGGNTATT TTTGAANGT 420
 TTAATAATTG TGTTTTNTGA ATACTGAAGT ATTTGGCTTT AAATTCCTAA NTAATAAATT 480
 TAATNTTTTA CTTTTTAAAT TGCTGGGTTT AAGATNGTTN AAGATTATCC TTGNAACTTT 540
 20 NNGGGGGANG TTNTATTTT NGAGTCTTTT NGGAANAGNC TTNAGGCTTT TNNACTTNGA 600
 AN 602

SEQ ID NO:855

SEQUENCE LENGTH:595

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00978

SEQUENCE DESCRIPTION:

30 GATCCCAAGG CTCCTGCCA TTTTAGTGTC TTGGTGTAGT GTAACCATTT AGTGGTTGGT 60
 GGCAACAATT TTATGTACAG GTGTATATAC CTCTATATTA TATATCGACA TACATATATA 120
 TTTTNGGGGG GGGGCGGACA GGAGATGGGT GCAACTCCCT CCCATCCTAC TCTCACAGAA 180
 GGGCCTGGAT GCAAGGTTAC CCTTGAGCTG TGTGCCACAG TCTGGTGCCC AGTCTGGCAT 240
 35 GCAGCTACCC AGGCCACCC ATCAGGTGTG ATTGACATGT AGGTACCCTG CCACGGCCTA 300
 TGCCACCTG CCCTGCTTCC TGGCTCCTTA TCAGTGCCAT GAGGGCAGAG GTGCTACCTG 360
 GCCTTCCTGC CAGGAGCTTT NCACCCACTN ACATTCCGTC CCCGCGGCTT AACTGNAGCA 420
 AGCGTGGNCC TAGGACAGNA GGAGCTTCGG GCCCNGTTN ACCTTGGCGT GGGGCTNANG 480
 GGTGGCATT TCTTGCTGG GGGCACTGGG TTNAAATTTT GGGNTGATNA TTGGGGNGAG 540
 40 GGGTGGGGTA AAAAAACAN TTTTGGNNAA GNTTGGGANG NTTTTGNCCT TAAA 595

SEQ ID NO:856

SEQUENCE LENGTH:581

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00979

SEQUENCE DESCRIPTION:

50 GATCTGGAAT TGCAGCCAC ATAACATAA AGGAGGATGT CCCTGGTCTG TTCCATCCCC 60
 ACGGATGGTG TTGCTGCTGG GCAACAGTGT TGGCTTCTTT NAAGTACCCC CTTTCCTCCT 120

EP 0 679 716 A1

CACCCACCTC CAAACTGACT AGCACTCAGA GGGACTTATG ATAAAGGTTT AGCTCCAGGG 180
 GTAGTACCTG AGTGTGTGCC ATGCCCCCTC AGACCAGCTG CTTCATCAG AATTCAGGG 240
 TCACAGCCCC AACAGAAGCA GCAGTGCCTC TGTAGGAGGG GTGCTGGGCT CTGGNCTTCT 300
 NATGCAGAGA GGTCCGGGAC AGGGTCAGTA TCGTGGGCAT GTNTATAGCT TCCCAAGTTC 360
 TTTTACAAGT CCCNTGCTGG GACTCCCTGA NTTTACTTTT GGTNGGNITC CTAGGTNCTA 420
 ATTGGTTTTA CAAACTTACA NTTTTNTAGG AATTGTANT ANGATTANCT TGNTTTAATT 480
 TAATTGTAGA NTTTNGGGGC CTTTTTGGGN CTCAAATTTT NCCATTACAA GGNNTTATTN 540
 GGGAAANAAA GNGTTTNA TNAATCCT TGGCCAGGAA A 581

SEQ ID NO:857
 SEQUENCE LENGTH:569
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00980

SEQUENCE DESCRIPTION:
 GATCTAAATC AGACAGGAGT TGGTCTACAT AGTAGTAATC CATTGTTGGA ATGGAACCTT 60
 TGCTATAGTA GTGACAAAGT GAAAGGAAAT TTAGGAGGCA TAGGCCATTT CAGGCAGCAT 120
 AAGTAATCTC CTGTCCTTTG GCAGAAGCTC CTTTAGATTG GGATAGATT CAAATAAAGA 180
 ATCTAGAAAT AGGAGAAGAT TTAATTATGA GGCCTTGAAC ACGGATTATC CCCAAACCTT 240
 TGTCAATTC CCCAGTGAGC TCTGATTCTT AGACTGCTTT GAAAATGCTG TATTCATTN 300
 GCTAATCTAG TATTTGGGGT ACCCTGCTCT TNTGGCTGTN CTTTTTTTGG AGCCCTTCTC 360
 AGTCAAGTCT GCCGGATGTC TTTTTTACC TACCCCTCAG TTTTCCTTAA AACGGGNACA 420
 CAANTCTAG NGNGGTGTTA NGANTAATNG TTAGTNGGGT TANTGGGGTA NTTNNTGGGG 480
 TNTNGGTTT GGGCTAGGCA TTGTGGTAGG TTTTNAANAA TTAGNGGGT GGNCCCCNTT 540
 NGNTGGGGTG NTTTCANGGT NGAATNAAN 569

SEQ ID NO:858
 SEQUENCE LENGTH:566
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00981

SEQUENCE DESCRIPTION:
 GATCCACCCC NGGCCTCTCC TGGAACTCTG AACCTGCTGT GGAAGGAATT GGCCATGACC 60
 TTCACCTCTG GAGAGTAGGG TCTATGGCGA GGGAAAAGGG NNTTCACCAT GATAACCTAG 120
 TGCCCTCCATA GAGGGGTTTG GAAAAATTC AGTCCGATTT CTTTGTGTGT CAGCTGACTT 180
 CCTTAGCTGA TTGTTCCAC TTGCACCTCT CCACCTTTGG CACTAGAACT CCTGAGACAC 240
 CACTTCTCAT GCTTCTCCCT CCCTACCAGC GGTCAAGGCT TTGGAGCCAC TCTTTGTAA 300
 CTCCAGATTA TTAAAGAGA AAAGTACAAG ACAGAAATCT TCTAGCACTT TGTAACACA 360
 GTTGATTAAC CCTCTTGGGN GTATTTTGG GGTCTTATAT AAAANCANGG TTTTAAATT 420
 NGTAAAGTNT AAGTGCCATT AGGAANATGC ACCAGGGCAT ATTTTGGTT NAAGGTGGTT 480
 TTTCAATGG TTTTNCAGGN TTNCATTTT AAAAAAANGG TTTTAAAT GGAGGTGTT 540
 NTTNAAANNT TCNTGANTGG TGGAAA 566

SEQ ID NO:859
 SEQUENCE LENGTH:556

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00982

SEQUENCE DESCRIPTION:

GATCTACAAT TACTAATTAA AGCTGTGAAT CTNTTCCCTG CTGGAACAAA TTCAAGATGG 60
GAAGTTATTG CTAATTACAT GAACATACAT TCTTCCTCTG GAGTCAAAAAG AACTGCCAAA 120
GATGTTATTG GCAAAGCAAA GAGTCTCCAA AAACCTGACC CTCATCAAAA AGATGACATA 180
AATAAAAAGG CATTGTATAA GTTCAAAAAA GAACATGGNG TGTACCTCA AGCAGACAAC 240
GCAACGCCCT CAGAACGATT TGANGGTCCA TATACAGACT TCACCCCTTN GACAACAGAA 300
GNACAGAAGC TTTTNGAACA AGCTTTGAAT ACATACCCAG TAAATACANC TGAAAGATGG 360
GNANAAATAG CAGTAGCGGT GCCTGGCAGG NCAAGGAGG GNGTGCATNN ANCCGGTTNC 420
AGGGGACTTT GTCGNGTGG GTAAAGCCAA AGGAAGCTTG TTCCAGGTCN ANGTGCTGGA 480
TGCAAGTTGG GGCNTGGNAT TNNCNATTT TTGTTGGGGT GTTCCTTTT TTANTAAACC 540
TGNANTTCTT TTAAA 556

SEQ ID NO:860

SEQUENCE LENGTH:555

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00983

SEQUENCE DESCRIPTION:

GATCTGGATT ATTTGTCTAA GTGAGAGATT GCGAATATCA AAATATCTGT CTCACTTCTT 60
CTGTGAATNA CACAGAGTAG AAATAAATTC ACTTTAAAAA TATGACTGAA TTTTAAAAAT 120
CAAGACTGAA TCTCACATAG CTGCAGACAG GAACTAAGCC AGCCTCTTG TATGTGGTAA 180
CAAGTACAGT ATAAGANTGA AAGATTTACC ATCCTTGAAA GCTCTAATGA AAATCAAAATC 240
CAGCAATATA TATTCAACTG TGTACAGGAT TTAAGAAGTT ATTTTATGAA GGAGTAATAG 300
TGTGTAGATA TAGATTCTGA AGTCTTTAAA CGTGCCTTAA TAAATNAAGT TCNCTGGCAT 360
TGAGNTGANN ACCAGGTGAC CNTTGGGGNC AAAAACCNC ACAAGTGATT NGCACACCAG 420
TATACNTTCA CCANTATACT NTNTGCACAC ACANCNTTGG TTTNGGTTCA GGGTTTGGCA 480
AATNGGTCAN ATGTATTGGC ACTGGCGTCT TTGNATTGTG TAAGTGGNTA TTTTNTGAGG 540
NTAGCGTGGT NNCNN 555

SEQ ID NO:861

SEQUENCE LENGTH:554

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00984

SEQUENCE DESCRIPTION:

GATCCATGTC TCAGCCTCCA CCCCGCCACA CCTGTCTGTG CAGCCCACCG GCCTTACCTT 60
CTACCCTGCC GTGGATGTCC AGGCCTTTGC CGTCCTCCCC AACTCCTCCC TGGCTTCCCT 120
CTTCCTGATT GGCATGGTAA GCAGTTCCTG GGTGGACAG ATGAGGAGCC CCAGACAGTC 180
CCAACAGCAC TGTCTTTGGA GTCAGGAGAC CATGTGAATC CTGTCTGGAT TCAAACCTGG 240
ACTGTGTAC TCCGGAGCCT GAGGCTTGAG TCACTGTACT CAATGGTGCC GACTCCTGGA 300
GGTATTCATT CACCCAGCCA TTCACTAGTG CGTTTGTGTTA CTTATTCATT CAATTATTCA 360
TTCAGTCAAT TTCTCATTCA TTCANTTATT CATTCCATGT TGGCTTGAAA TATGTGTACT 420

GTNCCAATTN ATCCATTTAT ATCTTTAGTC ATTCAATTAT GCATTNGTGG TATTTGTTCA 480
 TTNATTCAANT TTTAATTTN ATTNAGTTAN TNNNTNGGTT GGTGNCITGG NGTANNGTNA 540
 TACATTTGNG GAAA 554

SEQ ID NO:862

SEQUENCE LENGTH:549

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00985

SEQUENCE DESCRIPTION:

GATCCTATGG TTCAGGAGGC CAGAAATTTT CACCTCTAGG AGGTGGTGGT GGCATAGGTT 60
 ATGAAGCTAA TCCTGGCGTT CCACCAGCAA CCATGAGTGG TTCCATGATG GGAAGTGACA 120
 TGCCTACTGA GCGCTTTGGG CAGGGAGGTG CGGGNCTGTG GGTGGCAGGG TCCTAGAGGA 180
 ATGGGNCCTGG AACTCCANCA GGAATATGGT AGAGGGAGAT AAGAGTACGA AGNCCAAACA 240
 AAAAACCCCG ATTTTAGATG TGATATTTAG GCTTTCATTC CAGTTTTGTT TTGTTTTTTT 300
 GTTTAGATAC CAATCTTTTA AATCNTTGA TTTAGNAAAG AAGCTATCTT TTAATGGTTG 360
 TAGCAGTTAT TGACCTAATA TTTGAAATGG CTGTTGGCAG TAAATTATGA ATCAGTTTTT 420
 GACCAGGNGA TTTTTTNCN TNTATTCCTT ANTTTCCTGT TNCCTGATATN CCCCCAAGTA 480
 TGCAGTTNCT NNNCNCNTAA TTCCANGGNN CCATTTTTTT TTCNGGGTTC AANAATNGAA 540
 TNGNTTAAA 549

SEQ ID NO:863

SEQUENCE LENGTH:543

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00986

SEQUENCE DESCRIPTION:

GATCAGCAGT CTTCTGCTGC CTTCTTAATG TTTCACCTAA GTTCCCATAG TTGCTCTCAA 60
 AAAGTTTCTT GGCCCTCGTG GGCCAGTNTG GAGGGGCTGT ATCATCATTC ATNAGGAGCG 120
 TCACTTGGTG GTTTAGGGGG AAATAATCTA TTCTNAAGAT TGAAGAGAGT GCAGGATTTG 180
 GGGGGTTGAC TCTACATCCT TCAGTATCAG GGCTTATCTC CTGTNTTAC CTCCTAGGAG 240
 ACCCTCCTGT TCTTAACGTG GGGCGATGAG AAAGGTGGTG GACTCTTCTT ACTGGCAGGG 300
 CCACCTGCGT CTGTGGAGAC CCTGGGGCCC AGGGTGGCTG AGGTCCTGGA AGGCAAAGGA 360
 GCAGGGAAGA AAAGGCCGTT TTTAGGGCA AGGCCACCAA GATGAGCCGG CGGATGGAGG 420
 GCGCAGGCGG TTCTCCAGGN CTACATCAGC AACGNAGAGT NCTAAGNANT TANGGCTTTA 480
 GGGCACTTAN CTNCTGGTTT CCACAGGAAT CTTTNGTCA ATNAAATTAG TTGCCTCAG 540
 AAA 543

SEQ ID NO:864

SEQUENCE LENGTH:538

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00987

SEQUENCE DESCRIPTION:

GATCATTTCT ATAAAAGAAA TGGTCATTTT ACTTAGATGC CAGTCTACTT TATAAAGACA 60

AATGGATTAT AGACTTAAAA ATAGTCATTT TTCTTATTCA TAAATCTGAC AGGCATAAAC 120
 CCAAAATCAAA GATAATTTGG TGCCCATTTAT GAATTTGAAG TTAAGTGATA GCTCACTTGT 180
 AAAAGTACTA CCTTAATGTG TATAGAGACC CCAGTCTACT ATTATTTGGG AAAATTGTTT 240
 AGGTTATATG GGAAAAGTAG CTCTTTAAAA ATCATATTGC CCAACAGAAA CCTTAGGCTG 300
 AATTTACAGG TATGATAATT TTTGTAATTA ATTTTCTTAG AATTGTGCAG GCTGGGATGG 360
 GGATAATGNC ATACTCTTTT ACACGTGACC AGCAGCATTT ATTNNCTNG GACCTTTTAA 420
 CCNTTTTAGG GGTTAGGGTN CTNGGGGAAC CAACCTTAAT TNGGNCATCC TCCATTNNC 480
 TTNTNTNCCN NNNNCCCNNT TTTTTTTTG GNCCCNNTN GGNCCCTTA AACNACCN 538

SEQ ID NO:865

SEQUENCE LENGTH:533

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00988

SEQUENCE DESCRIPTION:

GATCAAACT ATANGTGGCT ATGGCGGATA TGATTATACT GGGTATAACT ATGGGAACTA 60
 TGGATATGGA CAGGGATATG CAGACTACAG TGGCCAACAG AGCACTTATG GCAAGGCATC 120
 TCGAGGGGGT GGCAATCACC AAAACAATTC CCAGCCTTTC CACATTGGCT TTCCCATGTA 180
 GTCCTTAGTG TGTCTGCTNC TCCTCTCTCT CCTCATCACA GTTCCCAGCC CCCACCTTCA 240
 ACTGAACTCA AAAAAATCTT CAACCTCATA CAGTAGTCAC ATTGTTAGTA ATAACACTGG 300
 GCATTTTAT TTTGATANAN TAGACCGTTT AAATTTTGA GATTCTACCT TATATTTTTT 360
 GAATTATATA CTAAAGCANA TAAGTAGGTG NTGTAATGTC CATTGGGGNC CAAGNTTTTT 420
 AGGTGTAAT GGNAAAAGGG TANCAAAATTT NAANTCAAG TAAACACCCT GTAGGCTTTC 480
 CCCATGNTT GGGGNATNTC CGGATTAAGG NCAGGGTTTT CCNTTTTCTN AAA 533

SEQ ID NO:866

SEQUENCE LENGTH:532

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00989

SEQUENCE DESCRIPTION:

GATCTGAAGT GGTGGATTCC TTGTTTTTGC TAGTATCTCA TTTAGAGTTG AGATGGACCT 60
 TAAAACTCAT CTGTTTTAAC TCACTTTTTA ATAGATGAGT TAACTTAAT TTACTTAAGG 120
 ANNNNCAGTT AGAGCCTGGA ACTTCAACCA TTATTCACCT CCCATGCCCT GTTCCCCCCC 180
 ACTTCGAAAT TAAATGCGGT TAGCATCATA TAGTTCATTT TCCCCCTCCA TGCTGCTGTG 240
 TGATTCTTGA CCTTGGGTAT GAGTTTTTCA TCCTTCATGC AGGGTTCTGT CAGTTCATGG 300
 TATAGTGATT CAGTGTTAAA ATGGTGGTGT CTCAGCTGTG CTGTGCACAT TTCCAACCTT 360
 GTCAAAATAA TAGTCCTGAG CAAGCAAGAA AAAGAGGTAA TAACATACCC ATTTTCTTTT 420
 ATGGANTATA AGCTTAATAA TATTTTTTTC NATGNGCCTA TTTTACCT GNGCAAATN 480
 GTATGGNCTC ACATGGTTAA CCCCAATNAA TTANTCTTGG NCAATTTTAA AA 532

SEQ ID NO:867

SEQUENCE LENGTH:528

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00990

SEQUENCE DESCRIPTION:

5 GATCGCAAAT NCACCTAAAC AATACATTTA CAAAGCCATC TTTACATGCA TTAACGAGG 60
 GCTACAACAA TATTGTTTTA CAAATACTAG CACTTTTTTC CTGTTATGTA CTTAGTGTTA 120
 GAGGGTCAAA ATAATCTTTC TGCTTAGCAT CTCTTAAACC ATACCTGCAA ATATAGCAGG 180
 ATNTTTACAT TTACAGTACT TTAATACTTG TATAANCTAT GCAGAAATTT TTAATAAAGT 240
 10 GTAATATATT TNATAAGCTA ATAAGACTGA ATGGGTAAAG GTTTTTNGCA TGC GTTAGTA 300
 TACTTG CAGA TACTGAAACA TTTTGGTAAT CTTTCTTACT AAAGGATGTG AATGTTTAAT 360
 GTACCTTCTC TGTTCCTACT CTGTAGTCCA ATGGGAATTC AGTAATGNCA TTTGNCATG 420
 TCAACCTGGG GACCATAAAN TTGGTCTGG TCCAGGCCCT CATNTCCTAT ATCCAGTATG 480
 CAATNTTATN TNNTNTNCCT GGTNAATNAA CCCCTCCGGG NTTTTAAA 526

SEQ ID NO:868

SEQUENCE LENGTH:526

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00991

SEQUENCE DESCRIPTION:

20 GATCTTTCCT CAGTATGTGC TGATGTTTGG GTTGCTTGTG GAATCACAGA CACTCCTAGA 60
 GGAGAATGCT GTTCAAGGAA CAGAACGTAC TCTTGGATTA AATATAGCAC CTTNATTAA 120
 25 CCAGTTTCAG GTACCTATAC GTGTATTTTT GGACCTATCC TCATTGCCCT GTATACCTTT 180
 AAGCAAGCCA GTGGAACCTC TAAGACTAGA TTTAATGACT CCGTATTGA ACACCTCTAA 240
 CAGAGANGTA AAGGTATACG TTTGTAAATC TGAAGACTG ACTGCTATTC CATTNGGTA 300
 TCATATGTAC CTTGATGAAG GGGATTAGGT TGGATACTTC ANGTGAGGCC TCCCNCTGGA 360
 AACAAAGCTGC AGTTGTTTTA GNTANTCCCA TCCNGGTTGA NATTGGGNGN GGNCCCTGNN 420
 30 CCTAGCATTN CGCATCACNA AGGCAATGTC NGCNTACAG TTANGGCATT GNGGGGCCGT 480
 TTNCCATGN GNACTGGGTT ATTGGGGNCT NACCAGGTCC AANTTN 526

SEQ ID NO:869

SEQUENCE LENGTH:526

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00992

SEQUENCE DESCRIPTION:

40 GATCCTGTTG CTTCTGCAGG CCATTTTCTG AAAACCCCTG TTAGGAAGGT TGGATTGGC 60
 GTGACTTGCT TGAGCAAGAG TCCTGGGGAG AGATTTTNAG GTTTAATTTA ACGGTATATC 120
 CAGAGCTAAC AGTGA CTCAA CTCGTCTAGT TCTGCAAGTC AGATGTACAC TTAGAGTCTC 180
 TCTGTGAAGG GTTTGGGTCT GAGCTGTATA GTATGTCAAA CTGCCAGTAA GCCAGCCCCT 240
 45 CACCNTCTGA TAGATATTCC TTTAATGCAC CAGACTTCAT GTTTGATAAA TGATTAATGG 300
 TTGAAATTGT TTCTCTTCTT TTGTGTTTTC CCAGTTAATA GATGGTCACT GTTCCACAA 360
 TGT TTTATAC TTTCCAGCTT TTNGTAACTN AACCTATAAT TACTTNAATT TTAATTTTTT 420
 TTAAGCTTN GTTGGTGGNC CTAATGNGAA GGTNTTTTTC CAGTGCATNA ATGGTTTTTT 480
 50 NTGGNGCTTC TGNNAATGN CCNTCCCAAT TGTGGGTTGG GTTTTN 526

SEQ ID NO:870

SEQUENCE LENGTH:520

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00993

SEQUENCE DESCRIPTION:

GATCAGGACG GCTGGATTCA GGTGTCGTAC GAACAGTACC TGTCCATGGT CTCAGTATC 60
 GTATGACCCT GGCCTCTCGT GAAGAGCAGC ACAACATGGA AAGAGCCAAA ATGTCACAGT 120
 TCCTATCTGT GAGGGAATGG AGCACAGGTG CAGTTAGATG CTGTTCTTCC TTAGATTTT 180
 GTCACGTGGG GACCCAGCTG TACATATGTG GATAAGCTGA TTAATGGTTT TGCAACTGTA 240
 ATAGTAGCTG TATCGTTCTA ATGCAGACAT TGGATTGGT GACTGTCTCA TTGTGCCATG 300
 AGGTAAATGT AATGTTTCAG GCATTCTGCT TGCAAAAAA TCTATCATGT GCTTTTCTAG 360
 ATGTCTCTGG CTCTATAGTG CAAATGCTTT TATTAGCCAA TAGGAATNTT AAAATACCAT 420
 GGACCTTACA CAAAAGGCTT TCATGNCCTT ACTTTNTNAA AAGGGGTTAT TGTATTCATT 480
 GGATATGTGC CGTAGCAATN NNGGGNTGTT AGCGGNTAAA 520

SEQ ID NO:871

SEQUENCE LENGTH:517

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00994

SEQUENCE DESCRIPTION:

GATCTCCGTG GCTTTGGGTT AAAAGACACA CTTGTCCACA TAGGTTTAGA GATAAGAGTT 60
 GGCTGGTCAA CTTGAGCATG TTAAGTACAG AGGGGGTATT GGGGTTATTT TCTGGTAGGA 120
 ATAGCATGTC ACTAAGCAG GCCTTTTGAT ATTAATTTT TNAAGGCA AAATTATAGA 180
 AGTTTAGATT TTAATCAAAT TTGTAGGGTT TCTAGGTAAT TTTTACAGAN TTGCTTGTTT 240
 GCTTCAACTG TCTCTACCT CTGCTCTTGG AGGAGATGGG NACAGGCTG GAGTCAAAAC 300
 ACTTGANNTT TTGTATCTTG ATGTCTTTGT TAAGACTGCT GAAGATTTAT TTTTTCNN 360
 TTATAATANG GGGNTAANCC CCACCTTAT TCCTTCAATT CACCTACCA TTTTCNNGG 420
 TTCTTNGTGT TGGGCTTGTG GCAGGNCAG CTNTGGGTT TTCCTTTTNN CCATGCCAAN 480
 NTTNTNAATT NCCCATGTAC CAGTTTGTN CAAAGGN 517

SEQ ID NO:872

SEQUENCE LENGTH:517

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00995

SEQUENCE DESCRIPTION:

GATCAGAAAT ACAGATTTTG ATAGCAAAGC GACGTTAGNT NGANGCTCTT GTGAGGAAAG 60
 TCATTGGCTT TATCCTCTTT AGAGTTAGAC TGTGGGGTG GGTATAAAG ATGGGGTCTG 120
 TAAATCTTT CTTTCTTAGA AATTTATTTT CTAGTTCTGT AGAAATGGTT GTATTAGATG 180
 TTCTCTATCA TTTAATAATA TACTTGTGGA CTAAGGATA TAAGTCTGT ATAAANNCNN 240
 CCAATTATGT TAACTAGCA TATCTGCCTT TATTGTGTTT GTCATTAGCC TGAGTAGAAA 300
 GGCTTTTAAA ATTTTTTTAG AAAGCATTTG AATGCATTTT GTTGGTATT GTATTTATTC 360
 AATAAAGTAT TTAATTAGTG CTAAGTGTGA ACTGGACCCT GTTGCTAAGC CCCAGCAAGC 420
 AATCCTAGGT AGGGTTTAAT CCCAGTAAA ATTGCCATAT TGCACATGGT CTTAATGGAN 480

GTTTGAATCT TAAATAAATT GGATATTCAC TTTTAAA

517

SEQ ID NO:873

SEQUENCE LENGTH:515

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00996

SEQUENCE DESCRIPTION:

GATCTGCGAA AGACCAACTT TTAGGCAGTG ATACTTTTCT CCCATTCCCT GGGGTGGGGG 60
 GAGTATGCAG TTGGTGCTTT CTGTAATTCC CTGTNCTGT TTTGTTTCTG TAAGCTTTTC 120
 CCCTGGTGTC ATGGAAAGGA CTTCTTAAAT AACCACATTG TGGGTGGCTG TATCCAAAGT 180
 TTAAATAATT GGCCAGAAGT GCAGAGTATC CTTTCCTGGA TTCGTGTCAG AAAAGGGCTC 240
 CTTGCCACAA CTGAACCTTAC TGTATAAAAA CCTGGCTAGG GAGATTTAAT TTTACTAAAA 300
 TTACAGTTTA ATGTTACCGT CTAGCCACAA ATCAAGCAGC AAAAGCTATT TTGATGATGA 360
 AAGGGGGTCC CGTTGAGCTG GCCATCTAGT GCAGTGTGCT CTCAGATNCC ATGTTTGTG 420
 ATTGTGTGCT TCACAAGNCC NTCTCTGGTG CTTGAATTGG ATTGAATTC TTGGTNAGAA 480
 GNCTCAGCAT CTCCTTGGGG TNGGCTTGGG CCAA 515

SEQ ID NO:874

SEQUENCE LENGTH:514

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00997

SEQUENCE DESCRIPTION:

GATCAGNNA TNAAGTGCAG CAATATCATG AATTCTCAGA AGCCCTTTCA GGGAGCCAGT 60
 NAGTCATACA GTATCCACAG TTGAGTCACT TAAAGATGTC AGTATACGAA ACATTATTCA 120
 CAATCCTTGG GCAATCTCAT TTTTTTTTCC TTCTCCCTC CTCCCCTGCC CCCCATACAT 180
 TTNTATCCTT GAGTTAGTTT TGGNGGGGCA GGAAGTACTT AACATCTCAG AAGCTAGATT 240
 GGGAAACATG CTCAGCTATA AGAACTGAGC TTAAATTTT GAGTTTAAAA ATGTACATCA 300
 GGAGCAGNTG GGGAGGGTCT TTTTTTNA AAAAACTTT CCAATTTTGG GTTTTCTNTG 360
 CCATATGGCC GTTTTGTA A TTTTNGGG GTTTTNTATT NTTTTNGAAA GTGNTGAAA 420
 TCTTGTTNG GGNTTTTTTT CCCCAGAAACA TTTNNAATAT AACCCNGTTT ATTTTTNNAT 480
 GNAAATTA A CCTTNTTGG GTAAAAAGGT TAAA 514

SEQ ID NO:875

SEQUENCE LENGTH:513

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00998

SEQUENCE DESCRIPTION:

GATCTTCTAT TAAANTGATT CCTCTTTATT AGAGAAGGAA AATTTAGTTG CTATACATCT 60
 TATATTNCA CAGTTTATTA AAGTCAGTNC CCTAAAGGTA CCTNCTTNC TTTGTGGCAT 120
 ATATGGCATC TNCCTGCTTC AGATTNCTT ACACTTTTGT GATTTATAAT GTTAGTGATT 180
 GGTGCCCTTAT TCTCTGAGGA AAGATGGAGG GTTCATAAAG CAATGCCTTA TCCACAGCAG 240
 ATTTNCTTGT ATATTAAGTT AACAGAATT CTGTAAATTA TTATGAAGGG TTCAAGCTCT 300

TTAGGGGGAG TTTTTTTTTC TTGTTGGTTA ACAAATTGGT TGCAATCTNT TATATTTTCGC 360
 AATTGGNTTA GATATTACAG TCTACTTATT TTTNCANGNG TAAATTAATT GTNTAAGGTT 420
 TGGGTTNGGT ATAAATGGNT AAAATATTAA TATNGTGGGG GGTAATAATT GATTNGGNGT 480
 TTTTTTTTTT NAAGGCCNNN GGNTTTANGG AAN 513

SEQ ID NO:876

SEQUENCE LENGTH:510

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00999

SEQUENCE DESCRIPTION:

GATCAGTATG AGANGCAATA CCTAATCCTA TGTGCTATT GTATTTTNC CTAGTTGGTG 60
 TGCCTGCTCA GAAAAACATA TACTGTATGT GTATACATAC CTGTGTATAT ATAAAAGGTC 120
 AATTATATA TTNCTATA GGAAATGGA GTAACAAGTT CCCTATCTCC CATATTTATT 180
 TGTCCATAGT AAAATGGCCA CATTGATGAT AATTTCTAGA ACTAGTTTCT GAGATTGTCA 240
 GCCCTTTGTC TAAAAAATG GCAGTATTAA TGATTGACTT CTGTCACTGC CATAGTTACC 300
 TGGATTGTCA GCCTNGGTAG CCTTTGTCTA AAGTCCTAAA GAGTTCCAAA AAAAATGTGT 360
 TGAATAAATT GCTAAATAGT GGTGGGTGAT TCTTNCAGTA GGNATTTGTA ATAATTTCNT 420
 GGCAANAAG GTTATTNCCT GCTATTGGTA TTGGATNATT NGNCTTNTAT NCNGGTATTT 480
 TNAAAAAGGC AGGNNTATAN GGNTNNCCN 510

SEQ ID NO:877

SEQUENCE LENGTH:504

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01000

SEQUENCE DESCRIPTION:

GATCTTCCAT CCTCAAATGA CTCTTTTTC TTTATATGTT AACATATATA AAATGGCAAC 60
 TGATAGTCAA TTTTGATTTT TATTCAGGAA CTATCTGAAA TCTGCTCAGA GCCTATGTGC 120
 ATAGATGAAA CTTTTTTTAA AAAAAAGTTA TTTAACAGTA ATCTATTTAC TAATTATAGT 180
 ACCTATCTTT AAAGTATAGT ACATTTTACA TATGTAAATG GTATGTTTCA ATAATTAAAG 240
 ACCTCTGAAA CANTCTACAT ATACTTATTA CCCAGTACAG TTTTTTCCC CTGAAAAGC 300
 TGTGTATAAN ATTTATGGTG GATAACCTTT TATGGTTTCC CTTTCCAAAG GCCCAGGGTG 360
 GGAGGGGGGA TTAAGGGGGC CTAAGGTNTA TGCCTCCNNG GTTTAAANT TAAATNCCT 420
 CNNGGTATTT AAATTANNTT TTNCNANGG TTTNTNGGGG GANTGGGGGG GTTTANANTT 480
 GCCTTNTTN GGGGTTTGGG GAAA 504

SEQ ID NO:878

SEQUENCE LENGTH:500

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01001

SEQUENCE DESCRIPTION:

GATCTGGGCT CTGAGCACAA GTCAGGAAAC ACCAACATAT TCACACTCTC CCAGTAGGTT 60
 CCTCAGTCCG ATGGTGAATG GCTATTCGTA AATGGCTGGT CTGGCTCTTT GGTGTTGGAG 120

CCTTTCCAAT AGCCCCATGA AAAGAAGCAT CACCCAAGGA TATTGTAAAA AGGATGTAAC 180
 AAGGAGATAG GGTAGACATT GTACTCAGTG GGCCTTGGGG CCTAGCCCAG CTCTGAGCAG 240
 AGGACTGTGG CATTCACTGT CTTGAGTGT TTCACCTTCT TGGATAACAC ACGGGCCTTC 300
 TCTTCTGGAT TTCATCAGAG ATTACAGCCA GATGGGGGCT GAAGACCATC CTCTTTGACC 360
 ACAGAGGGTG TGA CTGTGGG GAATTCCTCC CAATTTATGG TTTCCNAGGA AAATCTTAGT 420
 TCCTTTTATT TATAGGAATG CATGNCNTTT TGGTGTTAAG GAAACCCAAG GGGNANTTAA 480
 NGGGACCANT CCTANTNAAA 500

SEQ ID NO:879
 SEQUENCE LENGTH:500
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS01002

SEQUENCE DESCRIPTION:

GATCTCCAGC CTCCCAGAAG CCTGCTGTGC TTTCGTCCCA CAGCTTTCTG CCCATTGTTT 60
 CTTACTAGTT TCTTGAATTG TNCTTGTGGA CTTNCCCTCA GGGATACATT GGCCTGCAGG 120
 TCCCAGTTCA CATGTAGTCC CCTGCTCACC ATTGGAGAAT CAGCTCACTG CTCTCTAGAA 180
 ACGTGGCGTT GGTGAACGGA CCATGCTTCC GTAGCTCTGA CCTGGGCAGC TTGGACCTGG 240
 TCATCCTCTA CTGCCATACC TTTCCTTGGG GGCTTGAACA CAGAACAGGG AGATGGACAA 300
 CCACTTCAAA GAAAGACCCA CCGAATGCAG TTTCTGCTTG ANTGACTGGG NCTGCAGTTC 360
 CNTTNTCCTG GGA CTTAGAG GTGGNCAGAT NTANGGCCCC TTTACTCATC CANCTTNGTN 420
 TTCAACTGGN ACTNCCNAAT NANTNAAAGA GCCTNAAATT TAAACTNGN TGTGGATNGG 480
 GNATATGGGA NTAGGGTTGN 500

SEQ ID NO:880
 SEQUENCE LENGTH:500
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS01003

SEQUENCE DESCRIPTION:

GATCGTCAGC AAGTACTGTA NCTGTAAAGG AAAATCTCTC TCTCTGGAGA ACCCACACAA 60
 ACCATTGACC TGAGTGC GCA TGACAGCCAC TGGNNATNTT TTCTATGATT GAAAATCTGC 120
 CATCGCTGAC TGTTGGCCAG TTTCAAAGGG ACCCATTGTA TACAGGGTGC AAATGTATTA 180
 TACGGATGTT TCCTTTTGTG CACTTCATTT TTACAAGTTT TGCTACTCAC AAGCTTTATG 240
 TAGTGGAGGA TAGAGGTATT TTTGGTCTTT AGAAGCTTGT CGGGGTGAGG GCTGCTAACT 300
 TACACTTCAG AGGCCTGTGT CCCAAAGGCC TGGCTGCGTT TGCCGTGCTG TCGGAGGACC 360
 TGTGTACACA GGCAGGTGTT CGCCTGCCCC AGCGCGAGTA GCTCTTTGTG TAGTNGGTGA 420
 AAATGCTTGC AGGCATCTGT TTAATTAAAA ATTNCCTGCT GTTAAAGNCA GGGGTAAAAA 480
 ATNTCCACAA TTTANGGAAA 500

SEQ ID NO:881
 SEQUENCE LENGTH:498
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS01004

SEQUENCE DESCRIPTION:

5 GATCAGGATT CAGANGTGA CATCTTCCCC GCAGACTNCC CTACTGAGCC ACCTAGCACT 60
 GCCACGAACC GGTGGGGCTA GGAAGAAGT AAAATATTTT GCAGAGTCTG ATGAAGAAGA 120
 AGATGATGTT GATTTTGCAA TGNNTAATT AAGTGCCCAA AGAGCACAAA CATTITTCOA 180
 CAAATATCTT GTGTTGTCCT TTTGTCTTCT CTGTCTCAGA CTTTGTACA TCTGGCTTAT 240
 TTTAATGTGA TGATGTAATT GACGGITTTT TATTATTGTG GTAGGGCCTT TTAACATTTT 300
 GTTCTTACAC ATACAGTTTT ATGCTCTTTT TTTACTCATT GAAAATGTCA CGTACTGTCT 360
 10 GATTTGGCTT NGTAGGAATT GTTTATAGGN CTGCCCCGTC ATTAGGCACA GGATTTTAA 420
 ATGTCCATG GGTNCCANC CTACCAGACC CTGCTTTTTT NGNNAATNGG AATTTTNAAC 480
 CATTNANAAA TNGGAAA 498

SEQ ID NO:882

15 SEQUENCE LENGTH:494
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01005

SEQUENCE DESCRIPTION:

20 GATCTTACTC CACGNATACT TTTTGGTNTG TGAAGGCATC GGTAAAGGGC ACAAAGACAG 60
 CCATGGGGAC ATTTATGTAA ATACGTCTCT AATTGCCACA CTGCAGCTGA ACAGTGTGTA 120
 GTATTTTCCC AGTCAGCTTT GCCATACTGA CGTCAATCAT TTGAGAGAAA TTATTCAGAT 180
 TTNATTTTGG TATCTGTGGT AACAAAACAT TAACAAAAG ATTTNTGTG CAGAAGCCTC 240
 25 CCCGNCCCC CAAGCTATTT GCTCACATTA ACANATTAAA GTGCCTGAAG CATAATTCAT 300
 TCTTTACCTG TATACTAAAA ACCCTGTTGT ATTGGITTTT TTTNTAATAA GCCTTTTAC 360
 CTCTGTGTAA ANANATATAT ATACCAGGTG TATGATGGTN CATTITGGGT CTTNANCTTT 420
 TTTTAAATGG TTTCTAATNT GTNTGNCCNA ATGTTGGCNT TGNTTTANA NTTGTNCCGG 480
 30 GGTNNATTTT TANN 494

SEQ ID NO:883

35 SEQUENCE LENGTH:493
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01006

SEQUENCE DESCRIPTION:

40 GATCTTGATG CTGTGGAAGT AGTTTGAGGA ACATCCTATG AGTTTNCCTA GAATGTATAA 60
 AGGTTGTAGC CCATCCAAC TCAAAGAAAA AAATGACCAC ATACTTTGCA ATCAGGCTGA 120
 AATGTGGCAT GCTTTTCTAA TTCCAACCTT ATAACTAGC AAAAAAGTGT TTGCTTATTC 180
 CACCACTTCT ACTGTGACAT ACTCGAGTAT AAAGACATGT AGCAATAACG GGGAGTGGGG 240
 GGGGAGTCTC ACAGTGCCTT TGAAGGGGCC CGAACTTGCC TTAATCTTC CTCAACCAA 300
 TAAGTATTTT ATTAGTGCTT GAGAGAATCT GGAATGTAGG NTGGGTTCAA CTGCACAAAN 360
 45 GGAAAANGNT TTTTACCACT NTTTTATAT AGNTATAAAG TGNAGCAACC GCCTTAGTGC 420
 CTGAATATGT AGTCCATGAN TATGCCTTGT NTAATTTCCA GAAATCCAN ACCTTGACT 480
 GTTTTTTTT CCN 493

SEQ ID NO:884

50 SEQUENCE LENGTH:492

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01007

SEQUENCE DESCRIPTION:

5 GATCAGCACT GCCAGTGGAG ATGGGCGTCA CTA CTGCTAC CCTCATTTC CCTGCGCTGT 60
GGACACTGAG AACATCCGCC GTGTGTTCAA CGACTGCCGT GACATCATT AGCGCATGCA 120
CCNNNGTCAG TACGAGCTGN NCTAAGAAGG GAACCCCAA ATTTANTTAA AGCCTTAAGC 180
10 ACAATTAATT AAAAGTGAAA CGTAATTGTA CAAGCAGTTA ATCACCACCATAGGGCATG 240
ATTAACAANG CAACCTTTCC CTTCCTCCGA GTGATTTTGC GAAACCCNCT TTTTCCCTTC 300
AGCTTGCTTA GGATGTTCCA ATTTTAGGAA AGCTTAAGGC GGCCTACAGA AAAGGGANAA 360
ANGGGCCACA AAAGTTTCTT TTTAACTTTT NAGTAAAAAT TAANTTAAAN CAGCAGCAGC 420
AACCANTTTA AATTGGATT AANGGGTCCN AATTGGAATT NAATTTTTTG GNTTNNNNGC 480
15 GGNTTTNAAA AN 492

SEQ ID NO:885

SEQUENCE LENGTH:490

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01009

SEQUENCE DESCRIPTION:

25 GATCGAGTTT NATGCATCAC AGTTAACATG TCAGCTGGCC CTCCAGGCC CCGCCCCCAT 60
CCCGTCCACG TTGCTGTGTC GTGAGGTGCA GCGGGTCACC CTGTGGCCCG TCCTGTGACC 120
CATATTTAGC CGTGTGTTGG ACTCCGTGTC TTCAATGGTT TGTTAGTTGC CATTACAAC 180
TTGTCTGGGT AGAGTTTTTG AGTTTTNCA GTTCAGTATC CCTCTGTCTA TTCACACTTC 240
GTGTTAGTGG TAACTCAGTT TGTCTTTAAA TAGTTACAGA AGGGATACGT CATTGTGNA 300
30 TGCTTTTGTG AAGTGAGTTA AACGAGCTTT CTGTATTTTA ATGCTTTAGT GTTTCAGTTT 360
TATAAGTGAA GATTTTATTT TAAAAACCAG TGGGAAAGAG TGGGGGGTTT CTTTTATGT 420
CTGGGTCAAT CAGGCAGTAC ATCTGNTTTA AAGCTGAATG TAGGACANTT AATGAAATCC 480
ANATCTGAAA 490

SEQ ID NO:886

SEQUENCE LENGTH:487

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01010

SEQUENCE DESCRIPTION:

45 GATCAGCTAT ATACTATTTA TATACAAGTN ATAATACAGA TTTGTAACAT TAGTTTTAAA 60
AAGGGAAAGT TTTGTCTGT ATATTNNNTT ACCTTTTACA GAATAAAAGA NTTACATATG 120
AAAAACCTC TAANCCATGG CACTTGATGT GATGTGGCAG GAGGGCAGTG GTGGAGCTGG 180
ACCTGCCTGC TGCAGTCACG TGTAACAGG ATTATTATTA GTGTTTTATG CATGTAATGG 240
ACTATGCACA CTTTTAATTT TGTGAGATTC ACACATGCCA CTATGAGCTT TCAGACTCCA 300
GCTGTGAAGA GACTCTGTTT GCTTGTGTTT GTTTGTTTGC AGTCTCTCTC TGCCATGGCC 360
TTGGCAGGCT GCTGGAAGGC AGCTTGTGGN NGGCCGTTGG NTCCGNCCAC TCANTNCTTC 420
50 TGGNGCACTG GTTNTNCTT TANAGTTANG GTNCCATGNN NCAAGGGGGG TTCCNANGNG 480
GAGGN CN 487

SEQ ID NO:887

SEQUENCE LENGTH:485

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01011

SEQUENCE DESCRIPTION:

GATCGCAAAT AACTAAATG TGGAGTGTAG GAACCAAAAT GAAACCTGCT GTATGGAAAC 60
 TACTTTCACT TATGGTTCAT TGGTTTTTGT ACCAATATTT TTTATGCACT TCAGTGCAAG 120
 TTTTGTCACT TAACCTTACT TTATGAGTAA GCTAAATAAC CCAAATTACA TTTNTTTAAA 180
 CCTGTTTTAC TACTATGGCA CTTTGATAAA ATGGTCAGGA ACCAACTTTA CTGGCAAAAG 240
 GGTCCATGTA CCACCATGTG CTGGAGCATC TGTCTACAT GTGGATATCT ATGANTGGTA 300
 ATGTTTTTCT TCATGTAAGT GCCTATTGAG AGTTTCAGAA TTTTAAATG CCAAATATTT 360
 TCATGGGTCA TTTGCATGTA GTAAGCCAGA AAATATTCAA NGGGATTTTG GAAAACCAAT 420
 TGGTATTTAA CCAGCCTCAA ATTGTGCAAC CATGGTTGTA TAATAANGGA TTTGGAACCC 480
 GGAAT 485

SEQ ID NO:888

SEQUENCE LENGTH:485

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01012

SEQUENCE DESCRIPTION:

GATCTAATGN CATATTCCAA AAGCTCAACA GCAACACCCA GGTAGTTTTG CTGTCAGCCA 60
 CAATGCCTTC TGATGTGCTT GAGGTGACCA AGAAGTTCAT GAGGGACCCC ATTCGGATTG 120
 TTGTCAAGAA GGAAGAGTTG ACCCTGGAGG GTATCCGCCA GTTCTACATC AACGTGGAAC 180
 GAGAGGAGTG GAAGCTGGAC AACTATGTN ACTTGATGA AACCCTGACC ATCAGCCAGG 240
 CAGTCATCTT CATCAACACC CGGAGGNAGG TGGACTGGCT CACCGAGAAG ATGCATGCTC 300
 GAGATTTCAC TGTATCCGCC ATGCATGGAG ATATGGACCA AANGGAACGA GACGTGATTN 360
 TTTGGNANTT TCGTTCTNGC TCTAGCAGAG TTTTGATTTC CANTGACCTT TTGGNCAGAG 420
 GAATTNTTGT TTNGAAGGT TTTTTTTTAG TCATCANNCT NTTGTCCTTT CAACTATCAG 480
 GGGTN 485

SEQ ID NO:889

SEQUENCE LENGTH:492

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01013

SEQUENCE DESCRIPTION:

GATCGCAACG CCAAAGGTGA AGAACCANCT CAAGGAGACC ACTGAGGCAG CCTGCAGATA 60
 CGGAGCCTTT GGCCTGCCCA TNACCGTGGC CCATGTGGAT GGCCAAACCC ACATGTAATT 120
 TGGNTCTAAC CGGATGGAGC TGCTGGCGCA CCTNCTGGNA GANAAGTGA TGGNCCCTAT 180
 ACCTCCAGCC GTGAATGCNA GATTTTAAGA TTGCCCGGAG GAAGCAAACCT TTTCGTATAA 240
 AAAAAGCAGG CCATCTGCTT AACNNTTGGN TCCACCATAA GGCCTGGGA CTNGGATTTT 300
 TNTATCTGAT AGAGGTATTT NTTGTGGCCC TGGGAGCTGT CTGNTTTTCC CCTACCCCA 360

AGGNTGCCAG GAAGACGTCC ACCATTAGCC ATGTGGNAAC CTTTACTTCT ATGCTTACAA 420
 GTGCCTTTNA GNGAGCCCCA ATTCTGGTTT TNCCACAAAA TAAACCTAAT GCNNTCAGGG 480
 AAAACNNTTA AA 492

5

SEQ ID NO:890
 SEQUENCE LENGTH:478
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01015

10

SEQUENCE DESCRIPTION:

GATCTTGCTT CCAGGCAGCA GCTTGAATTC CCGAATCTNC CTGCAAGCNG CATACAAATG 60
 CAGCGTGAGA ATCCATACAC GTAATCCATA TTCACCTTCC CATCCATCCC GCAGAAGAGG 120
 CATGGTGACA CCCAGGCTAC TGTCCATGCT TGAGAGGACG TATTTGAAGG TTCTGTTACT 180
 ACAAGTTGGG AATATTCACG GGCCATGCCT GAATACCCGG NCTGTANCTC ACACNGTGGT 240
 CTGTGTAAGG GGNTACCCTN GGGGCGGCCT GGTTTAATCN TGATTAATAT CTGAAAGCNT 300
 GGGTTNNNTG GGGAAATGTNA GGGTTTTCCT AATGCCATTA AATTTTTTTT TAGGCNGTAA 360
 AAATTAATAAT NCATTTTNTT ATCCAGCAGG CCTCTTTTAT ACCTTTATNG GGGAAATCTNC 420
 CATACTTACT TTCCGGCCAN NTTTTCAATA ATNAAATTTA TTTTGGAAN TTTTAA 478

20

SEQ ID NO:891
 SEQUENCE LENGTH:474
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01016

25

SEQUENCE DESCRIPTION:

GATCTTACAC TCTGCTTTTG TCCAAATAAA ATGCAATAGT ATCAATATCA ATTCAGAAA 60
 AATGGACTGA ATATGCTTTT TTGGTGATGA AATCTCATGT ACGATATTTA TAGTGATGTG 120
 CTTTTATTN CTCATGAGAT ACTAAATATT AATTGTGTTG TACATTGTN CTTAGCATAT 180
 ATTAAAGTTT TGAACCAAAT GTGTTAAAGC TTACGCTTTG CCATGTAAAT TTCCAGAA 240
 TTGTGTAGCT CAAATGTATC CTACATCCAG CTGTAGAAAT TTGTCAGAAA TTGTTTAAAT 300
 TTTGTATATA ATTGTACTGT TTAATTCTAG CCATTGCGCT GAACAGTATT TGAGTTACCA 360
 TATAATATGG CTTTACACAA NGGNAATGTG TGGCTTTTGT TTTGGTATT TTTCCAGTAT 420
 AGGAAGTTCC CTGTGGCCTT ATTTAAATA AAGGTTATTA GGTAAACTG GAAA 474

35

SEQ ID NO:892
 SEQUENCE LENGTH:473
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01017

40

SEQUENCE DESCRIPTION:

GATCACAGCT CACTGCAGGT TCAGCCTTCT GAGTTCAAGC AATCCTTCTG TCTCAGTCTC 60
 CTCAGTAGCT GGGGCTTTAG GTGGGCACTG CCACACCGTA CTAATTTTNG TATTTTTTGT 120
 AGAGACGAGG TCCCACCATG TTGCCAGGC TGGTGTCAA CTCCTGGGCT CAGTCAGTCC 180
 CCCCATCTCA CCCTCCCCAA GTGCTGGAAT TACAGGCGTG ANTTACTGTG CCCAGCCTTA 240
 CGGACATCCT TTTGAATTAT CTTTTTCACT CATAGAATAT GAATACATT ATTTAGACTT 300

50

55

TTTCTAGAAC TTTCTGTTT TCATGCTTT GNTTCACCTG GAATTGGGT TAACACCCTT 360
TTATAAAGTT TGTGGTTGN AAAATTTCCA TTGGGGCCAT CAATACGGAA ATATATTTGG 420
TAANATNNGG GGGTTCNATT TTTAATTAA AATGGCAAAT GANNGGCAGG AAA 473

SEQ ID NO:893

SEQUENCE LENGTH:473

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01018

SEQUENCE DESCRIPTION:

GATCGGGTTG AGGATTGGGG CTAGCTCGAT NACANTAAGG CCCCCAATC GNGGGACCTG 60
CTGTGGCGCG GATTCTTAGG AACGCTGTTT TAGCCGGCCC CCTCTCCAGG GGTGCGCGTG 120
GCCGGCATT TTTCTAGTT CTTCTGTAA CCCTGAGGTG CCAGCGCGGG GAGTGAGGAG 180
GGGTCAAGGG GCTAAGGATG CAACCTCTGA CGTTCTGCGC CTTCTAGGA GAGTCTTACA 240
TGTNTTGAGA TTTCACAAGC AATGCGAGTT GTAAAATACC AGCTCTACAN GAAGCTAGGC 300
TCTGTGACGG CATAGTTTTC AGTAGCTNTA TCACAATATT CACAATGGAG AATTATATGA 360
CATGGTAAGC AGAAATAGGC CCTTTTAAAT GNGNTGCTTC TATTTTACCT CANATTGGTG 420
GNTNTAGGNT AATCANTAAA AATCNATCCA NNGCNTTCA CAACACTNNN AAA 473

SEQ ID NO:894

SEQUENCE LENGTH:468

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01019

SEQUENCE DESCRIPTION:

GATCAGGGGG CCAGGCCAGC AGCTCGGGGG CCACAAGGAG ATGGATAATG TGCCTGTTTT 60
TTAACACAAC AAAAAAGCCT ACCTCCAAAA TCCCCTTTTT GTTCTTCCTG GACCTGGGCA 120
TTCAGCCTCC TGCTCTTAAC TGAATTGGGA GCCTCTGCCA CCTGCCCCGT GTATCCTGGC 180
TCTCAGCTCA TGGGGAAGCC ACATAGACAT CCCTTTCTTC CTTGTCACGC TCGCTAGCAG 240
CTGGTAAGGT CTTACACCCC TGATTCTCA AGTTTTCTGC TTAGTGGCAC TGACATTAAG 300
TAGTGGGGGG ACAGTCCATG CCAGGACACC CTGGAGTAGC CTTCCCCCTT GGCCGTGGGG 360
CAGGNCCTAA CTCAGTGTG CTTTGGAGTT GAGGGTGTCT TTTCTTNTTC TTTCTTTAGT 420
TCCTGTATTG TAAACATTAG TAAAAATAAA TGTTTTTTAC ACAGGAAA 468

SEQ ID NO:895

SEQUENCE LENGTH:462

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01020

SEQUENCE DESCRIPTION:

GATCCTGCAG GACTACAAAT CCCTCCAGGA TATCATTGCC ATCCTGGGTA TGGATGAACT 60
TTCTGAGGAA GACAAGTTGA CCGTGTCCCG TGCACGGAAA ATACAGCGTT TCTTGCTCA 120
GCCATTCCAG GTTGCTGAGG TCTTCACAGG TCATATGGGG AAGCTGGTAC CCCTGAAGGA 180
GACCATCAAA GGATTCCAGC AGATTTTGGC AGGTGAATAT GACCATCTCC CAGAACAGGC 240
CTTCTATATG GTGGGACCCA TTGAAGAAGC TGTGGCAAAA GCTGATAAGC TGGCTGAAGA 300

GCATTTCATCG TGAGGGGTCT TTGTCTCTG TACTGTCTCT CTCCTTGCCC CTAACCCAAA 360
 AAGCTTCATT TTTCTGTGA GGCTGCACAA GAGCCTTGAT TTGAAGATAT ATTCTTTCTG 420
 ACCAGTATTT AAGGGTTTCC AATAAAATGT ACACCNTCA AA 462

SEQ ID NO:896

SEQUENCE LENGTH:462

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01021

SEQUENCE DESCRIPTION:

GATCTAAATC CTCATTTATC TCTNCTATGT CTAGTATTTT ACTGTCACTG GAGGCTCTGT 60
 GGGCTGTCAT AGTTAATTGA CCATAATTAG CAATATACTT TTAAAGTGGG AAAGCTGAAT 120
 GACACTNTTT AAGACAATGA ACATTATCAA AACAAAATGT ATAATTNCTT AATTTGAATA 180
 ATAAATTAGG CGTTTAAATG CTATTTGTAG TCTTGATATA CAGAAATAAA ATAATTAGGG 240
 TTGGTCTTTT TTATTTTAGG TTGTTTTATG TTGAATGTTT TATATCTTAT TAGTTAATTN 300
 GTATATTINA TTAGTATTN GGGAAATAGC ATATCTGAGA CTGAAGGGGA AATTGGCCAA 360
 TTCACTTATT TGTGGTTTTT TTCCTCAGCT ATTCTGAGCT TATTTATTAA TTGNATGGCC 420
 TAATGGCTAA CCATTACAT TAAATGGTT TTTTCCCCA AA 462

SEQ ID NO:897

SEQUENCE LENGTH:459

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01023

SEQUENCE DESCRIPTION:

GATCTNCTCT TTCCTCTCCT TTCCTCATT TATTCCTAAA GGAATCTGAC CATTAAAAAG 60
 NCTCTACGGC CCAAAAAAG ACAAAAATAA AAATTCCTTT TTATTCCTGT CAACTGGATG 120
 GAAACACAAA TTTCATGGAG CTGTGTACCA TCGAAGAAAC CTGGTGTCTG GCATGAAATT 180
 ACTGTAAAGA ACTTCCTGTA AAACACGTTT TTTAACAAC TGAAATGAAA AGCATTGGAG 240
 CGTCTGANTG AAAGACGTA CCTCCTGCTG GGAATCTGAT GGTCTTCAGC ATTCACCTTC 300
 GTGTGTCTTC AGTGTCTCAT TGTATCCCT NGCTTCTGGN TTGGNCCTTA GGAGTNGTTT 360
 GGGATATAAC CTNAAATTGT NGGATGGTA AANGGAAAT TTNATGNNG TTTTTTTGGT 420
 TTTTAAAAAT NATTTTNAAT NCGGGGTCAN TTTTAAAA 459

SEQ ID NO:898

SEQUENCE LENGTH:457

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01024

SEQUENCE DESCRIPTION:

GATCCACCTG AGCGACCTCC GGGAGTACAG GCGCTTTGAG AAGGAGAAGC TCAAGTCCCA 60
 GTGGAACAAT GATAATCCCC TTTTCAAGAG CGCCACCACG ACGGTCATGA ACCCCAAGTT 120
 TGCTGAGAGT TAGGAGCACT TGGTGAAGAC AAGGCCGTCA GGACCCACCA TGTCTGCCCC 180
 ATCAGCGGGC CGAGACATGG CTTGCCACAG CTCTTGAGGA TGTACCAAT TAACCAGAAA 240
 TCCAGTTATT TTCCACCCTC AAAATGACAG CCATGGCCGG CCGGGTGCTT CTGGGGGCTC 300

GTCGGGGGGA CAGCTNCACT CTGACTGGCA CAGTCTTTGC ATGGGAGACT TGAGGAGGGG 360
 AGGGGNTTNA GGTGGGTGAG GTTAAGGTGC GTGTTTCCTG GTGCAAGTCA AGACCATCAG 420
 TCTTATTAAA AGGTGGGTGC CAATTTTTTT TACNAAA 457

SEQ ID NO:899

SEQUENCE LENGTH:457

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01025

SEQUENCE DESCRIPTION:

GATCCAGTAT CTCCTCGGC TTTTAGGGA GCAGGAAAAA TGCGTCTNAN AGCAACTTTT 60
 TTAAAAACC TGCCCTGTTG TATATAACTG TGTCTGTTT ACCGNGTGNC CTCCCAAGGG 120
 GTGGGGAAC TATATAAAC GTTAAAGGG GCCACGATT GCCCGAGGGT TACTCCTTTG 180
 CTCTCACCTT GTATGGATGA GGAGATGAAG CCATTCTTA TCCTGTAGAT GTGAAGCACT 240
 TTCAGTTTTC AGCGATGTTG GAATGTAGCA TCAGAAAGCTC GTTCCTTCAC ACTCAGTGGC 300
 GTCTGTGCTT GTCCACATGC GGTGGGCGTC TTGGGACCTT GAATGCCTGC CCTGGTTGTG 360
 TGGACTCCTT TAATGCCAAT NATTTCTTCA NTTTCTCTTG GGACACCNAG GGNTGCCNGT 420
 TNGACAAAGT TTTGGNGAAC NTCCTAATTT AAAATGN 457

SEQ ID NO:900

SEQUENCE LENGTH:454

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01026

SEQUENCE DESCRIPTION:

GATCCGANGA CCACATCAAT GGGCGCGTGC TCTACTATGC CACCTGCAAG TAATGCTACA 60
 GCTTCCAGCC CGTTGCCCA CTCATCTGCC GCCTTTGCTT TTGGTTGGGG GCAGATTGGG 120
 TTGGAATGCT TTCCATCTCC AGGAGACTTT CATGTAGCCT AAAGTACAGC CTGGACCACC 180
 CCTGGTGTGT AGGTAGTAAG ATTACCCTGA GCTGCAGCTG AGCCTGAGCC AATGGGACAG 240
 TTACACTTGA CAGACAAAGA TGGTGGAGAT TGGCATGCCA TTGAAACTAA GAGCTCTCAA 300
 GTCAAGGAAG CTGGGCTGGG CAGTATCCCC CGCCTTTAGT TCTCCACTGG GGAGGAATCC 360
 TGGACCAAGC AAAAAAATT AACAAAAGTG ATGTAAANT GAAAAGCCAN ATAAAAATCT 420
 TTGGAAAAGA GCCTTGGAGG TTCAACGGGG GAAA 454

SEQ ID NO:901

SEQUENCE LENGTH:453

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01027

SEQUENCE DESCRIPTION:

GATCTTNCCT NTAAAGTGA TAAGACAGTC CCACAGTCCA GCCTAACTAT GGGACAGCTT 60
 TACGAGAAGG AAAAAGATGA AGATGGATTC TNATATGTGG CCTACAGCGG AGAGAACT 120
 TTTNNAANCT GAGGGCCATT GCTGGGCTAG GTGCACCGTA ACTGCTTGTG TATCTGTAA 180
 ATAGCCAGCC ATTTCAGTT ATTATACCAG AACCTCTTCA CATAGACCTA TTAGTGCATT 240
 TGTAACGGN TTTATTTCTT AATATATTGG AAGGTTTGTG TCCTTAGNCT AGTAAATTAT 300

CATACAGNGT TTTATTTTGA GGTITTTCTT NNNTGTGCAT TNCCTCATG GCCTGTAAAC 360
CNCAGGAAA CCTTTTCTT CTNGGAAATC ATATTTGAAA TGATAATTN TATATCCGAN 420
GTGAGGNTAG GNNCCGGGTC CTCCAATAA ANN 453

SEQ ID NO:902

SEQUENCE LENGTH:452

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01028

SEQUENCE DESCRIPTION:

GATCTTAAGT GAAGAAGGAA GACTTGGCCT TTTGTATTGC TTGAATATTA ACTGTCTTGG 60
AAGGAAAGTTA TGCTACAAGA AGTCATACTT TCATAAAATT ATTTGCATCT GTGTCAAATG 120
CAGTTTAGTC AGAACGTAAG ACATAATAGG TGTGGACATG AACTCTGGAG TGTGAAATAA 180
AATCCACAGT TACTTAAGCA GTCTGTTTTG ATGGAAAGTA TCTTGGGATA ATACTTTCCT 240
CTGTGGGATT TTGTTCAATT TAGATGGTGC ANGGNAGTAT CAGTCTTTAA TTTTTTGT 300
GTTGTTTTTA TCANTCAATT GCTCTGATGG TATGATGCAT GGGCTTCAGG ACTCCAGCTG 360
CACCAGTGA TAAACTCAG TTCAGGTTN CTAGCGGTCN TTGGNTAATT TTCGGGGCNT 420
ANCCGATNC CAATTNTTTT TAATGTGNTA AA 452

SEQ ID NO:903

SEQUENCE LENGTH:448

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01029

SEQUENCE DESCRIPTION:

GATCAGGGAC CCTCCNGCT TTCCTGGGCC TCTNAGTTGA ACAAAGCAGC AAAACAAAGG 60
CAGTTTTATA TGAAAGATTA GAAGCCTGGA ATAATCAGGC TTTTNAATG ATGTAATTCC 120
CACTGTAATA GCATAGGGAT TTTGGAAGCA GCTGCTGGTG GCTTGGGACA TCAGTGGGGC 180
CAAGGGTTCT CTGTCCNGG TTCAACTGTG ATTTGGCTTT CCCGTGTCTT TCCNGGTGAT 240
GCCTTGTTTG GGGTTCTGTG GGTITGGGTG GGAAGGAGGG CCATCTGCCT GANTGTAACC 300
NGCTAGCTCT CCGANGCCCT ACGGGCCTGN CTNGTGTGAG CGTGTGGACA GTGGTGGCCG 360
GCGCTGTGCC TNCTCGTGTG GCCTACANTG TNCNTGGCTG TTGAGGCGCT GCTTCANGCC 420
TGCAACNCGT CCNTNGTCTC ANTACAAA 448

SEQ ID NO:904

SEQUENCE LENGTH:461

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01030

SEQUENCE DESCRIPTION:

GATCGGTTTA CAGATGAGGA AGTGGATGAG CTGTACAGAG AAGCACCTAT TGATAAAAAG 60
GGGAATTTC ATTACATCGA GTTCACACGC ATCCTGAAAC ATGGAGCCAA AGACAAAGAT 120
GACTGAAATA ACTTCAAATT CCAGCCAAAC GTTCCTTGTG GCCACTTTGG GTATTCTGAG 180
ATTTCTCTT GCATGCCCTT AGCTTTACAG CTTTGCATT TCCTGTTGTA TTTATTCTCA 240
GCCATTTTGG GCATATGTAT CTTTATAATC AGACTGGAAA CGGGACTTTC TATTAATATC 300

ATTTTTCAGA ATAAAAATA GGGTAATTTA ACCTACCAGC CTTTCTCCCC CAATAACTGT 360
 GGGCCTATAC AGNGTCAATA TATTTTTTNC AGNGAAAGGT TTATTCGGCT CGATTTTTTT 420
 CTGGAANTCC ATAATTTAAC CTTTTATGGG TTAAANTTAA A 461

SEQ ID NO:905

SEQUENCE LENGTH:453

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01032

SEQUENCE DESCRIPTION:

GATCAGGGAC CATGAAAAGA AACTTGTGCT TCACCGAAGA AAAATATCTA AACATCGAAA 60
 AACTTAAATA TTATGGAAAA AAAACATTGC AAAATATAAA ATAAATAAAA AAAGGAAAGG 120
 AAACTTTGAA CCTTATGTAC CGAGCAAAATG CCAGGTCTAG CAAACATAAT GCTAGTCCTA 180
 GATTACTTAT TGATTTAAAA NCAAAAAAAC ACANAAAAAT AGTAAATAT AAANCCAAAT 240
 TAATGTTTTA TAGACCCTGG GAAAAAGAAT TTTCAGCANN GTACAAAAAT TTANCGCATT 300
 CTTTCTTTA ATTTTGTANT TCTTTACTGT GGGAAATAGCT CAGAAATGTCA GTTCTGTTTT 360
 ANGTAACAGN NTTGGATAAC TGAGCAGGGN ANCGNAATT TGGNTTTNTA AAATTCCTTG 420
 CTTTNANTAN ANNTCCCTT NCCCGGTGG AAA 453

SEQ ID NO:906

SEQUENCE LENGTH:445

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01033

SEQUENCE DESCRIPTION:

GATCCGATGG AGAAGGGGGG ACCCAGGCCA GCAGGAGACA GGACCCCGA AGCTGAGGCC 60
 TTGGGATGGA GCAGAAGCCG GAGTGGCGGG GCACGCTGCC GNCTTCCCCA TCACGGAGGG 120
 TCCAGACTGT CCACTCGGGG GTGGAGTGAG ACTGACTGCA AGCCCCACCC TCCTTGAGAC 180
 TGGAGCTGGC GTNTGCATAC GAGAGACTTG GTTNAACTTG GTTGGTCTT GTNTGCACCC 240
 TCGACAAGAC CACACTTTGG GACTTGGGAG CTGGGNCTGA AGTTGNTCTG TACCCNTGAA 300
 CTCCAGTTT GCGAATTATA GAGACAATCT ATTTTGTTAC TTGCACTTGT TATTCGACCA 360
 CTGAGAGCGA GATNGGGAAG CATAGATATC TATATTTTAA ATTCNCTAT NGAGGGCCTN 420
 GTAAATAAAT TTCTAAAAGC CTAAG 445

SEQ ID NO:907

SEQUENCE LENGTH:444

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01034

SEQUENCE DESCRIPTION:

GATCTCAATG AAATTAAATT AATAACTATA TCTAGAAAAA CTCCAATAT GTGAATATTA 60
 AGCAACATAC TTATAAAAAA TTCATAGTTC ATGGATGAAA TCAAAAGAGA ATTCAAAATA 120
 TTTCAAAATA AATTATGATG ATTATATAAN ATGTAGAAAT GTGTGGGATG CCACTACACC 180
 AGTTCTTAGA GTGAAATGCA CAGCTTTCAA GGCTTCTGTT AAAAGAGTTG GGAATTACAA 240
 AACAAGGAGC AGCGACTGCC AATGGGTGTG GAGTCTTTTT TGGGGTGATG ATGAAAATGT 300

TCAAAAATTG ATTTTATTGA TGGTTACACA CGTCTATAAA TATATTNNAN CGGNAGAATT 360
 ATATGGATAT ATATGTGATA TATGGAGGTA TATCCTCTGT AAAATTCCTA NGGGTTTAAN 420
 GGAGGATTGG GTATCCACAC CAAA 444

SEQ ID NO:908

SEQUENCE LENGTH:440

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01035

SEQUENCE DESCRIPTION:

GATCCCAGTG TTGCCTTAAC AGGGTGTCTG TCGTGCCGCA GTAGAGCACT GCTGCTTCCT 60
 CCAACCCCAA AATTATGTT CCTAAGTAAG TCAGGTCCCT AAGCCCCGTC CCAAGAAGTG 120
 ACACAAGTGG CCAACATCCA CACTGTAGGC TTGCAGGCTA CCCGCCCTGA GATTTGGTAA 180
 AGAACACTGC CTTGTTCCCC ATCAGTAAAC AAGGTTACCT ACCTCAGGAG GCTGCTTGTTG 240
 AGAGAGCAAA TGCAGTATCT TCAGANTGAT TTATTTTTTT ANTTAATTGT AAAGACTTGT 300
 GCCATTGGCT GCTCTTTCTA GTCCCCTAAN TTTCTGTTCT AGTTTAAANT TTCTCTAGAN 360
 CTTGCAATNG TTGGGGGGTT TTTATANTGG TGTTTTINCA ATGNTTTGTT TCNTTANNNT 420
 AAANCCTTAA AAGTTCCAAA 440

SEQ ID NO:909

SEQUENCE LENGTH:439

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01036

SEQUENCE DESCRIPTION:

GATCGGCGTG GGGGTGCTGC TCATCTTCCT TGTCAAGTAC GACCTTAACA ACCNGGACAA 60
 GCACGCCAAG CTGGACTTCC TCAACAACCT GGCCACGGGN CTGGTGTTCA TCATCGTGGT 120
 AGTCAACATC TTCATCACGG CCTCGGGGT CCAGAAGCCC TTGATGGACA TGGCACCCCA 180
 GCAGTAGGAC ACCCAGGACC NTGGATGCTG CCTGCCNNTG CAACTCAGCT GCCCGACCCC 240
 AGGAGTCGCC ATACCTGTNA GGTGTCCACC TCCCTGCACA TGGCACTACC CAGANTGCCA 300
 GAGCCCAGGC TGGNCTCATC TGCACCATGT CCCCAGGACA GCCCTTGCTC TGANTGCGGG 360
 CCAAGNACCA NTAGGAGGN CACTNTTGT TNTNAGCAGN TTTTCCAGG NGGGNAGTTN 420
 NNTTCTGGGA AATTGGGGN 439

SEQ ID NO:910

SEQUENCE LENGTH:435

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01037

SEQUENCE DESCRIPTION:

GATCCAAGGA CCCACACTTT GTCACCTCAT ATCTCTCTCT CTCTCCCACT TTCGCTTTCT 60
 CTGTCTCTTC TTAGTTCTGC TTTCTCCAC TGTGCTTCG CTCTCAGAGA GAGCTCTCCC 120
 CTGGCAGTGA CAAGATGGCT GCAGCAGCTC CAGCAACCTC AGAGGACTCC CCCATCCAGG 180
 GTCCTTGTA GCTCCTCATC TGTAGGATGT GCAGTAAACA CTCACGTGTC CTTTCCTGAG 240
 GAGCCCAAGT GCTGGGGTGG GGGCTGAGGG GCAGCCCTA TGCCCTCACA GTGCAGCAAC 300

CTTGGTTAGC TCACCCATCA GGGCAGACTT GGGCAGAAAT CATGTCTTGG CATATTGTTT 360
 TGTAACTGCG TTTTAAATTT GTCATATAT ATTATGAGCA TTTCCCTATA ATATAACAATA 420
 TTCTTCCACA TTAAT 435

SEQ ID NO:911
 SEQUENCE LENGTH:433
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01038
 SEQUENCE DESCRIPTION:

GATCATATGA AAAAGTAACA AGCTGTTCCN TGTTTCTGAT ACATAAAATN ATTTTAAGCA 60
 TTTTATCAAT CATTAAAAAT TACTGCCAGT TGTGAGTGGC TTTTAAATTA ACTTGTCTTT 120
 CATTGCACTT CACTCTGCCT GTTTTCAAGG GGAGTAAGAT TGGTAACATT TGGGGAGACT 180
 GTATCTGTCT ACTTAGCGTG GCTGTTTTGA GGGACTGTCC CATCAGTGAA CAACTGCAT 240
 GGCCTTGGAG AGAGACTCTG GGCTCTTGGC TCAGATGTGT TCATCAAATA CTCCTTTCAG 300
 AGCTGTTGTG GGTGTAAGTG ACATGATGTG GCCAAAAAAT CCAAACTGTG CAGTTGCGNT 360
 TGTGACAACC ATGCAATGTG NCTGTAAAAA TTNANTTNCA GTTTAAATN ANATNNTTTA 420
 TATTNNGTGG AAA 433

SEQ ID NO:912
 SEQUENCE LENGTH:431
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01039
 SEQUENCE DESCRIPTION:

GATCTTTCTA ATTCGAAAGC TGTGTTCTTT TTGAATACCG TGCATGGGGG TTAAGCTGAT 60
 GTTAAACAG TTTGCAATAA AAAAAATGA ATNAGCTTAA GTCATTTAAT CATTCAAGT 120
 GCATTCTGCA TCCTTTAAAA ATAAGTTTAA GAAATTTAAG AGAATTGTGT TTTCAATTAAG 180
 TTTTGCAAT CTTTGTAT GCCATGTAAA TNCCTTTTN CGTATGATTA AAGGAAGGTT 240
 ATGATAAAT GATTAGTTCA TTTACATTCA CTTGTAGCAA TTACATGAGA ATTTGAATTT 300
 NGTCGTGTTT GGGTTGTNC ATTCTGTGA ATGATGGTNC AGTTAGGTGA GATTNCTGT 360
 TATGGNACCC CAACTCACCA TTTGGNCCTC TTTAATCTTT GGGGGGTTC AATAAAATTT 420
 GGTCACNTAA A 431

SEQ ID NO:913
 SEQUENCE LENGTH:431
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01040
 SEQUENCE DESCRIPTION:

GATCCAAANT TTAAGGGATA TTGCCTATTT TGGAAGAATA AACTAAAAAT GTTAAACTG 60
 TTGAATTACA GAGAACAGAT GTACTCTGAG ACATAATTTT AAACAAATAT TAAAAATANG 120
 GCAGGTAAAC ATTTGCGTTT AGGCACAATA AATCTGTATT AAAGGGAAGC ACATCAAGGA 180
 AATATATACA TGTGANTAA TGTAACNTAA AAATATTTT TAAAAACCAC TAAAAATGA 240
 NAAATAATTT GATGGGTACT TTAAGCATTG TAGATAGAAA TTAATGTATA ATAGTGTCT 300

CCCNGTCTTT GTATGAAAAA TTAANAATC TCTAGTCCTT TAATGAGCAT GANTTTTATA 360
 CTTCTACATT TTGTTGCCA GGNAAAATN TCCTCNGTA CCTTTGAGGT NATTCGGAT 420
 TTTATGGTTT N 431

SEQ ID NO:914

SEQUENCE LENGTH:430

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01041

SEQUENCE DESCRIPTION:

GATCTATAGA GAGAGATATA TACACTTTTG ATTGTTTTCT AGATGTCTAC CAATAAATGC 60
 AATTGTGAC CTGTATTAAT GATTAAAGT GGGGAACTA GATTAATAA TTTGTTTTT 120
 AACTAGTTTA TTAGTTTCTN TGGAACTCTG CTGTGTCCCT GGGTTTGGGT TTTGCTCTTG 180
 GCAGCAGCAG GTGCCCTCTG GGTGCTCCTC CTGCTCCTGC CTGCAGCCCT AAGAGCAGGT 240
 GGGTGCCGAG TGTCTGGCAC AGCTTGGATG CCGCCCACTG AAGACAGCAG AGGGGGGTTG 300
 TTTGAAGCT CCCGNGACAG AGTCAAGCAT CTTCTGAGNC TTCGATGTCT TCGGNAAGTA 360
 AAAATGGGGN TTTAGTAAAA CCCTGCCCCN GTTTNTCACA GGGGGTTNTT TTGCAAGNNA 420
 AANTGATAAA 430

SEQ ID NO:915

SEQUENCE LENGTH:428

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01042

SEQUENCE DESCRIPTION:

GATCAGATTC TAATTTGACA GGCAACCAGT CAATGAAACA GACACACCTG CACAGTTGGA 60
 AATGGAGGAT GAAGATACAA TTGATGTGTT TCAGCANCAG ACAAGAAGTG TCTACTGNAA 120
 AAGGANCCTG CTTCTTTACT CTAGAACTTT GTTCTTATAG ACCAAGATTA CATTCTCAAT 180
 TAGAAAACCTG CAATTTGGTT CCACCACATC ATGACTATTA CTATAGTATA GTTTTCTCTA 240
 TTCTTTTATT TTTCCCTTTA CCCATTCCCT TATTTGTACA TAAAATAATG GGTGTATGTT 300
 CACAAGCATT TTGCTGTTT TNAATATTA ANTGGCCAAT GACATCCACT TGATGTCANT 360
 CAANACNATA TCTGTGGGGG NAAANTACCG NTTCTTGAA ATTTNCCTCC NNTTTTCCA 420
 TNAGTGGN 428

SEQ ID NO:916

SEQUENCE LENGTH:428

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01043

SEQUENCE DESCRIPTION:

GATCGCCAGG TTCTACAAGC TGCACGAGCG GAGGTNTGAG CCCATTGCCA TGACAGTNCC 60
 TCGAAAGTCG GACCTGTTCC AGGAGGACCT GTACCCACCC ACCGCAGGGC CCGACCNTNC 120
 CCTCACGGCT GAGGAGTGGC TGGGGGGTCG GGATGCTGGG CCCCTCCTCA TCTCCCTCAA 180
 GGATGGCTAC GTACCCCAA AGAGCCGGGA GCTGAGGGTC AACCGGGGCC TGGACACCGG 240
 GCGCAGGAGG GCAGCACCAG AGGCCANTNG CACTCCCAGC TCGGATGCCG TGTNTCGGCT 300

NNGAGGAGGA GATGCGGGAA GTTCCAGGCC ACGGTGCAGG ANCTCCAGAA GNNGTTNGGA 360
CAAGGNTTGG AGGAGACAAG TCCAAGNCA AGTAGNAGCC CCTGAAGGNN TTNCAATCAN 420
GGTTTCAN 428

SEQ ID NO:917

SEQUENCE LENGTH:424

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01044

SEQUENCE DESCRIPTION:

GATCCAATAT TCAATTCATT TGTGTACTCC CACATGCAAA ATGCTAAATT ACAATGCAGA 60
CATTAAAGAAA AAGTATTGAC TGGAGGGGTT GAATTCCTTG AGAATTTATT TTATAGTCTA 120
AATCACAAAT ACTTTACTCA ATTTAGTTTT TAAAATAGTA AACTGAATAT TTTTGTGTA 180
AGCCTATCAG AGTCAATCCT TCGTTTGGA TTTTTCCT GTTTTNCCTT ACTATAAATC 240
ATTTAAAAAC TGAATTCATT TTCTTAGATG GCATAAGTCT GTCTCTTGAG AAATAAGTAA 300
AATACTCCTA TTTTCAGTAT CTGTAGCACC TGAATAGGT CTTTGTATAG CCAGAANCAA 360
GTTATGNTTG AAGTTAGCTT TTCTTTGCA CCAGTTTGG NCAATAAAAA TCTGAANGTT 420
TAAA 424

SEQ ID NO:918

SEQUENCE LENGTH:422

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01045

SEQUENCE DESCRIPTION:

GATCAACATA ATGGACCACT CCTGAATGAG ACTTAATTTT GTCTTTCAAA TTTACTGTCT 60
TAAATCAGTT TATTAAATCT GAATTTTAAA ACATGCTGTT TATGACACAA TGACACATTT 120
GTNGCACCAA TTAAGTGTG AAAAATATCT TTGCATCATA GAACAGAAAT ATATAAAANT 180
ATATGTNGAA TGTTAACAGG TATTTTCACA GGTTTGTTT TGTATAGTTA CTCAGACACT 240
AGGGAAGGT AAATACANGT GANCAAAATA NGCAACTAAA TGAGNCCTAA TAATTGGCCT 300
TCGATTTTAN ATATNGTTC TTATAAACCT TGTCAATAAA AATAAATCTA AATCAAAAAA 360
AANTTGGTTC CACCTNTGCA GGTTTTTATA ANTGGTGCCA ATTAAAGGTT TTTGTTTTTA 420
AA 422

SEQ ID NO:919

SEQUENCE LENGTH:422

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01046

SEQUENCE DESCRIPTION:

GATCCTTACT AAGTNTTCA TGGGAGACTT CCTTCATCAC ATCTTATGTT GAAATCACTT 60
TCTGTAGTCA AAGTATACCA AAACCAATTT ATCTGAACTA AATTCTAAAG TATGGTTATA 120
CAAACCATAT ACATCTGGTT ACCAAACATA AATGCTGAAC ATTCCATATT ATTATAGTTA 180
ATGTCCTTAAT CCAGCTTGCA AGTGAATGGA AAAAACNNNC AAGCTTCAA CTAGGTATTC 240
TGGGAATGAT GTAATGCTCT GAATTTAGTA TGATATAANG AAAACTTTTT TGTGCTAAAA 300

ATACTTTTAA AAATCAATTT CNTTGATTGT AGGTAATTC TATTGCACT GGGCCTTTCA 360
 ACTCCAGAAA CATTCTGANG GTGGTACTTG GGGTTTAANT TAAAAAGGTC CACTTTGGTA 420
 AA 422

SEQ ID NO:920
 SEQUENCE LENGTH:410
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01047
 SEQUENCE DESCRIPTION:

GATCGCTGTT TCCAGAACGG GGAGGAGTAT CTCATTGTGA AACAGACTCT AGAGTGGTTC 60
 TATTGGTCT TCAGTGTITT AGCCTCATT GTTCATATTT GGCATGCAGC TTGTGGTGAG 120
 TACTGTTCTA GGAAGTGGCA AAAATGGGCA AAATGTATCA CTCCAAACAC TACTGATTCA 180
 GCATTGTTTT CATGTCTTAA AATTGCCACC TGCACCTTTGT TTCTGCACTA TTATGTAGTG 240
 CATTTTAACT TAAATTTTTT CCAGCAACAT GTTACTTATT TANGATACAT TACTGATATT 300
 TCATTATAAT TANGTTCATC TTCCCTGTGA AACAAGAGAA TTGTAATAATG TTGTGGGAAA 360
 ATGATACATA TGTGGGATGC TAATGNAAAT CATAGGTATT TTTGTGTAAA 410

SEQ ID NO:921
 SEQUENCE LENGTH:409
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01048
 SEQUENCE DESCRIPTION:

GATCACANTT GANCTGGCAG CGGGATGGCG AGGACCAAAC TCAGGACACC GAGCTTGTGG 60
 AGACCAGACC AGCAGGAGAT AGAACCTTCC AGAAGTGGGC AGCTGTGGTG GTGCCTTCTG 120
 GAGAAGAGCA GNGATACACA TGNCATGTAC AGCANGAGGG GCTGCCAAAG CCCCTCAGCC 180
 TGAGATGGGA GCCATCTTCC CAATCCNCCN CCCCCATCGT GGGCATTGTT GCTGGCCTGG 240
 NTGTCCTAGC AGTTGTGGTC ATCGGAGCTG TGGTCGCTGC TGTAATGTGT AGGAGGAAGA 300
 GCTCAGGTGG AAAAGGAGGG AGCTACTCTN AGGCTGCGTG CAGCGACAGT NCCCAGGGCT 360
 CTTAATGTGT CTTTNACAGN TTGAAANGCC TGAGACAGCT TGTTTTGTN 409

SEQ ID NO:922
 SEQUENCE LENGTH:407
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01049
 SEQUENCE DESCRIPTION:

GATCCAGGCT GTCATGTGAT TTATGGTGGC ATGTGTTGTG TATTGTTGG CTACTTGTGT 60
 CTTGAAATCT AGAATTATTT CACGCAGAAT TGTCAGTGTG TGTCAGGAAG AGAAAATGGG 120
 CTAGTGGAAG CCCAGTCTTG AGTTCTGTG TTGTTACCAT TAAAAATTGA CATTTAATTT 180
 TCAAATCACT GTTGGTGCCT AATCACTNAA GTTATTAATT TATTCTGTTG TATTCTTTTT 240
 TTTNAAATNG TAACATATTT ATCCGGTGGG TGGGACAGGA GTGTGTTCAA GTGGGTCATG 300
 TTTTNTCTGT GGTGACACAT GGTACAGGCT TGGAGCTTGC AGGTCCCTTT CTACTGTGGT 360
 TTTGGAGCAG GNCAATTAAA GTCCACTANG AAATNCACCN CTTTAAA 407

SEQ ID NO:923
 SEQUENCE LENGTH:411
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01051

SEQUENCE DESCRIPTION:

GATCCAGGTT CCTCCAGAAA TAAGATATAC AGATTACTTT GTNATTGTAA GTGGAAC TTC 60
 TACCCGACAC TTACATGCCA TGGCCTTCTA CGTTGTGAAA ATGTACAAAC ACCTGAAATG 120
 TAAACGTGAC CCTCATGTGA AGATAGAAGG GAAGGACACT GATGACTGGC TGTGCGTGGA 180
 TTTTGGCAGC ATGGTGATTC ATTTGATGCT TCCAGAAACC ANAGAAATCT ATGAATTAGA 240
 GAAATTATGG ACCCTACGTT CTTATGATGA CCAGTTAGCT CAGATAGCAC CTGAGACAGT 300
 ACCTGAAGAC TTTCATTCTT GGAATAGAAG GTGATACTTN ATCTGTNACT NCANTGGGNG 360
 TTAAAATGTG GATTAAATTN TTTTANTGCA NTGNNGTTAG TCATTTTCAA A 411

SEQ ID NO:924
 SEQUENCE LENGTH:109
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01052

SEQUENCE DESCRIPTION:

GATCAGAGCN TATNTTATGA TTGTTGATAA CTAACCAAAG TAGNTGCCTG CAGAGACTTT 60
 AAAATGTAAA ATAAAGATGT ATGCTGCCTG TCAGCTATTC TCATTTAAA 109

SEQ ID NO:925
 SEQUENCE LENGTH:405
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01053

SEQUENCE DESCRIPTION:

GATCCGAGGC TGGGAAGAAG GGGTTGCCCA GATGAGTGTG GGTCAGAGAG CCAAAC TGAC 60
 TATATCTCCA GATTATGCCT ATGGTGCCAC TGGGCACCCA GGCATCATCC CACCACATGC 120
 CACTCTCGTN TTCGATGTGG AGCTTCTAAA ACTGGAATGA CAGGAATGGC CTCCTCCCTT 180
 AGCTCCCTGT TCTTGGGTAA GAAATGGAA TACTGAAGGG CCCTTCACTG CTTTGTCTCC 240
 TCCCATGTGA TGCCAGCGT TTGATGGGTA GCAGAGAGGA CANANATCAC CACATGGCTA 300
 TTTTCCNC TGAATNCTGT CTNGNATTGN GTACCTNTCA AGTGTTATTA GTGNATGCTT 360
 TNGAAATGAA AAATTTGGGC NACCTTATGG GNAGGGNGTN GGAAA 405

SEQ ID NO:926
 SEQUENCE LENGTH:405
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01054

SEQUENCE DESCRIPTION:

GATCTTAAGC AGTAATCTGT CAGTGTTTGT ATTTGTATTC TCTGCAATTT TACTGTGAAA 60

AAAAATTGT TTTCAACAAT TGGTGTCAAT TTCTTGATGT CACTATTGT NGGAGAGTTA 120
 AATGGTCTCT NCCCTTTGTG TATCTTACCT AGTGTTTACT CCTGGGCACC CTTAATCTTC 180
 AGAGGTGCTA AATTGTCTGC CATTACACCA GAAGGATGCC TCTGATAGGA GGACAACCAT 240
 GCAAATTGTG AAATAGTCCT GANGTTCTTG GATTACTTTA CACCTCAGTA TTGATTTGTC 300
 CCAGAATTTN CTGGCCTTNC ATGGCANTGA AANTNTTNGG GGGAAAGATT TAANGTATTT 360
 NANTTTTAAN GAGTGTGTTA TAANNATANT TGTACTGNNT NCTNN 405

SEQ ID NO:927
 SEQUENCE LENGTH:404
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01055

SEQUENCE DESCRIPTION:
 GATCTATGTT ACATTTACCA CACTGAAGTT TTTTTTGTG TTTTTTGTG GTTTTAAAG 60
 AATCACCCTC ATTGTTGAAA GTAAATGTAC TCTTAGGGTG CGAATATTAG TGTCCAATA 120
 AGCATGTGAT TATATTAAGG TGGTGGTAGC GGGGAAGATAA TTCTGATTCC ATTGGGAATC 180
 TTAGGTTTTT GTAAATTTAT TGGGAAAATA GTTTTTCCTG TACTGCTGAA GTTCTTTTT 240
 GGTAAACAGT ATCTTTCTAA AAGAAAAAAG CATGAAGGGA GAAATTGAGG TGTGTATACA 300
 TTTCTCAAA TGACCAGCAT TGTATTCGTG AATACTGTGT ATCTTGAGT GAACAGTGTG 360
 GAAGCTGTTT ATTTTCAAT CTGAAGTAAA ATACTTTCAA GAAA 404

SEQ ID NO:928
 SEQUENCE LENGTH:399
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01057

SEQUENCE DESCRIPTION:
 GATCANGTGT AAATGTGACC TTGTACAGTT TACTAAAATT ACTGATATTT TTTACTACAT 60
 TGAGACAGTT ACTGTGAGAA TAGGACACAA ACACCAGCTA TTGCCTGCAT CTGGGAAATT 120
 GCTGAATCGC ACAGCAGTCA TGTACATATC AGAAAATTAC TGCCAAATAA TTGTAATAAT 180
 TGTAAAGTAT AAAGTATATA AAGTAGATAC TAAATACAGN CACTTCANTA TTTGTTGAA 240
 GCTATTGACT GTACANTTAG ACATTTTCAN ANGGGTGTAA TTTATTTANN GTTGTCTCAT 300
 TTTGGTAAAA TTTATGTGAA CTTTAAAGC TAANTATTAA NCCITAATAT GCTATGTAAT 360
 TTTTTTCNT NTATACCATT TNCGTGGTGT NTTTTTTN 399

SEQ ID NO:929
 SEQUENCE LENGTH:397
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01061

SEQUENCE DESCRIPTION:
 GATCTGCAGA AGGTATCTGG TGATGCAGAG ACTCTTTCCC CGCATCCNTC ACATGAAAGA 60
 CCCCATCGGT GACAGCTTCC AAAACGACAA GCTGGTGGTC TGGGAGGCGG GCAAAGCCGG 120
 CCTGGAGGAG TGTCTGGTGA CTGAAGTACA GGTCTGTCAG AAAACTTGAG ACTGGGGTTC 180
 AGGGCTTGTG GGGGTCTGCC TCAATCTCCC TGGCCGGGCC AGGCGCCTGC ACAGACTGGC 240

TGCTGGACCT GCGCACGAGC CCAGGAATGG ACATTCCTAA TGGGTGGTGG GCATGGGAGA 300
 TGCCTGTTTA ATTCGTCCG AAGCTGCCAA GGAAGAAGAC CAGAACTTG TGTGTTTATT 360
 TCATGATAAA GTGATTTTTT TTTTTTTTNA ACCTAAA 397

SEQ ID NO:930

SEQUENCE LENGTH:402

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01062

SEQUENCE DESCRIPTION:

GATCCCAAC AATGTCAAGA CAGCCGTCTG TGACATCCCA CCTCGTGGCC TCAAGATGGC 60
 AGTCACCTTC ATTGGCAATA GCACAGCCAT CCAGGAGCTC TTCAAGCGCA TCTCGGAGCA 120
 GTTCACTGCC ATGTTCCGCC GGAAGGCTTC CTCCACTGGT ACACAGGCGA GGGCATGGAC 180
 GAGATGGAGT TCACCGAGGC TGAGAGCAAC ATGAACGACC TCGTCTCTGA GTATCAGCAG 240
 TACCAGGATG CCACCGCAGA AGAGGAGGAG GATTTCCGGT AGGAGGCCGA AGAGGAGGCC 300
 TAAGGCAGAG CCCCCATCAC CTCAGGCTTC TCAGTTCCTT TAGCCGTCTT ACTTCAACTG 360
 CCCCCTTCT NGTCCNTCAA GAATTTNGTG TTTTGCTTGC CN 402

SEQ ID NO:931

SEQUENCE LENGTH:396

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01063

SEQUENCE DESCRIPTION:

GATCTGCCGA CTTGCTATA GATGCCATGT TACCAATGAT TTCCTGTGGT GGGGGCTTGC 60
 CATTNTTAC TCTCTATT ACCAACTTCT GGCCTAGGCA TGACAGTGGG CACCTTCCCC 120
 CAGCCCTGGN TGGGCCCAGC GCCTNTTTC TGTGTTAGAA AGGTTTATA TATATATAAA 180
 ATTACATATA TATGTAGAAA TATATGTAAT NTTGGGGGCC CTGTTCCCTG CACATTTTAC 240
 AGTTACCTCA TTTTNCCTCA TGTATGTATT TGAGAAAATG CTAATATATA GNGAAAAAAA 300
 TGGGTTCTTA AAGCTNAAAT GTNGGTTT TNCATTCCA GGGGNTCACA TTNGGTTTGN 360
 GGCATNGACN ATACCTNGTA TGTCGNNTA TAAANN 396

SEQ ID NO:932

SEQUENCE LENGTH:394

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01064

SEQUENCE DESCRIPTION:

GATCCGTGGA TTTTGGTGC AATTCCTT TTATTTCTTG TCTGAAGAAA GCCTACTGCC 60
 TTCTGTTGGG ACCAAAGAGG CCATAGTGCC CATGGAGGTT TGGACTTAAG AGATATTCAT 120
 TGGCAGCTCA AAGACTTCCA CCCTGGAGAC CACACTGCAC ACAGTGACTT CCTGGGGATG 180
 TCATAGCCAA AGCCAGGCCT GACGCATTCT CGTATCCAAC CCAAGGACCT TTTGGAATGA 240
 CTGGGGAGGN CTGCAGTCAC ATTGATGTAA GGNCTGTAAA CATCAGCAAG NCTTTATAAT 300
 TCCTTNTGCC TAANTTGTAA AANGGGGGNC TGCATTCTTG TTGGAAGNAT GNACTNTNTT 360
 TNNGGAAAAC CACATTTTAA AAANTTCCCG TAAA 394

SEQ ID NO:933

SEQUENCE LENGTH:393

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01065

SEQUENCE DESCRIPTION:

5 GATCCACAGG CTTTGTACT CAACGCTGAC AACAAACCCTA AGAGGTAGGT ATCATTATAT 60
 CAACCATTTT ATGAATAAGA AAACAACAGC ACAGAGAGAT GCAGTCACTT GCCCAAGGTC 120
 10 ACACAGGGCC AGGGGTGGG CCAGGATTCG AAGCAGGCAG GCTGTCTCCT GGGTCTGAAC 180
 TCTCAACTAC TACACCCTAA TCAAACAATC CCTCTGGTCA AATGTGAGTG ATAATAATAG 240
 TACCCACCTC GTGGGTGTTG AGGGTGAGCC CAAGTTAGCA TTCAGCGTGG GCATGTGAAC 300
 AATTATAGTC AATATTGANT GGAGACCTAT GATGCTTTA TGAAGGTTT TATTTTGGGT 360
 15 TAAAAAATGC ATAAAATTTC TCCTGACCAG AAA 393

SEQ ID NO:934

SEQUENCE LENGTH:393

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01066

SEQUENCE DESCRIPTION:

20 GATCACCTTA AGTGAAATNA TTTNCCTTTA ATCTTTNATG TATTTATTCA CTTTGGGAAG 60
 CTAGGAATGA GCAACACAAA TTTTACTCTG AAGTCAGAAG AGCTCATATA TAATANTTCT 120
 25 AATGTCCAC CTATTTTCAC TTGTCCATTC CATGTACCAG CTTAGTTATG ATANNNGTC 180
 ACATAATTAT CTTTGATAAA GGTAGAGGCA CAAAGAGGCA AACTAAGCAA GTCAAATTCT 240
 AATGTGTGTA CTTCATAATA ATTTTTATC CATTTTCATC TTTATATTCT GTAACATGAA 300
 NCTTACCTAA TCTTCAAATG TTAGCTTCCA TTTTACCT TTGAAATACT TAAATCTTTC 360
 30 TGGANTAAAT ATAATGGGGC CTNTAAAANT AAA 393

SEQ ID NO:935

SEQUENCE LENGTH:392

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01067

SEQUENCE DESCRIPTION:

40 GATCCTGTTT TTTCAGCAGG TGAAAAATAA AACGCANTCA AATTTCATGG TTTTAATTTT 60
 NAACTCAGAA GCACTCAAAA ATGCAAAATG TGATAATGGG CACTTGTTTA AAAGANTTAG 120
 TGTATCCAGC CTTCACTCCA GCTGGTAAA AATGTTGCAC TTATCAGCAA CCNNACCACT 180
 TTCATCTGCT GAAAGGNCAA ATGTGCTTGG TTTTACTATT ATGTAATCAC AACTTTCTTT 240
 TNTGCTTGTA GTTGCTTAAA ATTATGTATT TGGTCTNGGG CTGCAATTG GTTTNATGCT 300
 45 NTATNTGATT ATTACNGCAG TAGGTTGCCT NTCCNGTATG GAAAAATAA AGTGGAATNG 360
 CCCNAATTAA ACCNCCTCTN TCTTAAGGTA AA 392

SEQ ID NO:936

SEQUENCE LENGTH:391

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01068

SEQUENCE DESCRIPTION:

GATCAGGCAG CCTCCTGATG CCAGANCACC TCAGGCAGAG CCTACTCAGC TGTACCTGTN 60
 TGCCCTGGACT GTCCCTGTG CCCGCATCTC CCCTGGGACC AGCTGGAGGG CCACATGCAC 120
 ACACAGCCTA GCTGCCCCCA GGGAGCTCTG CTGCCCTTGC TGGCCCTGCC CTTCCACAG 180
 GTGAGAAGGG TCCTGTCCAC CAGCACACTC AGTTCNTTC CCTGCAGTGT TTCATTTNAT 240
 TTTAGCAAAN ATTTTGCCTG TTNNTGTTNA AACATGATAG TTGATATGAG CTGAACCCCT 300
 GGGTTNGGNG GGAATTGGTC AGAGTGGCAA CCTGGGACTG TGAGCCCTGT TCGGNACAGN 360
 NTATGGATAT GAAAANTCTG NCCNNNGCNA N 391

SEQ ID NO:937

SEQUENCE LENGTH:390

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01069

SEQUENCE DESCRIPTION:

GATCTTTCCC AAGATTGTAA CTGAAACTG CTGTCTCTTG TTTTNTTCGT TTTGGGGGTG 60
 GTGGTGCTGG CTGGGCCATG CTTGTAAAGT GATGTGTGTC TCTGATTAA CCGATTCACT 120
 GTTTTCTCTG CTAATTGAGA GAGCGTTATT TACATTATTT ATTTGTTTTG ACACAAGTNC 180
 TTTCACTGTT TTATCCTAGC TAATGGCTTC TTAAGGTAA TAAACCCCTT CCAACGTAAT 240
 TGGTCAGATA AAACTTTTT CCTTGATGTC TTAATAAAG CAATTAGTGA AGCACTTCTA 300
 TCCAAAATGA CTTTTTTGTC CTTTTTTAAA ACCAATTTAC TGTTACTGGA AACTTTGTAC 360
 AATAAAGCAA ATCAGCGAGA TTAANGGAAA 390

SEQ ID NO:938

SEQUENCE LENGTH:389

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01070

SEQUENCE DESCRIPTION:

GATCAGAGGG AAAGAATGAC CAACCNNGCA ATAAGTGATC TAACTCTAC GCTCTGGTTA 60
 ATGTAATGTA CTCTCCTGGA CTGAATGCAG TGTATAATTN CTGTCTACAG CTAGAAGCTG 120
 TGCCCCAGTT CCACATTGA TTACACATGT NAGATTGCT GCTGTTGCAG TATAAACACT 180
 AGGTATAATA GGATTTGAAA TTGCATTACA GTTCATAAAA NTNGAAAATG AGGAATTAAA 240
 CCNGCAAGTG AACATTGAA CGNTTATNCT NTCTACATAA GACATGGTTG GGACATCAGT 300
 ACTNACAAGA TGGTTTANGT ATGGTACTAG NGNANTTAAG NTTCTTTCT CTCTGGTTTA 360
 TNGATNGGGT TATTTCCATT ATGTATTNN 389

SEQ ID NO:939

SEQUENCE LENGTH:390

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01071

SEQUENCE DESCRIPTION:

GATCTCACGC TGCCTCTGTG GTTCCCTCCC TCATTTTTC TGGACGTGAT AGCTCTGCCT 60
 ATTNACAGGAC AATAATGGCT ATTCTAAACG CTAAGGAAAA AAAACAAACA CAGAACTGTT 120
 TCAAGTACTC AAGACTGACT TACAGACCAA CCAACCACCT TGCTGGAACC CTTGCTAGCA 180
 GGCATTCTTA TAAAAGAAAC TTTCGAGCCT CCTTATATTG CTGGAACTC AGCTGTGCTC 240
 CAGACTAGAG CCTCCTTACC TATGCTATGG ATTTTAAATT TATTTCTCT TATTTTATGT 300
 ACACTGCTTT TTTTGGTTAC AGTGTATGAT GGATGTGTAT GAAAAAATG TATCTTTGGG 360
 GAACCAATTA CAGTTTGTGTT AATTTGAAAA 390

SEQ ID NO:940

SEQUENCE LENGTH:543

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01072

SEQUENCE DESCRIPTION:

GATCCACACA CGTTGGTCTT TTAACCGTGC TGAGCAGAAA ACAAACAGG TTAAGAAGAG 60
 CCGGGTGGCA GCTGACAGAG GAAGCCGCTC AAATACCTTC ACAATAAATA GTGGCAATAT 120
 ATATATAGTT TAAGAAGGCT CTCCATTTGG CATCGTTTAA TTTATATGTN ATGTTCTAAG 180
 CACAGCTCTC TTCTCCTATT TTCATCCTGC AAGCAACTCA AAATATTTAA AATAAAGTTT 240
 ACATTGTAGT TATTTTCAA TCTTTGCTTG ATAAGTATTA AGAAATATTG GACTTGCTGC 300
 CGTAATTTAA AGCTCTGTTG ATTTTGTTC TGTGTTGATT TTTGGGGGAG GGGAGCACTG 360
 TNGTTTATGC TGGAAATATGA AGTCTGAGNC CTTCCGGTGC TGGGGACCAC ACANGNGTTN 420
 GTTGNAAGT TTGACCAAGN AGNCCTGCGC ATNNNCTCTG GATGCCTNTG GTATCCATTC 480
 TTNGANGCAA TCCGCTCGGG NCCCGTGGGC CCAATAAANC NGGTATTTNT CCCAANGGGG 540
 AAA 543

SEQ ID NO:941

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01073

SEQUENCE DESCRIPTION:

GATCTCAAGA TTTCTAAATT GTCAAGATT ACATGGCATT GTGGTGAAC TAGTTAACAC 60
 TTAGAGCTTT TGGTATGTAA TAACTATTG CTATGGACTG ATTAATGTT TCAAAAGATT 120
 GTGTTCTTCA AA 132

SEQ ID NO:942

SEQUENCE LENGTH:387

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01074

SEQUENCE DESCRIPTION:

GATCAGCACT AAGTCCTGCA TTCCTGTAA AGCCACTTGG GTCATAAGAA GGGAGTAAAA 60
 AATGAAGTCT GACTAGNAAC CTATTGCAGA GGCCAAGTAC ATTTAGTATG GCATTGAGTT 120
 GTGATATAGT TTTACTTTGA TGTGCATTTT GAATTCAGC TACACCTAGA TAGACGTAAA 180

ATGATAATTA AAATGCTGTA ACCAACTTAT CTAATAAAAT TGGCAACCAG CCACTATTTT 240
 GTTGACTATG AGAAAGTTAA AAGTTTATGT TAATTTTNG GGTCTGATAG AATATTTTAT 300
 GTGTATTACA GTGGTATTCA TATGCTATGT CTCTAAACTT TATTTTCAAA AGCTTANGGC 360
 CCANATACAA NCTTCTCTGG GNNTAAA 387

SEQ ID NO:943

SEQUENCE LENGTH:386

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01075

SEQUENCE DESCRIPTION:

GATCAGANAA AAAGTCCATA TGGACTGTGG ATACCTATCT AAAAGAAGAA AACTGATGGC 60
 TAAGTTTGCA TGAAACTGC ACTTTATTGC AAGTNAGTGT TTCTAGCATT ATCCCATCCC 120
 TTTGAGCCAT TCAGGGGTAC TTGTGCATTT AAAAACCAAC AAAAAAGAT GTAAATACTT 180
 AACACTCAAA TATTAACATT TTAGGTTTCT CTTGCAGATA TGAGAGATAG CACAGATGGA 240
 CCAAAGGTTA TGCACAGGTG GGAGTCTTTT GTATATAGTT GTAAATATTG TCTTGTTTAT 300
 GTAAAANTGG AATTTTTTAG ACACAGTAAT TGAAGTGTAT TCCTGTTTTG TATATTTAAT 360
 AAATTTCTTG GTTTTCATT TTTAAA 386

SEQ ID NO:944

SEQUENCE LENGTH:383

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01076

SEQUENCE DESCRIPTION:

GATCTTCTAG CTACCATNCA TTTTCTTCAC TGTTACAAA AGATGAGTGT GAAATTCAGT 60
 GAATGCTGTT ACTAATCCTG TTACGAGATG AATCTCATTT CACCAAAATT AAATTATGTT 120
 TTTCCGCTAA AATGATGATA CAAGTTGAAG ACACATCACT CTGAAATTGG AAGACCTCAC 180
 CACTTAAGGC TCCACAGTGG CTTACTCAGC TGAAGTCTAG GTTACTACTC TTTACTTTGT 240
 TCACCCATTG GGGGGTGCAG TTTTTTAAA ATGTTGGGAG ATGGCCATTC TAACTACTGT 300
 TGAATGTCTC TGTTTTGGGA AGGTATAACA NGAANTAAAA ANGNNTATAT ATGANGGGAG 360
 AGNCTGGTTA TCTCCTCCCC AAA 383

SEQ ID NO:945

SEQUENCE LENGTH:382

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01077

SEQUENCE DESCRIPTION:

GATCTCTCCA TGTACCCTGC AGGGGGCTTG GTACTGTGAA ATNAGTAACT TAATCCTGAC 60
 AACCGTAGTG CAAGGTATGG CCCATCTCCT GTACGCTTGG AGCGACCTTT GGCTACGTGG 120
 CTGGCCTTGT TATTTACCA CTCTGGATAT ACTGGAATAG AAAGCAACTT ACATACAAGA 180
 ACAATTAAGT GGAGCAAAGG GAGATATTTT TTTGTGCAGA TTCTGTAAGG GCTGGGCAGA 240
 AATGTGTATG GTCAAAGCCA AGCAGTTCCA TTTACAGCTC TGTTTTTTAC GTAGTTACAA 300
 CATGATGTGA TTGTAGCTTT TTAACTATG AAACCCCTGA GAGATTGTAC CTTCTAGTT 360

GAAATAAAGT ATTTATAATA AA

382

SEQ ID NO:946

SEQUENCE LENGTH:381

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01078

SEQUENCE DESCRIPTION:

GATCCGAACA CCTCCAGATT CCGGCTTCTA CATGGNNCAG ACGGGGACGC ACAGGCCACC 60
TTCTTCTGG CAGGGACTCT TATTTATTCC CATTGCTCTA GGGCTTTCNN TTTCCNTTC 120
TTCCGGTAGG CCGCGTAGAG GCATGCACCG GGTAGGTTTC CGCGGTGACC CCGCGGCGGC 180
CTGAGGGACG CTCCTGCCC CATCCCGGCT GTTGGGCTGG GCCGTTTGC CTCTGCTTCG 240
NCCTGTGCTG TGTTCCTCAG CTTTGTAGCA GCAGCTTGAC AAACCCAGGC GCACTGTACC 300
AAGGCAATGT AACTTTTAT TTTCCGTCAG TTTAAGTTCT TTTGTCACC AAATATTAAT 360
AAACCAAGTT TGGACTTNA A 381

SEQ ID NO:947

SEQUENCE LENGTH:380

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01079

SEQUENCE DESCRIPTION:

GATCTGAGTC CAGAGTTGGC CACTTTGTGT GGGTCCTCAC AAGCAAAGAG AGCACTAAAC 60
TTGACATTGG GGGTCCACCA CTCCAACCTT NCTTCTGAA GGTTTTGGTG TACATTGAGC 120
CCCAGAAGGA AAGGAGAGTA TCTGTGAGTG GGGGCCTCCC TTGACCCAG TACGAAGTCT 180
ATGCCCTGAA TCCCAGAGT AGCCCTTCCT GGTGCCCAAC TGGCCTGGGG ACAANCAGCG 240
TCCACTACAT CTAGGCTGCC GGCTAAGTGG CACACTTCTT GACCTCCTAC CAGGACTTTG 300
GTAAAAGCTA GCTTTGGGGA GGGGTGGGTT AAATATGAGA GGTGGAGGNG CCANTGGTAG 360
ATAACATGG GTAGACTAAA 380

SEQ ID NO:948

SEQUENCE LENGTH:380

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01080

SEQUENCE DESCRIPTION:

GATCTGCATC AGTTGTAAAG GGGAAATTGGT ATATTCACAG ACTGTAGACT TTCAGCAGCA 60
ATCTCAGAAG CTTACAAATA GATTTCATG AAGATATTN NNNCAGAAT TAAAACTGCC 120
CTTAATTTTA ATATACCTTT CAATCGGCCA CTGGCCATTT TTTCTAAGT ATTCAATTAA 180
GTGGGAATTT TCTGGAAGAT GGTCACTAT GAAGTAATAG AGTTTGCTTA ATCATTGTGA 240
ATTCAAACAT GCTATATTTT TTTAAATCAA TGTGAAAACA TAGACTTATT TTTAAATTGT 300
ACCAATCACA AGAAAATAAT GGCAATAATT ATCAAACCTT TTTAAATAGN TGCTCATATT 360
TTTAAAAATA AGGTTTAAA 380

SEQ ID NO:949

SEQUENCE LENGTH:399

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01081

SEQUENCE DESCRIPTION:

GATCAAAGCA TGCAATAAGC AATACAAAAT ACCAAGCCTT ATACTTAAAA GAAGTTTAAC 60
 ATATTGGTTA ATATACTGGT TAATATACTG GTTAAACATA TTGAATGTAT ATAAGTGGCA 120
 AAAC TAGATT TTTAAGGAAG TGTACATTAT AATATTGGAG CTCAGTACTG CATGANGAGA 180
 CTTCAATAAA ACTAAGAAAN CATTATTG GGGAGAAATT TTAGGCATT AAGANCTTGT 240
 ATTTTCTAT TTTAAAAAGT TAAATTATTC CGTAATTTGG ANGGAAAGTT CGTTGAATGT 300
 AGGCCATAAC CGTTTGANGG GTTTTCCTTT GGANAACCTG GTGTNTTNG GTGCCCTTAN 360
 TATTTGGTC CTTTAATAA AAATGCNCCT GNATTTTCN 399

SEQ ID NO:950

SEQUENCE LENGTH:379

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01082

SEQUENCE DESCRIPTION:

GATCAGGCC TGGCCCCC TGCATCTTT ATAGCAGTGG GTGTCCAGTC CAGGACACTG 60
 GTGCTTTTT ATACAAGAGA ACGAGCCAGA GTTCACTCCT TCCTCCTGGC TCTCTATATA 120
 CCTGTGAATA TGTGAATAG TGTAATATG AAAGAAGTTG TACCTATCAC TTCAACCCCT 180
 GCCTTGTA TAATACTATT CCATCCACAC AGTTTCCACC CTCACCTGCC CCNTCATACG 240
 GAGTTGGATG GGGGCCGAGT NAGGTAACCA GGTGGCATCT ACCNNATGTT TTATAAGGAA 300
 TTTGTACAG TCTTNGTGAA ATAAAATAAC GTGCTTCATT TGNAAAAATN NNGTTNNNTT 360
 TNTNTTNT NGNGGGTTN 379

SEQ ID NO:951

SEQUENCE LENGTH:376

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01083

SEQUENCE DESCRIPTION:

GATCTAGTAG AACTAAGGG ATGGGAAAAA CCTTTTCATT TTTCATCTNC TTTCCAACAA 60
 TATGAATTTT TTAGTTTCA AACTATACTC AGGAAAGCTG GGCTTTAGGA TTTAACATGT 120
 AGTGATGAGT TCTGTGTGA TTTAATATT TNACTCAGGA TTCCTATTAA TTGAAAAAAA 180
 TTTTAACTT TTTTATTATA AATCTTTTTT TCAGGGAGGN GATATCACC AACATGATGG 240
 AACAGGCGGA CAGTCCATT ATGGAGACAA ATTTGANGAT GAAAATTTTG ATGTGAACAT 300
 ACTGGTCCTG GTTACTATC CATGGCCANT CAAGGCCAGG ATTACCAATA ATTCNTCATT 360
 TTTGTTATAC CACTGN 376

SEQ ID NO:952

SEQUENCE LENGTH:375

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01084

SEQUENCE DESCRIPTION:

5 GATCAAGCCA CCACGTGCCC TACGATGGCC TAACAGGAGT GCCCATTGGC AGATTACACA 60
 TGTAAATATG ACCTCAGACA AAAAGGAACC AGAGGCCCAA GGGCAATAAT AAGGTGGAAT 120
 TTNCAGGTCA GCCCAGGAAT TGGCAGAGGA AGTAGGTGTC TGATAACCCT TTGTGGAGAA 180
 TGAGATTCCC CCCACCTGTG TGAGAAAAAT AAACAGCTCT GGAGTCTTGT NCCTGACTCC 240
 AGAGGAACGA GAGCATTCCA GGAAAGAGAG ATTCCTGGA AAATTGAAAA TGTGAATCCT 300
 10 AGGGGGAAAT TGGGGATTGT NTCTTTCCT GTTGAAAATG TTTNGNTGGG AATAAATATC 360
 TTCAGGAACC ATAAA 375

SEQ ID NO:953

SEQUENCE LENGTH:374

15 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS01085

SEQUENCE DESCRIPTION:

20 GATCTTCTNC ACACACCCCA TCACCCAGAT AATTACAGT TCTGTTAACA GTGAGGTTGA 60
 TAAAGTATTA CTGATAAAAA ATTATCTAAG GAAAAAACA GAAAATTATT TGGTGTGGCC 120
 ATCTTACCTG CTTATGTCTC CTACACAAAG CTAAATATTC TAGCAGTGAT GTAATGAAAA 180
 ATTACATCTT ACTGTTGATA TATGTATGCN CTGGTACACA GATGTCATTT TNGTTGGTCA 240
 CAGCACTACA GTGAAATACA CAAAAATGA AATTCATATA ATGACTTAAA TGTATTATAT 300
 25 GTTAGANTTG ACAACATAAA CTA CTGTGNGC TTNGAAATGA TGTATGCTTC AGTAAATCA 360
 TATTCAAATN TAAA 374

SEQ ID NO:954

SEQUENCE LENGTH:376

30 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS01086

SEQUENCE DESCRIPTION:

35 GATCAAAGCA AAGAGCGCCT TTCCATGTAT CTCATGAAAG CTGACCTGAT GCCTTTCCTG 60
 TATTGGAATA TNATGCTAAG GGGTTACTGG GGAGGACCAG CGTTTCTNCG CAAGTTGTTT 120
 CATCTAGGNA TGAGTTAAGN ATGGCTCAGC ACTTGCTCAT CTTGGATGGC TTCTGGGCCA 180
 AAAGTGCAGT CACTGAATGA CCAAGAGCAG CACGAAGGAC TTGGAACCTA TCCTTGTAAT 240
 40 GAGTTCCTTG ATGGGTAATG GTGACCAAAT GCCTCCCTTT TCAGTACCTT TGAACAGCAA 300
 CCAATGTGGGC TACTCATGAT GGGCTTGATT CTTGGGAAT ANTAATTTGA AATANTACTT 360
 TTNTTTTCTG AATAAA 376

SEQ ID NO:955

SEQUENCE LENGTH:371

45 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS01087

SEQUENCE DESCRIPTION:

50 GATCAGAACC TCCAAATACT GCCATGAGAA ACTAGAGGGC AGGTCTTCAT AAAAGCCCTT 60

55

TGAACCCCT TCCTGCCCTG TGTTAGGAGA TAGGGATATT GGGCCCTCAC TGCAGCTGCC 120
 AGCACTTGGT CAGTCACTCT CAGCCATAGC ACTTTGTTCA CTGTCTGTG TCAGAGCACT 180
 GAGCTCCACC CTTTCTGAG AGTTATTACA GCCAGAAAGT GTGGGCTGAA GATGGTTGGT 240
 TTCATGTTTT TGTATTATGT ATCTTTTGT ATGGTAAAGA CTATATTNG TACTTAACCA 300
 GATATATTTT TACCCAGAT GGGGATATC TTTGTAATAA ATGAAATNA NAGGTTTTTT 360
 NAANTGGNAA A 371

SEQ ID NO:956
 SEQUENCE LENGTH:368
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01088

SEQUENCE DESCRIPTION:

GATCTGGGGA GGGCTAGCCC AAAACCTCCC GCATCGGGCA GGCACCCCT GAAGTACTTC 60
 CTTCAGGGTT TCCCTTTGT NAGGGTGTG AGTAGCCTCA CCGGCTGTN TGGAGGAGCA 120
 GCTGGCTCTG CTCTGAGAAA CTCTGGCAAG TGGACGCCAT TCTNTGCCC TTAGGATTCA 180
 CTGCTCTCTC CTACAGCCGC CAGNCCTGGG GTCCTGAAAG ACCTTGGGTG GTAAAGCTGT 240
 ACTTGGTGGG AGTNAGGGCG TGGGGAGGAA CCATGCAAT CGCCTTCCAT GGGTTTTTAA 300
 NTGCAGTAAA TAACATTCT GGATGAGACT NGTTTCCAAA NTAAACNNG CTATTATCTG 360
 TTTTGAAA 368

SEQ ID NO:957
 SEQUENCE LENGTH:369
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01089

SEQUENCE DESCRIPTION:

GATCCGAGCT CTGGAGCGTG GATACGGAT GTCTCGCCCA GAGAACTGCC CAGAGGAGCT 60
 CTACAACATC ATGATGCGCT GCTGGAAAA CCGTCCGGAG GAGCGGCCGA CCTTCGAATA 120
 CATCCAGAGT GTGCTGGATG ACTTCTACAC GGCCACAGAG AGCCAGTACC AACAGCAGCC 180
 ATGATAGGGA GGACCAGGGC AGGGCCAGGG GGTGCCCAGG TGGTGGCTGC AAGGTGGCTC 240
 CAGCACCATN CGCCAGGGCC CACAACNCGN TTTNCTACTT TCCNAGACAA CNACCNTCGG 300
 TTTCAGGCCA CAGTTTTCTT CATCTGTCCA GTTGGGGTAG GTTTGGGACT TGGNAAAATN 360
 TTTTTTTN 369

SEQ ID NO:958
 SEQUENCE LENGTH:366
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01090

SEQUENCE DESCRIPTION:

GATCGAGCCA CTGCACTCCT GGGGCAACAG AGCAAGACTT CGTCTCAAAA TAAATAAATA 60
 AATAAAGTGG CTCTGGGGA AAAGCAATTT AATGTACCAC GATGAATAGC TAACTGTTCC 120
 CAAGTGTGTT CTATGTGCAA CACACCGCGT GAGAGTGTTA CCTGCATTAT TACATTAGGC 180
 TGAGAGGTAA AATAATTGC CCGAAGACAT ACAGCTAGTG ACGAATGGAC TGATGGTTTG 240

AACTTAACGT CTATTGACT TAAGGTCCTG CACCCTGCCA CTTGTAATTT TCAGANTCAC 300
 TGATAATCTG AAATAATGCA GCTTAAACCA TGTTTCTTA ATTAAGTA TAATTGGATG 360
 GTGAAA 366

SEQ ID NO:959
 SEQUENCE LENGTH:364
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01091

SEQUENCE DESCRIPTION:
 GATCCTGAAG GTGAAATGAA ACCAGGAAGA AAAGGTATTT CTTTAAATCC AGAACAATGG 60
 AGCCAGCTGA AGGAACAGAT TTCTGACATT GATGATGCAG TAAGAAAAT GTAAAATTCG 120
 AGCCATATAA ATAAACCTG TACTGNTCTA GTTGTCTTT TCTGTCTTT TACATTGGCT 180
 TTTGTTTCT AAATGTTCTC CAAGCTATTG TATGTTTGA TTGCAGAAGA ATTTGTAAGA 240
 TGAATACTTN CCTTTAATGT GCATTATTAA AAATATTGAG TGAAGCTAAT TGTCAACTTT 300
 ATTAAGGATT ACTTTGTCTG CCCACCACCT AGTGTAAGT AAANTCAAGT AATACANTCT 360
 TAAA 364

SEQ ID NO:960
 SEQUENCE LENGTH:364
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01092

SEQUENCE DESCRIPTION:
 GATCTGGGGC CGNCCTTACG GGGCAGGGCT CAGTCCTGAC GCTTGCCACC TGCTCCTACC 60
 CGGCCAGGAT GGCTGAGGGC GGAGTCTATT TTACGCGTCG CCAATGACA GGACCTGGAA 120
 TGTACTGGCT GGGGTAGGCC TCANTNAGTC GGCCGGTCAG GGGCCGCAGC CTCGCCCCAT 180
 CCACTCCGGT GCCTCCATTT AGCTGGCCAA TCAGCCCAGG AGGGGCAGGT TNCCCGGGGC 240
 CGGCGCTAGG NTTTGCACTA ATGTTCTNT CCCNGCGGGT GGGNGCGGGG AAATTCATAT 300
 CCCCTGTTTC GTNTNATGTT GTGTCNNCG NNCCCAAATT TAAAAAGGNA ATTTNAAAAAN 360
 GGTTN 364

SEQ ID NO:961
 SEQUENCE LENGTH:362
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01093

SEQUENCE DESCRIPTION:
 GATCGAGGGG CGGGGGTCAG CTATGCAGCC CATCACGTGT GTTTTTCATC TGGGATGAAA 60
 AAGCCTGGTT CTCTTTTGAA ATGCTTGATT GTACTTATTG AGCTAAACAA GNCTTGGTGA 120
 CTNITGTTGA TTGCCTCAA AAGTTTAAAG TCCTGGGTTT TCAGACTACT GTGTAGCAGC 180
 TGTGTGTTTA ACATACTGTA GCTTTTCTC CCTTGGGGGC ACATACAAAT AGGATGTGTT 240
 GATGTGGACT CTAAACTGTA ATTTTCTGT AACTATTTTG GAATGATGCA TATTTCTAAT 300
 GTTTGTTATA CTGTACAGA GTATTGCTG TTGGTTGCTT TTTTTTTTIN TTCANNGGGA 360
 AA 362

SEQ ID NO:962

SEQUENCE LENGTH:360

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01094

SEQUENCE DESCRIPTION:

GATCCAGGCC AAGGCACTGG CTGTNAGTGG CAGAGTTTGG CTGTAACCTT TGCCCCTAAC 60
 ACGAGGAACT CGTTTNAAGG GGGCAGCGTA GATTGTNTNA TTTGCCACCT GGATGAAGGC 120
 AGACATCAAC ATGGGTCAGC ACGTTNAGTT ACGGGAGTGG GAAATTACAT GAGGCCTGGN 180
 CCTCTNCTTT CCCAAGCTGT GCGTCTGGA CCAGCTACTG ANTTATTAAT CTCACTTAGC 240
 GAAAGTNACG GATGAGCAGT AAGTAAGTAA GTNTGGGGNT TTAAACTTGA GGGGTTCCCT 300
 CCTGACTAGC CTNTNTTACA GGANTTGTGG NAATATTAAN TGCAAATTA CAACTGCAAA 360

SEQ ID NO:963

SEQUENCE LENGTH:358

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01095

SEQUENCE DESCRIPTION:

GATCCAATTT GTAGCTTCCT GCCTGGCTTC AGAGAGCCCA GCAACCTTCT AGGCCTGCTT 60
 TCCAGACTTC TGAGATAGCC TGGGATGAGC AATCCTGTTA TAGTACATCT GGACCTTCCC 120
 TACCTGGGCT CTGGGGAGGC TGTGGGCCTG GAGAGGGAAA AGGAGGGAGG GGGTGTCTGC 180
 ACCACCTGGG AAGATAGCAC AAGGCCTAAT GAGGTCACCC TGACTCCCCA CCCCAGCATT 240
 TCATTCATAC CAGATAATAG CTGCATTACT GCCANCTGAC CTTATAACCC TCTGCACCTT 300
 CAAAAAGGTT CATGGTTTTT AATTGCTGCT TTTTAATAAC ATTTTGTNA AGNTTAAA 358

SEQ ID NO:964

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01096

SEQUENCE DESCRIPTION:

GATCGGGCCT ACTAAGATGC AGAGACCCCG NCAGAGCTNG CATTGACTAC CAGATTATT 60
 TTTNAAACCA GAAAATNTT TAAATTTATA ATTCCATATT TATAATGTTG GCCACAACAT 120
 TATGATTATT CTTGTCTGT ACTTTAGTAT TTTTNACCAT TTGTGAAGAA ACATTAAAAAC 180
 AAGTTAAATG GTAAA 195

SEQ ID NO:965

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01097

SEQUENCE DESCRIPTION:

GATCCAAGAC TGGCTGACTT CATTGAAAT GGTGAATCT GCTGTGTAAT AAAGTGGTTC 60

AACCATGATT AGGAACTGAA ATTTAGTAGA AGAGGGAAAA GGAGTTAATG TAACAAATTA 120
TTTTAGCTAC AAACCCCGGT AATAGAGCAC TTGGGGGATG GGATGGGGTG GGTGGGTGAG 180
ACAATCAGAA TGGTAAATG ATTAATGCT CCTAACCTG TAATTTGTG CATAGAGCAC 240
CCTATGCTGT GGAAATAACT GTTCTTAGAT TTCATTGTAA CTGGACTGTT CAGGTGCCC 300
AGAGGGAAAG ACCATTCTTA ATTCTAATAA AATAACCTTT TATTTGTTA TTCAA 356

SEQ ID NO:966

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01098

SEQUENCE DESCRIPTION:

GATCTCCACC ACCATCTCCC CTCTACTTCT CATTCCCTAA CTCTCTGCTG AATATGGGGT 60
TGGTGTCTC ATCTAATCAA TACCTACAAG TCATCATAAT TCAGCTCTTG AGAGCATNCT 120
GCTCTNCTTT AGATGGCTGT AAATCTATTG GCCATCTGGG CTTACAGCT TGAGTTAACC 180
TTGCTTTTCC GGGAAACAAA TGATGTCATG TCAGCTCCGN CCCTTGAACA TGACCGTGGC 240
CCCAAATTTG CTATTCCTCGT GCATTTTGTG TGTTCCTTCA CTTATCCTGT TCTCTGAAGA 300
TGTTTTGTGA CCAGGTTTGT GNTTCTTAA AATAAAATGC AGNGACATGT TTTAAA 356

SEQ ID NO:967

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01099

SEQUENCE DESCRIPTION:

GATCTTCCAC AAAACATCTA GCCATCTAAA ATGGAGAGAT GAATCATTCT ACCTATACAA 60
ACAAGCTAGC TATTAGAGGG TGGTTGGGGT ATGCTACTCA TAAGATTTC GGGTGTCTTC 120
CAACTGAAAT CTCAATGTTT TCAGTACGAA AAACCTGAAA TCACATGCCT ATGTAAGGAA 180
AGTGTATTTC ACCCAGTAAA CCCAAAAAAG CAAATGGATA ATGCTGGCCA TTTGCTTNN 240
CTGACATTTT CTTGGGAATC TGCAAGAACC TCCCCTTTCC CTTCCCCCAN TAGGNCCATT 300
TAAGTGTGTG TTAACANCT ACAGNATACT ANNTAANAAG TTTGGCCAAN NCCAAA 356

SEQ ID NO:968

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01100

SEQUENCE DESCRIPTION:

GATCAGATTT TTGGGTCATG TCTGTTGTAT TTTCAGTAAT GTGATTTTCA ATGGTCATCT 60
GGATTCTCCC ACTTCTCTAC TCCATTATTT CTCTACTTTT CTTCCAGCA NACCTGANNC 120
GTGAGGGAGA TGGATTAATG TGAGTAACAG GAATGTGTCT TTAATAAGCT AGAGTGGTTA 180
CATTTAATCA GGCAGTAAGA TAATTGGGT TCTTGAGTTG TTTTGGNGTA ATATCCCACA 240
ACTGGGGTAG GAAGCTCAGG ACTTTTTTNT TTAAGCTAG TCATTTCAAA AGCATATTGT 300
ATTTTTTTGA NTGACTACAG TATGCCCAAN TTCAANANCC AAANCCNCT TTGGGN 356

SEQ ID NO:969

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01101

SEQUENCE DESCRIPTION:

GATCCAACAA TTTTNAAGAG CTCTCTCTTA ATCTCTGACA TAATGAGTCT GAAACAAAGA 60
AAAGTTACCT TACCGTGTCT TTAATTCTT TCTTCTGGG TGTGAACCTA AGTGCCTTGA 120
GGGCCAGCTA AGAGCTTTTT GGGATATTTG TCTAACTTAA TTGAACCTGT ACTGAAAGAT 180
AAATTAACAA AATGGTTCAG AGTTTTGGAT TAAGACCTTT GTAACCTAAT GACCGTCAGC 240
ACAGGAGCTT CGGTTTCTCT CTCTGTAAAA CAGGGCTCCT CATTCCAATT CCACCTATCC 300
TGTAGCCTTG TGGGAATAAA AGGAGGCACC ACGTGGAGGT GCTTGGCAGG NTGAAA 356

SEQ ID NO:970

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01102

SEQUENCE DESCRIPTION:

GATCATANAA NGGCCATCTG GGCCAGCTN GTGTACAGCG AGGGNGGGCA GCGCCCTCCA 60
CTCCACTCTG CTTCACAAA GTCGGCTCCC GAGAGCTCGA GGCTGCTTCT TTTTATATGT 120
GCAGGGCCCG GCGGGTGAA GGGTCAGAGA GACGGACACA AGGAGCCGGC AGGAGNGCGG 180
ANCGAGGATG TCCTTTCCCG GGAGACAAGT CGGGAAAGCC TGGCTGGACT GCCTCAGCCC 240
CGNGTGANTC CTGGNCTNAA GGNTTCCCG TCCTGAGCTC GGGAGATNTT CAGAGTCACA 300
CTGNCNCCT GTCTTGCCAC GGAGAGGTCA ACTTGCCACC GGNAGTNCNT GGTAN 355

SEQ ID NO:971

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01103

SEQUENCE DESCRIPTION:

GATCCAAACA ATATCTTCAA GGCATTCTTT GCGGCTCCTG GCGGCTTCAN CTTTGANGCA 60
TCTGGTCCAG GGAATTNNIT TTNCAATTT GGCTAATGAA GGGCAACCAC CCAGAACCCA 120
GAAAAATNCAG ATTCACTCAG TTAAATCTTG AATGTGGAAA CAGTTCACCT CCTCCCTTCA 180
TCACGTCTCC GTGTGCTTAG AGCAGTTTCG TTTTCTCAGT TGGATGCCCT GTGTCTCTGT 240
GAGTGGGGTG GAGCAAAGGG AACCAATGCC GAAGACCGAG GGCAGGGGAG GGGAGGCGGG 300
GGTNGGACAG NGAGGCAGCT TGTGAATTTT TGTTTTACTG TTAACTTTA TTTAAA 355

SEQ ID NO:972

SEQUENCE LENGTH:352

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01104

SEQUENCE DESCRIPTION:

GATCNTAGGC TGGGGCCAAC TGGAACCATT GGCAGCTGCA CGCTCATTAC TACCCCTCCGC 60
 TCCTGCGCTC TGCCACTGTC CGGAAATTCA TGGTTGGCTA CGAAATGCTT GCTCAGGCTC 120
 AGAGGGACCT CACCCCTGAG CAGGCTGCAG AGAGACTAAG GGCACCTCCT GAGGTTTCAAT 180
 ACCACCTGGG GCAGAAGGAC AGGGAGACAG CAACCATCGC CTGACCACGC CGACCACAGG 240
 GCCTTGAATC CTTTTTGTG TTCAACAGTC TTGCTGAATT AAGCAGAAAAG GGCCTTGAAT 300
 CCTGGCCTGG AATTGGGCA GATATAGCAT TAATAAACT GTGCATCTCA AA 352

SEQ ID NO:973
 SEQUENCE LENGTH:358
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01105

SEQUENCE DESCRIPTION:

GATCAAGGGG GTTGGGAGGG GGGAAAGAGA CCAGCCTTGG TCCCTAAGCC TCCACNNAAC 60
 GTCTTCTTAA TCCNCACCTT TTCTTACTCC CAAAAAGAA TGAACACCCC TGAATCTGGA 120
 GTGGTGTATA CTGCCACATC AGTGTGTTAG TCAGTCCCA GAGGAGAGGG GAACCTCCT 180
 CCATCTTTTT TGCAACATCT CATTCTNCC TTTTGTGTT GCTTCCNCN TCACACACTT 240
 GGTGTTGTTT TATCTACAT TTGAGATTTC TAATTTATG TTGAACCTGC TGCTTTTNTT 300
 TCATATTNGA AAAGATGACA TCGGCCCCAA GGNGCCAAA NTAAATGGG ANTTGAAA 358

SEQ ID NO:974
 SEQUENCE LENGTH:354
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01106

SEQUENCE DESCRIPTION:

GATCTTAGGC AAAATACCAG NTGATGAAGG CATCTGATGC CTTTCTGTG TCAGTCATCT 60
 CCAAAAACAG TAAAAATAAC CACTTTTGT TGGGCAATAT GAAATTNTA AAGGAGTAGA 120
 ATACCAAATG ATAGAAACAG ACTGCCTGAA TTGAGAATTT TGATTTCTTA AAGTGTGTTT 180
 CTTTCTAAAT TGCTGTTTCT TAATTTGATT AATTTAATC ATGTATTATG ATTAAATCTG 240
 AGGCAGATGA GCTTACAAGT ATTGAAATAA TTACTAATTA ATCACAATG TGAAGGTTAT 300
 GCATGATNGT AAAAAATACA AACATTCTAA ATTAAAGGCT TTTGCAACCA CAAA 354

SEQ ID NO:975
 SEQUENCE LENGTH:351
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01107

SEQUENCE DESCRIPTION:

GATCAGAGCT TGAACACAGG CTTATTTTAA AAANNANAAA TATTTTAAAC ATGGGTTTCC 60
 TTATTGAAAA ATCAGTGTAT TAGTCATAAA ACACCATCAT TAAGAATAAT TGAACAATAA 120
 AGTTTGCTTT CAGATGCAGT TTTCAAATTA TAATCTCATT TCAATTTATA ACGTTCTCAG 180
 TCCTTTGTTA TAATTTTCT TTTTCATGTA AGTTTAATTA TCTGCATTTA TCTTTTTTCC 240
 TAGTTTTTCT AATACTAATG TTATTTCTTA AAATTCAGTG AGATATAGGG NTAAATAAT 300
 GCTTTGAGGA GNATGTTTAA TAGGAAATTA AAATAACTTT TTCTGGCCAA A 351

SEQ ID NO:976

SEQUENCE LENGTH:420

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01108

SEQUENCE DESCRIPTION:

GATCCAGAAC ACTTCAAGAA CTCGTCAAAC AGCTCGATAA GCCTTTTNA CTGTNTACAT 60
 CTGTACCGGG AATAACATTC CTAGGCTGAA ATTTCCACAA AGAATAGAAC CTGTACCCAG 120
 TTCTTCAGGC TGATTTCCCT GACCTCTTGG GCATTTGTAT TTGTAGTAAA GTATTGCAGA 180
 GATTCCCTAAG TTTTTATAG CAGCCATCAA ATTTGGACTT TGTATTGTTT ATTCATAAAA 240
 GACACTTGGT AATAGACTTC AGTGAACCTC GTATGAATGC AGTAGTGTGC GTGCAAAATC 300
 CGCTTCCTGA GCGTAGGGTG CTGAGCTGGC GCTAGGGCTC GGTGTGTGAA ATACAGCGTA 360
 GGTCAGCCCT TCGCTNAGT GTAGAAACCC ACGGTCTTTA AGGTCGGGC CTTGGTCCAN 420

SEQ ID NO:977

SEQUENCE LENGTH:349

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01109

SEQUENCE DESCRIPTION:

GATCCTCATG TACTCAGAGG CACTTCCCTC CTAAGTCAA GACCATCCTC ACTGACTATG 60
 TGCCAACGCC TCGTTTCAGG CTTGTNACTC AACAAAGGGC TTTCCATTG ATAGAAGCAG 120
 TTTGGGATTT GTAGTTGCGA CTTCTTCGAT AGTTACCTGC ACGTCCATTG CTGGCAACTG 180
 ACTTGTCTATT AAAACCTGGC TCCTTGTTTA AGGGAGCTAC GCTGTGGTTT ATTCTTAAGT 240
 TACGTGGATA AACTAACCTC TAACAGAAAT ATACTTTGGT TAATTTTGAA ATGTGTCATT 300
 TTTAAACAAT CTAAAAAGTA ATACAGAATT GTGATTTATT AATTTTAAA 349

SEQ ID NO:978

SEQUENCE LENGTH:349

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01110

SEQUENCE DESCRIPTION:

GATCAGAGTG GGTTAAGCTG ACCAGGAACA CCCATTTAAC CCCTTTTCTC TTTTGCTTTC 60
 ATTTTATAA AGGAAAAGAG GACCTGTCAG ATAGGCAGCC CCATGCTACG TGATTCTTTA 120
 TGTGTGTGTG TTTGTTTTG TAAATTGTAT AATTTTAAA TATCTGAGTT TTAATAAAG 180
 AAAAAAGTAC AAAAAATCT TGTTATGGCC TTAAGAAGGG NNTAGTGCAT CTTTCAGGGG 240
 TCACTCTGCC ATGGGGATAA AATAGCTGTT TCACAAACAG TTTTATTTAA AAAANCAANN 300
 ACCANNAAN ANTCAAAATN TCATGNAANN TTTTNAACCT TCATTTTNN 349

SEQ ID NO:979

SEQUENCE LENGTH:345

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear